

GenCore version 5.1.4-p5-4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 6, 2003, 16:28:24 ; Search time 29.3732 Seconds
(without alignments)
1816.682 Million cell updates/sec

Title: US-09-993-234-6_COPY_25_198
Perfect score: 1038
Sequence: 1 QGGTRSPRCDCAGDFHKKIG.....CPTSTLGSCPERCAVCGWR 174

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-O=/cgn2_1/USPTO_spool/US09993234/runat_27032003_115457_15378/app_query.fasta_1.2346
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdl
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09993234_@CGN_1_1_116_@runat_27032003_115457_15378 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1038	100.0	1254	3	US-08-815-469-3 Sequence 3, Appl1
2	1038	100.0	1634	4	US-08-928-069-11 Sequence 11, Appl1
3	1038	100.0	1634	4	US-08-828-683A-9 Sequence 9, Appl1
4	1038	100.0	1783	3	US-08-815-469-1 Sequence 1, Appl1
5	950	91.5	1438	4	US-08-928-069-5 Sequence 5, Appl1
6	950	91.5	1438	4	US-08-828-683A-5 Sequence 5, Appl1
7	666	64.2	433	4	US-08-928-069-2 Sequence 2, Appl1
8	666	64.2	433	4	US-08-828-683A-2 Sequence 2, Appl1
9	212.5	20.5	1049	4	US-08-804-166-1 Sequence 1, Appl1
10	212.5	20.5	1049	4	US-08-910-991-1 Sequence 1, Appl1
11	211	20.3	1956	2	US-08-762-308-10 Sequence 10, Appl1
12	205.5	19.8	1301	4	US-08-804-166-7 Sequence 7, Appl1

13	205.5	19.8	1301	4	US-08-910-991-7	Sequence 7, Appl1
14	205	19.7	600	1	US-08-050-319B-47	Sequence 47, Appl
15	205	19.7	600	2	US-08-465-982-47	Sequence 47, Appl
16	203.5	19.6	1202	4	US-08-804-166-3	Sequence 3, Appl1
17	203.5	19.6	1202	4	US-08-910-991-3	Sequence 3, Appl1
18	203	19.6	2062	1	US-08-050-319B-24	Sequence 24, Appl
19	203	19.6	2062	2	US-08-465-982-24	Sequence 24, Appl
20	203	19.6	2161	3	US-09-106-038A-1	Sequence 1, Appl1
21	203	19.6	2161	4	US-09-505-250-3	Sequence 3, Appl1
22	203	19.6	2175	1	US-08-321-668-1	Sequence 1, Appl1
23	203	19.6	2175	1	US-08-837-941-1	Sequence 1, Appl1
24	203	19.6	2175	1	US-08-126-016-1	Sequence 1, Appl1
25	203	19.6	2175	4	US-08-054-970-1	Sequence 2, Appl1
26	203	19.6	6889	1	US-08-286-740-2	Sequence 2, Appl1
27	203	19.6	6889	5	PCT-US95-09576-2	Sequence 2, Appl1
28	203	19.6	6896	2	US-08-627-151A-6	Sequence 6, Appl1
29	201	19.4	1147	4	US-08-804-166-5	Sequence 5, Appl1
30	201	19.4	1147	4	US-08-910-991-5	Sequence 5, Appl1
31	200.5	19.3	483	4	US-09-326-394-1	Sequence 1, Appl1
32	200.5	19.3	1478	4	US-09-149-922-6	Sequence 6, Appl1
33	191	18.4	543	4	US-09-513-007-3	Sequence 3, Appl1
34	191	18.4	2440	4	US-09-513-007-1	Sequence 1, Appl1
35	190	18.3	1724	5	PCT-US96-12374-1	Sequence 1, Appl1
36	189	18.2	1724	4	US-08-509-024-1	Sequence 1, Appl1
37	189	18.2	1724	4	US-09-333-279-1	Sequence 1, Appl1
38	182	17.5	579	4	US-09-146-950-3	Sequence 3, Appl1
39	182	17.5	591	4	US-09-146-950-19	Sequence 19, Appl
40	182	17.5	1596	4	US-09-146-950-17	Sequence 17, Appl
41	182	17.5	1929	4	US-09-146-950-1	Sequence 1, Appl1
42	182	17.5	4622	4	US-08-509-024-6	Sequence 6, Appl1
43	182	17.5	4622	4	US-09-333-279-6	Sequence 6, Appl1
44	170.5	16.4	477	1	US-08-050-319B-53	Sequence 53, Appl
45	170.5	16.4	477	2	US-08-465-982-53	Sequence 53, Appl

ALIGNMENTS

RESULT 1
US-08-815-469-3
Sequence 3, Application US/08815469
Patent No. 6153402
GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang
APPLICANT: Ni, Jian
APPLICANT: Dixit, Vishva
APPLICANT: Gentz, Reiner L.
APPLICANT: Dillon, Patrick J.
TITLE OF INVENTION: Death Domain Containing Receptors
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/815,469
FILING DATE: HEREWITH
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: NO. 6153402 Yet Assigned
FILING DATE: 06-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,711
FILING DATE: 17-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,285

FILING DATE: 12-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1254 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1251
US-08-815-469-3

Alignment Scores:
Pred. No.: 3.22e-86 Length: 1254
Score: 1038.00 Matches: 174
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-993-234-6_COPY_25_198 (1-174) x US-08-815-469-3 (1-1254)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGly 20
DB 73 CAGGGCGGCACTCGTAGCCCCAGGTGTGACTGTGCGGTGACTTCCACAAGAGATTGGT 132
QY 21 LeuphCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
DB 133 CTGTTTGTGACAGAGGCTGCCAGCGGGGCACTTGAAGGCCCTTGACAGGAGCC 192
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
DB 193 TCGGGCACTCCACCTGCTTGTGTGCCCAAGACACCTTCTTGCGCTGGGAGAACAC 252
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
DB 253 CATATTCTGAATGTGCCCGCTGCCAGCGCTGTGATGAGCAGGCGCTCCAGGTGGCGCTG 312
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
DB 313 GAGAACTGTTCAGCAGTGGCCGACACCGCTGTGGCTGTAAGCCAGGCTGTGTGGAG 372
QY 101 CysGlnValSerGlnCysValSerSerSerProPheTyrCysGlnProCysLeuAspCys 120
DB 373 TGCCAGGTCAAGCAATGTGTACAGCAGTTCACCTTCTACTGCCAACCATTGCTAGACTGC 432
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
DB 433 GGGGCCCTGCACCGCCACACACGCGCTACTCTGTTCCCGCAGAGATGACTGTGGGACC 492
QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
DB 493 TGCCTGCTGCTTCTATGAAATGGGATGGCTGCTGCTCTGCTGCCACGAGCACCCTG 552
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArg 174
DB 553 GGGAGCTGTCCAGAGCGCTGTGCCGCTGTCTGTGGCTGAGG 594

RESULT 2
US-08-928-069-11
Sequence 11, Application US/08928069
Patent No. 6462176
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-3 POLYPEPTIDE

NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,069
FILING DATE: 11-Sep-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/026943
FILING DATE: 09/23/1996
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1052R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1634 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-928-069-11

Alignment Scores:
Pred. No.: 4.57e-86 Length: 1634
Score: 1038.00 Matches: 174
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-993-234-6_COPY_25_198 (1-174) x US-08-928-069-11 (1-1634)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGly 20
DB 161 CAGGGCGGCACTCGTAGCCCCAGGTGTGACTGTGCGGTGACTTCCACAAGAGATTGGT 220
QY 21 LeuphCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
DB 221 CTGTTTGTGACAGAGGCTGCCAGCGGGGCACTTGAAGGCCCTTGACAGGAGCC 280
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
DB 281 TCGGCACTCCACCTGCTTGTGTGCCCAAGACACCTTCTTGCGCTGGAGAACAC 340
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
DB 341 CATATTCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCGCTCCAGGTGGCGCTG 400
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
DB 401 GAGAACTGTTCAGCAGTGGCCGACACCGCTGTGGCTGTAAGCCAGGCTGTGTGGAG 460
QY 101 CysGlnValSerGlnCysValSerSerSerProPheTyrCysGlnProCysLeuAspCys 120
DB 461 TGCCAGGTCAAGCAATGTGTACAGCAGTTCACCTTCTACTGCCAACCATTGCTAGACTGC 520
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
DB 521 GGGGCCCTGCACCGCCACACGCGCTACTCTGTTCCCGCAGAGATGACTGTGGGACC 580

QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
|
Db 581 TGCCGTGCTGGCTTCTATGACATGGCGATGGCTGCGTGTCTGCTGCCACGAGACCCCTG 640
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArg 174
|
Db 641 GGGAGCTGTCCAGAGCGCTGTGCCGTGTCTGTGGCTGAGG 682

RESULT 3
US-08-828-683A-9

: Sequence 9, Application US/08828683A
: Patent No. 6469144
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi J.
: TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
: NUMBER OF SEQUENCES: 28
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 1 DNA Way
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Winpatin (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/828,683A
: FILING DATE: 31-Mar-1997
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/625328
: FILING DATE: 1-Apr-1996
: APPLICATION NUMBER: 08/710802
: FILING DATE: 23-Sep-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Marschang, Diane L.
: REGISTRATION NUMBER: 35,600
: REFERENCE/DOCKET NUMBER: P1007P1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650/225-5416
: TELEFAX: 650/952-9881
: INFORMATION FOR SEQ ID NO: 9:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1634 base pairs
: TYPE: Nucleic Acid
: STRANDEDNESS: Single
: TOPOLOGY: Linear
: SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-08-828-683A-9

Alignment Scores:

Pred. No.: 4.57e-86 Length: 1634
Score: 1038.00 Matches: 174
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-993-234-6_COPY_25_198 (1-174) x US-08-828-683A-9 (1-1634)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGly 20
|
Db 161 CAGGGCGGCACTCGTAGCCCCAGGTGTGACTGTGCGGCTGACTTCACAGAAGATTGGT 220
QY 21 LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
|
Db 221 CTGTTTGTTCAGAGGCTGCCACAGCGGACACTACCTGAAGGCCCTTGCACGAGGCC 280
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
|

Db 281 TGCGGCACTCCACCTGCCTTGTGTGTGCCCAAGACACACTTCTTGCCCTGGGAGAACCAC 340
QY 61 HisAsnSerGlyCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
|
Db 341 CATAATTCTGAATGTGCCCGCTGCGTGCAGGCTGTGATGAGCAGGCGCTCCAGGTGGCGCTG 400
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
|
Db 401 GAGAACTGTTCAAGTGGCCGACACACCCGCTGTGGCTGTAAAGCCAGGCTGTGTGGAG 460
QY 101 CysGlnValSerClnCysValSerSerSerProPheTyrCysGlnProCysLeuAspCys 120
|
Db 461 TGCCAGGTCAAGCAATGTGTACAGCAGTTCAACCTTCTACTGCCAACCACTGCTAGACTGC 520
QY 121 GAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
|
Db 521 GGGGCCCTGCACCGCCACACACAGGCTACTGTCTTCCCGCAGAGATACTGACTGTGGGACC 580
QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
|
Db 581 TGCCGTGCTGGCTTCTATGACATGGCGATGGCTGCGTGTCTGCCGCCACGAGACACCCTG 640
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArg 174
|
Db 641 GGGAGCTGTCCAGAGCGCTGTGCCGCTGTCTGTGGCTGAGG 682

RESULT 4
US-08-815-469-1

: Sequence 1, Application US/08815469
: Patent No. 6153402
: GENERAL INFORMATION:
: APPLICANT: Yu, Guo-Liang
: APPLICANT: Ni, Jian
: APPLICANT: Dixit, Vishva
: APPLICANT: Gentz, Reiner L.
: APPLICANT: Dillon, Patrick J.
: TITLE OF INVENTION: Death Domain Containing Receptors
: NUMBER OF SEQUENCES: 17
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
: STREET: 1100 New York Ave., NW, Suite 600
: CITY: Washington
: STATE: DC
: COUNTRY: USA
: ZIP: 20005-3934
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/815,469
: FILING DATE: HEREWITH
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: NO. 6153402 Yet Assigned
: FILING DATE: 06-FEB-1997
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/028,711
: FILING DATE: 17-OCT-1996
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/013,285
: FILING DATE: 12-MAR-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Steffe, Eric K.
: REGISTRATION NUMBER: 36,688
: REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-371-2600
: TELEFAX: 202-371-2540
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1783 base pairs

TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 198..1481
US-08-815-469-1

Alignment Scores:
Pred. No.: 5.13e-86
Score: 1038.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 3
Length: 1783
Matches: 174
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-09-993-234-6_COPY_25_198 (1-174) x US-08-815-469-1 (1-1783)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
DB 303 CAGGGCGGCACTCGTAGCCCCAGGTGTGACTGTGCGGGTGAAGCCCTTGACAGAGATTGGT 362
QY 21 LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
DB 363 CTGTTTGTGTCAGAGGCTGCCAGCGGGGCACTACTGTAAGCCCTTGACAGAGGCC 422
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
DB 423 TGGGGCAACTCCACTGCTGTGTGTCCCAAGACACCTTCTGGCCTGGGAGAACCCAC 482
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
DB 483 CATTAATTCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCCCTCCAGGTGGCGCTG 542
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
DB 543 GAGAACTGTTCAGCAGTGGCGGCACACCCGCTGTGGCTGTAAGCCAGGCTGTTGTGGAG 602
QY 101 CysGlnValSerGlnCysValSerSerSerProPheTyrCysGlnProCysLeuAspCys 120
DB 603 TGCCAGGTTCAGCAATGTGTTCAGCAGTTCACCCCTTCTACTGCCAACCATGCTTGAAGTGC 662
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
DB 663 GGGGCCCTGCACCGCCACACAGGCTACTCTGTTCGCCGACAGATACTGACTGTGGGACC 722
QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
DB 723 TGCCCTGCTGCTTATGAACATGGCGATGGCTGCTGCTGCCACAGACACCCCTG 782
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArg 174
DB 783 GGGAGCTGTCCAGAGCGCTGTGCCGCTGTCTGTGGCTGGAGG 824

RESULT 5
US-08-928-069-5
Sequence 5, Application US/08928069

Patent No. 6462176
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-3 POLYPEPTIDE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,069
FILING DATE: 11-Sep-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/026943
FILING DATE: 09/23/1996
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1052R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1438 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-928-069-5

Alignment Scores:
Pred. No.: 4.3e-78
Score: 950.00
Percent Similarity: 93.68%
Best Local Similarity: 93.68%
Query Match: 91.52%
DB: 4
Length: 1438
Matches: 163
Conservative: 0
Mismatch: 3
Indels: 8
Gaps: 1

US-09-993-234-6_COPY_25_198 (1-174) x US-08-928-069-5 (1-1438)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
DB 449 CAGGGCGGCACTCGTAGCCCCAGGTGTGACTGTGCGGGTGAAGCCCTTGACAGAGATTGGT 508
QY 21 LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
DB 509 CTGTTTGTGTCAGAGGCTGCCAGCGGGGCACTACTGTAAGGCCCTTGACAGAGGCC 568
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
DB 569 TGGGCAACTCCACTGCTGTGTGTGCCAAGACACCTTCTGGCCTGGGAGAACCCAC 628
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
DB 629 CATTAATTCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCCCTCCAGGTGGCGCTG 688
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
DB 689 GAGAACTGTTCAGCAGTGGCGGCACACCCGCTGTGGCTGTAAGCCAGGCTGTTGTGGAG 748
QY 101 CysGlnValSerGlnCysValSerSerSerProPheTyrCysGlnProCysLeuAspCys 120
DB 749 TGCCAGGTTCAGCAATGTGTTCAGCAGTTCACCCCTTCTACTGCCAACCATGCTTGAAGTGC 808
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
DB 809 GGGGCCCTGCACCGCCACACAGGCTACTCTGTTCGCCGACAGATACTGACTGTGGGACC 868
QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
DB 869 TGCCCTGCTGCTTATGAACATGGCGATGGCTGCTGCTGCCACAGACGTAATTCCTA 928
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArg 174
DB 929 -----GCTGTGCTGGATGGAGG 946

RESULT 6
US-08-828-683A-5
Sequence 5, Application US/08828683A

Patent No. 6469144
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,683A
FILING DATE: 31-Mar-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/625328
FILING DATE: 1-Apr-1996
APPLICATION NUMBER: 08/710802
FILING DATE: 23-Sep-1996
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1438 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-08-828-683A-5
Alignment Scores:
Pred. No.: 4.3e-78 Length: 1438
Score: 950.00 Matches: 163
Percent Similarity: 93.68% Conservative: 0
Best Local Similarity: 93.68% Mismatches: 3
Query Match: 91.52% Indels: 8
DB: 4 Gaps: 1
US-09-993-234-6_COPY_25_198 (1-174) x US-08-828-683A-5 (1-1438)
QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
DB 449 CAGGGCGGCACTCGTAGCCCCAGGTGTGACTGTGCCGGTGACTTCCACAAGAAGATTGGT 508
QY 21 LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
DB 509 CTGTTTGTGTGACAGAGGCTGCCAGCGGGGCACTACCTGAAGGCCCTTGACAGGAGCCC 568
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
DB 569 TGCAGCACTCCACCTGCTTGTGTGCCCAAGACACCTTCTTGCTGGGAGAACCCAC 628
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
DB 629 CATATCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCGCTCCAGGTGGCGCTG 688
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
DB 689 GAGAACTGTTCAGCAGTGGCCGACACCGCTGTGGCTGTAAAGCCAGGCTGTTGTGAG 748
QY 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120

DB 749 TGCCAGGTACAGCCAAATGTGTACAGCAGTTACCTTACTGCCCAACCAATGCTAGACTGC 808
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
DB 809 GGGGCCCTGCACGCCACACACAGGCTACTCTCTTCCCGCAGAGATACTGACTGTGGACC 868
QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
DB 869 TGCCTGCTGCTTCTATGACATGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTA 928
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArg 174
DB 929 -----GCTGTGCTGGGATGAGG 946
RESULT 7
US-08-928-069-2
Sequence 2, Application US/08928069
Patent No. 6462176
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-3 POLYPEPTIDE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,069
FILING DATE: 11-Sep-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/026943
FILING DATE: 09/23/1996
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1052R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 433 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-928-069-2
Alignment Scores:
Pred. No.: 8.2e-53 Length: 433
Score: 666.00 Matches: 127
Percent Similarity: 93.48% Conservative: 2
Best Local Similarity: 92.03% Mismatches: 5
Query Match: 64.16% Indels: 5
DB: 4 Gaps: 0
US-09-993-234-6_COPY_25_198 (1-174) x US-08-928-069-2 (1-433)
QY 2 GlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGlyLeu 21
DB 22 GCGGCGACCTGTAAGCCCGAGGTGTGACTGTGCCGCTGACTTCCACAGAAGATTGGTCTG 81
QY 22 PheCysCysArgGlyCysProAla-glyHisTyrLeuLysAlaProCysThrGluProCys 41

Db 82 TTTTGTGACAGAGCTGCCAGCGGGCAACTACCTGAAGGCCCTTTCACGAGCCCTG 141
QY 41 sglYasnerThrcysleuValCysProGlnAspThrPheLeuAlaTrpGluAsnHisH 61
Db 142 CGC-AACTCCACCTGCCTGTGTGTGTCCCAAGACACACCTTCTTGGCTGGAGAACCA 200
QY 61 sasnsrGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeuG 81
Db 201 TAATCTGATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCGCTCCAGGTGGCGCTGA 260
QY 81 uasncysSeraAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 101
Db 261 GAACGTTCAGCAGTGCGCCGACACCGCTGTGGCTGTAAGCAGGCGCTGTTGTGAGTG 320
QY 101 sglN-ValSerGlnCysValSerSer-SerProPheTyrcysGlnProCysLeuAspCys 120
Db 321 CCAGGTCAGCCCAATGTGTGACAGATTTCACCCCTTCTAATGCCCAACCATGCCCTAGACTGC 380
QY 121 GAlaLeuHisArgHisThrArgLeuLeuCys-SerArgArgAsp 135
Db 381 GGGGCCCTGCAACGCAACACACAGGCTAATNTGTTCGCCGAGAGAT 426

RESULT 8

US-08-828-683A-2

; Sequence 2, Application US/08828683A
; Patent No. 6469144

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/828,683A

FILING DATE: 31-Mar-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/625328

FILING DATE: 1-Apr-1996

APPLICATION NUMBER: 08/710802

FILING DATE: 23-Sep-1996

ATTORNEY/AGENT INFORMATION:

NAME: Marschang, Diane L.

REGISTRATION NUMBER: 35,600

REFERENCE/DOCKET NUMBER: P1007P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-5416

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 433 base pairs

TYPE: Nucleic Acid

STRANDEDNESS: Single

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-08-828-683A-2

Alignment Scores:

Pred. No.: 8.2e-53

Score: 666.00

Percent Similarity: 93.48%

Best Local Similarity: 92.03%

Query Match: 64.16%

DB: 4 Gaps: 0

US-09-993-234-6_COPY_25_198 (1-174) x US-08-828-683A-2 (1-433)

QY 2 GlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGlyLeu 21
Db 22 GGGGGCACTCGTAGCCCCCAGGTGTGACTGTGCCGGTGACTTCCACAAGAAGATTGCTCG 81
QY 22 PheCysArGlyCysProAla-GlyHisTyrlLeuLysAlaProCysThrGluProcy 41
Db 82 TTTTGTTCAGAGGCTGCCAGCGGGCAACTACTGTAAGGCCCTTGACGAGCCCTG 141
QY 41 sglYasnerThrcysleuValCysProGlnAspThrPheLeuAlaTrpGluAsnHisH 61
Db 142 CGC-AACTCCACCTGCCTGTGTGTGTCCCAAGACACCTTCTTGGCGTGGAGAACCA 200
QY 61 sasnsrGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeuG 81
Db 201 TAATCTGATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCGCTGCCAGGTGGCGCTGA 260
QY 81 uasncysSeraAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 101
Db 261 GAACGTTCAGCAGTGCGCCGACACCGCTGTGGCTGTAAGCAGGCGCTGTTGTGAGTG 320
QY 101 sglN-ValSerGlnCysValSerSer-SerProPheTyrcysGlnProCysLeuAspCys 120
Db 321 CCAGGTCAGCCCAATGTGTGACAGATTTCACCCCTTCTAATGCCCAACCATGCCCTAGACTGC 380
QY 121 GAlaLeuHisArgHisThrArgLeuLeuCys-SerArgArgAsp 135
Db 381 GGGGCCCTGCAACGCAACACACAGGCTAATNTGTTCGCCGAGAGAT 426

RESULT 9

US-08-804-166-1

; Sequence 1, Application US/08804166
; Patent No. 6193972

GENERAL INFORMATION:

APPLICANT: Campbell, Robert K.

APPLICANT: Jameson, Bradford A.

TITLE OF INVENTION: HYBRID PROTEINS

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK

STREET: 419 Seventh Street N.W., Ste. 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 22207

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/804,166

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/011,936

FILING DATE: 20 February 1996

ATTORNEY/AGENT INFORMATION:

NAME: Browdy, Roger L.

REGISTRATION NUMBER: 25,618

REFERENCE/DOCKET NUMBER: CAMPBELL=2A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 628-5197

TELEFAX: (202) 737-3528

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1049 base pairs

TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 278..1047
US-08-804-166-1

Alignment Scores:
Pred. No.: 7.74e-11 Length: 1049
Score: 212.50 Matches: 52
Percent Similarity: 42.26% Conservative: 19
Best Local Similarity: 30.95% Mismatches: 82
Query Match: 20.47% Indels: 15
DB: 4 Gaps: 6

US-09-993-234-6_COPY_25_198 (1-174) x US-08-804-166-1 (1-1049)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGly 20
DB 329 CAAGAGGGCAGTGGCGATAGTGTGTGTCGCCCAAGAAATATATCCACCCCTCAAAATAT 388
QY 21 LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
DB 389 TCCATTTCCTGTACCAAGTGCACCAAGAACTACTTGTACCAATGACTGTCCAGGCCCG 448
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
DB 449 GGGCAGGATACGAGCTGCAGGAGTGTGAGAGCGGCTCTTCACCGCTTCAGAAACCAC 508
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGlnAlaSerGlnValAlaLeu 80
DB 509 CTCAGA---CACTGCCTCAGCTGCTCCAAATGCCGAAAGAAATGGGTGAGTGAGATC 565
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
DB 566 TCTTCTTGACACAGTGGACCGGGACACCGGTGTGGCTGCAGAGAAGAACCACTACCGGCAT 625
QY 101 Cys-----GlnValSerGlnCysValSerSerProPheTyrCysGlnProCys 117
DB 626 TATTGAGTGAACCTTTTCCAGTGC-----TTCAATTGCAGCCTCTGTC 670
QY 118 LeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAsp 137
DB 671 CTCAT---GGACCGTGCAC-----CTCTCCTGCCAGAGAAACAGAACACC 715
QY 138 CysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThr 157
DB 716 GTGTGACCTGCATGCAGGTTTCTTCTTAAGAGAAACGAGTGTGTCTCTGTCGGCGT 775
QY 158 SerThrLeuGlySerCysProGlu 165
DB 776 GCTGCCCCAGGT---TGCCACAGAA 796

RESULT 10
US-08-910-991-1
Sequence 1, Application US/08910991
Patent No. 6194177
GENERAL INFORMATION:
APPLICANT: Campbell, Robert K.
APPLICANT: Jameson, Bradford A.
APPLICANT: Chappel, Scott C.
TITLE OF INVENTION: HYBRID PROTEINS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 22207
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,991
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/804,166
FILING DATE: 20 February 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/011,936
FILING DATE: 20 February 1996
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: CAMPBELL-2B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1049 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 278..1047
US-08-910-991-1

Alignment Scores:
Pred. No.: 7.74e-11 Length: 1049
Score: 212.50 Matches: 52
Percent Similarity: 42.26% Conservative: 19
Best Local Similarity: 30.95% Mismatches: 82
Query Match: 20.47% Indels: 15
DB: 4 Gaps: 6

US-09-993-234-6_COPY_25_198 (1-174) x US-08-910-991-1 (1-1049)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGly 20
DB 329 CAAGAGGGCAGTGGCGATAGTGTGTGTCGCCCAAGAAATATATCCACCCCTCAAAATAT 388
QY 21 LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
DB 389 TCCATTTCCTGTACCAAGTGCACCAAGAACTACTTGTACCAATGACTGTCCAGGCCCG 448
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
DB 449 GGGCAGGATACGAGCTGCAGGAGTGTGAGAGCGGCTCTTCACCGCTTCAGAAACCAC 508
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGlnAlaSerGlnValAlaLeu 80
DB 509 CTCAGA---CACTGCCTCAGCTGCTCCAAATGCCGAAAGAAATGGGTGAGTGAGATC 565
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
DB 566 TCTTCTTGACACAGTGGACCGGGACACCGGTGTGGCTGCAGAGAAGAACCACTACCGGCAT 625
QY 101 Cys-----GlnValSerGlnCysValSerSerProPheTyrCysGlnProCys 117
DB 626 TATTGAGTGAACCTTTTCCAGTGC-----TTCAATTGCAGCCTCTGTC 670
QY 118 LeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAsp 137
DB 671 CTCAT---GGACCGTGCAC-----CTCTCCTGCCAGAGAAACAGAACACC 715
QY 138 CysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThr 157
DB 716 GTGTGACCTGCATGCAGGTTTCTTCTTAAGAGAAACGAGTGTGTCTCTGTCGGCGT 775

Score: 205.50 Matches: 51
Percent Similarity: 40.91% Conservative: 21
Best Local Similarity: 28.98% Mismatches: 83
Query Match: 19.80% Indels: 21
DB: 4 Gaps: 7

US-09-993-234-6_COPY_25_198 (1-174) x US-08-804-166-7 (1-1301)

```
OY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGly 20
    ||| |||::: ||| |||
Db 330 CAAGAGGCGACGTCCGATAGTGTGTCCCAAGAAATATATCCACCCCTCAAAATAT 389
OY 21 LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
    ||||| ||| ||| ||||| |||
Db 390 TCGATTGCTGTACCAAGTGCACAAAGAACCTACTGTGACATGACTGTCCAGGCCCG 449
OY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
    ::::: ||| ||| ::||| ||| ||||| |||
Db 450 GGGCAGGATACGCACTGCAGGAGGTGAGAGCGGCTCCCTCACCCTTCAGAAACCAC 509
OY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
    ||| ||| ||| ||| ::::: ||||| |||
Db 510 CTCAGA---CACTGCCCTCAGCTGCTCCAAATGCCGAAAGAAATGGGTACAGTGAGATC 566
OY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTyrPheValGlu 100
    ::|||::: ||||| ||||| ||||| ::|
Db 567 TCTTCTTGACAGTGGACCGGACCGGTGTGTGGCTGCAGAGAAACCACTACCGGCAT 626
OY 101 Cys-----GlnValSerGlnCysValSerSerSerProPheTyrCysGlnProCys 117
    ::| ||||| ||| ||| ||| |||
Db 627 TATTGAGTGAACCTTTTCCAGTGC-----TTCAATTGCACGCTCTGC 671
OY 118 LeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAsp 137
    |||::: ||| ::||| ||| ||| ::|
Db 672 CTCAT---GGGACCGTGCAC-----CTCTCCTGCCAGAGAAACAGAACACC 716
OY 138 CysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThr 157
    ||||| ||||| ||||| ::| ||||| |||
Db 717 GTGTGCACCTGCCATGACAGGTTCCTTTCTAAGAAACGAGTGTCTCTCTGT----- 770
OY 158 SerThrLeuGlySerCysProGlu-----ArgCysAlaAlaValCys 171
    ::||| ::| ||| ::|||
Db 771 -----AGTAACGTGAAGAAAGCCTGAGTGCACGAGTGTCTGC 809
```

RESULT 13
US-08-910-991-7
: Sequence 7, Application US/08910991
: Patent No. 6194177
: GENERAL INFORMATION:
: APPLICANT: Campbell, Robert K.
: APPLICANT: Jameson, Bradford A.
: APPLICANT: Chapel, Scott C.
: TITLE OF INVENTION: HYBRID PROTEINS
: NUMBER OF SEQUENCES: 22
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: BROWDY AND NEIMARK
: STREET: 419 Seventh Street N.W., Ste. 300
: CITY: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 22207
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/910,991
: FILING DATE:
: CLASSIFICATION: 530
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/804,166
: FILING DATE: 20 February 1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/011,936
FILING DATE: 20 February 1996
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.

REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: CAMPBELL-2B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 1301 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 279..1287

US-08-910-991-7

Alignment Scores:

Pred. No.: 4.49e-10 Length: 1301

Score: 205.50 Matches: 51

Percent Similarity: 40.91% Conservative: 21

Best Local Similarity: 28.98% Mismatches: 83

Query Match: 19.80% Indels: 21

DB: 4 Gaps: 7

US-09-993-234-6_COPY_25_198 (1-174) x US-08-910-991-7 (1-1301)

```
OY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGly 20
    ||| |||::: ||| |||
Db 330 CAAGAGGCGACGTCCGATAGTGTGTGTCCCAAGAAATATATCCACCCCTCAAAATAT 389
OY 21 LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
    ||||| ||| ||| ||||| |||
Db 390 TCGATTGCTGTACCAAGTGCACAAAGAACCTACTGTGACATGACTGTCCAGGCCCG 449
OY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
    ::|||::: ||||| ||||| ||||| ::|
Db 450 GGGCAGGATACGCACTGCAGGAGGTGAGAGCGGCTCCCTCACCCTTCAGAAACCAC 509
OY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
    ||| ||| ||| ||| ::::: ||||| |||
Db 510 CTCAGA---CACTGCCCTCAGCTGCTCCAAATGCCGAAAGAAATGGGTACAGTGAGATC 566
OY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTyrPheValGlu 100
    ::|||::: ||||| ||||| ||||| ::|
Db 567 TCTTCTTGACAGTGGACCGGACCGGTGTGTGGCTGCAGAGAAACCACTACCGGCAT 626
OY 101 Cys-----GlnValSerGlnCysValSerSerSerProPheTyrCysGlnProCys 117
    ::| ||||| ||| ||| ||| |||
Db 627 TATTGAGTGAACCTTTTCCAGTGC-----TTCAATTGCACGCTCTGC 671
OY 118 LeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAsp 137
    |||::: ||| ::||| ||| ||| ::|
Db 672 CTCAT---GGGACCGTGCAC-----CTCTCCTGCCAGAGAAACAGAACACC 716
OY 138 CysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThr 157
    ||||| ||||| ||||| ::| ||||| |||
Db 717 GTGTGCACCTGCCATGACAGGTTCCTTTCTAAGAAACGAGTGTCTCTCTGT----- 770
OY 158 SerThrLeuGlySerCysProGlu-----ArgCysAlaAlaValCys 171
    ::||| ::| ||| ::|||
Db 771 -----AGTAACGTGAAGAAAGCCTGAGTGCACGAGTGTCTGC 809
```

RESULT 14
US-08-050-319B-47
: Sequence 47, Application US/08050319B
: Patent No. 5633145
: GENERAL INFORMATION:


```
Db 103 GGGACAGGAGAGAGATAGTGTGTCCACAGAAAAATATCCACCCTCAAAAT 162
QY 20 GlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGlu 39
Db 163 AATTCGATTGTGCTGTACCAAGTGCACAAAGGAACCTACTGTACATGACTGTCCAGGC 222
QY 40 ProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsn 59
Db 223 CCGGGCAGCATACGCGACTGCAGGAGTGTAGAGCGGGCTCCCTTCACCGCTTCAGAAAAAC 282
QY 60 HisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAla 79
Db 283 CACCTCAGA--CACTGCCCTCAGCTGTCCAAATGCCGAAAGAAATGGGTCAAGTGGAG 339
QY 80 LeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheVal 99
Db 340 ATCTCTTCTTGACACAGTGCACCGGACACCGTGTGTGCTGCAGAGAACAACAGTACCGG 399
QY 100 Glucys-----GlnValSerGlnCysValSerSerSerProPheTyrCysGlnPro 116
Db 400 CATTAATTGGAGTGAACACCTTTTCCAGTGC-----TTCAATTGCAGCCCTC 444
QY 117 CysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThr 136
Db 445 TGCCTCAAT--GGGACCGTGCAC-----CTCTCTGCTGCCAGAGAAACAGAAC 489
QY 137 AspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysPro 156
Db 490 ACCGTGTGCACCTGCATGCAGGTTTCTTCTTAAGAGAAAAACGAGTGTCTCTCCTGT--- 546
QY 157 ThrSerThrLeuGlySerCysProGlu-----ArgCysAlaAlaValCys 171
Db 547 -----AGTAACCTGTAAGAAAAAGCCTTGAGTGCACGAAAGTTGTGC 585
```

Search completed: April 6, 2003, 23:29:46
Job time : 35.3732 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 6, 2003, 15:35:34 ; Search time 4846.17 Seconds

(without alignments)
2504.221 Million cell updates/sec

Title: US-09-993-234-6
Perfect score: 2323
Sequence: 1 MEQRRGCAVAALLLVLL.....ERMGLDGCVEDLRSLQKGP 417

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL-frame+p2n.model -DEV=xlh
-O=/cg2_1/USPTO_spool/US09993234/runat_27032003_115455_15349/app_query.fasta.1.2346
-DB=GenEmbl -QFMT=fastap -SUFFIX=trge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS-human40.cdi -LIST=45
-DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09993234_@CGN_1_1_8534_@runat_27032003_115455_15349 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*

29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2323	100.0	1254	6	AR119657	AR119657 Sequence
2	2323	100.0	1254	9	HSU72763	U72763 Human death
3	2323	100.0	1254	9	HSU78029	U78029 Human apopt
4	2323	100.0	1254	9	HSU94501	U94501 Human lymph
5	2323	100.0	1634	9	HSU74611	U74611 Human Apo-3
6	2323	100.0	1662	6	AX055442	AX055442 Sequence
7	2323	100.0	1662	6	AX201344	AX201344 Sequence
8	2312.5	99.5	1257	9	HSU94502	U94502 Human lymph
9	2281	98.2	1528	9	HSU83597	U83597 Human death
10	2281	98.2	1557	9	HSU75380	U75380 Human apopt
11	2271.5	97.8	1355	9	HSU94503	U94503 Human lymph
12	2267	97.6	1783	6	AR119656	AR119656 Sequence
13	2254.5	97.1	1743	6	AX331947	AX331947 Sequence
14	2254.5	97.1	1743	9	HSWSL1	Y09392 H.sapiens m
15	2242	96.5	1669	9	AF026070	AF026070 Homo sapi
16	2228	95.9	1250	6	AX150176	AX150176 Sequence
17	2218.5	95.5	1763	9	AF026071	AF026071 Homo sapi
18	2176.5	93.7	1198	9	HSU94504	U94504 Human lymph
19	2085.5	89.8	1143	9	HSU94510	U94510 Human lymph
20	2016.5	86.8	1119	9	HSU94509	U94509 Human lymph
21	1951	84.0	1087	9	HSU94505	U94505 Human lymph
22	1644.5	70.8	952	9	HSU94506	U94506 Human lymph
23	1575.5	67.8	4811	9	AB051851	AB051851 Homo sapi
24	1556.5	67.0	4825	9	AB051850	AB051850 Homo sapi
25	1556.5	67.0	53982	9	AL158217	AL158217 Human DNA
26	1404.5	60.5	838	9	HSU94507	U94507 Human lymph
27	1397	60.1	1665	10	AF329969	AF329969 Mus muscu
28	1255	54.0	1619	10	BC017526	BC017526 Mus muscu
29	1221	52.6	1581	9	AK094463	AK094463 Homo sapi
30	1221	52.6	2053	9	AK094488	AK094488 Homo sapi
31	1150.5	49.5	705	9	HSU94508	U94508 Human lymph
32	1051	45.2	809	9	HSU94512	U94512 Human lymph
33	1039.5	44.7	816	6	AX335086	AX335086 Sequence
34	1039.5	44.5	808	9	HSU75381	U75381 Human death
35	973	41.9	196368	2	AL772240	AL772240 Mus muscu
36	973	29.0	97483	2	AC118359	AC118359 Rattus no
37	673	28.7	651	9	HSU83599	U83599 Human alter
38	667	27.4	18015	10	AF134858	AF134858 Mus muscu
39	636	17.9	2004	4	SSU19994	U19994 Sus scrofa
40	415	17.4	1956	10	MUSTNFR2	M59377 Murine tumo
41	404.5	17.4	2048	10	MUSMTNFR1	M60468 Mouse tumor
42	404.5	17.4	2063	10	MMP55R	X59238 Murine mRNA
43	404.5	17.4	2086	10	BC004599	BC004599 Mus muscu
44	404.5	17.4	2115	10	AF329978	AF329978 Rattus no
45	404.5	17.4				

RESULT 1

ALIGNMENTS

AR119657
LOCUS AR119657 1254 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 3 from patent US 6153402.
ACCESSION AR119657
VERSION AR119657.1 GI:14102356
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 1254)
AUTHORS Yu,G.-L., Ni,J., Gentz,R.L. and Dillon,P.J.
TITLE Death domain containing receptors
JOURNAL Patent: US 6153402-A 3 28-NOV-2000;
FEATURES
location/Qualifiers
source 1..1254
BASE COUNT 201 a 420 c 407 g 226 t
ORIGIN
Alignment Scores:
Pred. No.: 2.64e-114 Length: 1254
Score: 2323.00 Matches: 417
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-993-234-6 (1-417) x AR119657 (1-1254)
QY 1 MetGlulnArgProArgglyCysAlaAlaValAlaAlaLeuLeuValLeuLeu 20
Db 1 ATGGAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTCCCTGCTGCTG 60
QY 21 GlyAlaArgAlaGlnGlnGlyThrArgSerProArgCysAspCysAlaGlyAspPheHis 40
Db 61 GGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTCCAC 120
QY 41 LysLysIleGlyLeuPheCysCysArgglyCysProAlaGlyHisTyrLeuLysAlaPro 60
Db 121 AAGAAGATTGCTGCTTTGTTGTGACAGAGCGTCCACAGCGGGGCACTACTGAAGGCCCT 180
QY 61 CysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAla 80
Db 181 TGCACGAGCGCTGCGCACTCCACCTGCTGTGTCTCCCAAGACACCTTCTTGCC 240
QY 81 TrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSer 100
Db 241 TGGAGAACCAACCATATCTGATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCGCTCC 300
QY 101 GlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGly 120
Db 301 CAGGTGGCGCTGGAGAACTGTCAGCAGAGTGCCGACACCGCTGTGCTGAAGCCAGGC 360
QY 121 TrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCysGlnPro 140
Db 361 TGGTTTGTGAGAGTGCAGAGTCAACCAATGTGTCAAGCAAGTTCAACCTTCTACTGCCAACA 420
QY 141 CysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThr 160
Db 421 TGCCTAGACTGCGGGCGCTGCACCGCCACACAGGCTACTCTGTCCCGCAGAGATACT 480
QY 161 AspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysPro 180
Db 481 GACTGTGGAGACTGCGCTGCTGCTTCTATGAACATGGCGATGGCTGCGGTCTGCCCC 540
QY 181 ThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTyrParGlnMet 200
Db 541 ACGAGCACCTGGGGAGCTGTCCAGAGCGCTGTGCCGCTGTCTGTGGCTGAGGCGAGATG 600
QY 201 PheTrpValGlnValLeuLeuAlaGlyLeuValValProLeuLeuGluAlaThrLeu 220
Db 601 TTCTGGGTCCAGGTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660

QY 221 ThrTyrThrTyrArgHisCysTrpProHisLysProLeuValThrAlaAspGluAlaGly 240
Db 661 ACCTACACATACCGCACTGCTGCGCTCACAAGCCCCCTGTTACTGACAGATGAAGCTGGG 720
QY 241 MetGluAlaLeuThrProProProAlaThrHisLeuSerProLeuAspSerAlaHisThr 260
Db 721 ATGAGGCTGTGACCCCAACCCAGCGCCACCACTCTGTCAACCTTGGACAGCGCCACACC 780
QY 261 LeuLeuAlaProProAspSerSerSerGluLysIleCysThrValGlnLeuValGlyAsnSer 280
Db 781 CTTCTAGACACTTCTGACAGCAGTGAAGATCTGCACCGTCCAGTTGGTGGTAACAGC 840
QY 281 TrpThrProGlyTyrProGluThrGlnGlnAlaLeuCysProGlnValThrTrpSerTrp 300
Db 841 TGGACCCCTGGCTACCCCGAGAGACCCAGAGCGGCTGTGCCCGCAGGTGACATGTCTTG 900
QY 301 AspGlnLeuProSerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSer 320
Db 901 GACCAGTTGGCCAGCAGAGCTCTTGCGCCCGCTGTGCGCCCACTCTCGCCAGAGTCC 960
QY 321 ProAlaGlySerProAlaMetMetLeuGlnProGlyProGlnLeuTyrAspValMetAsp 340
Db 961 CCAGCGCGCTCGCCAGCAGCATGATGTCTCAAGCCGGCCCGCACTCTACGACGTGATGAC 1020
QY 341 AlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGluAlaGlu 360
Db 1021 GCGGTCCAGCGCGCGCGCTGGAAGAGTTCTGTGCGCACGCTGGGGCTGCGCAGCAGAG 1080
QY 361 IleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGluMetLeuLys 380
Db 1081 ATCGAAGCCGTGAGGTGAGATCGCGCGCTTCGAGACCAAGTACGAGATGCTCAAG 1140
QY 381 ArgTyrParGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMet 400
Db 1141 CGCTGGCGCCAGCAGCAGCGCGCGCGCTCGAGCCGTTTACGCGCGCTGAGCCGATG 1200
QY 401 GlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 417
Db 1201 GGGCTGGACGGCTGCTGGAAGACTTGGCAGCCGCTGACAGCGCGCGCCG 1251
RESULT 2
HSU72763 1254 bp mRNA linear PRI 15-NOV-1996
LOCUS
DEFINITION Human death receptor 3 (DR3) mRNA, complete cds.
ACCESSION U72763
VERSION U72763.1 GI:1669511
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE
1 (bases 1 to 1254)
AUTHORS Chinaiyan,A.M., O'Rourke,K., Yu,G.L., Lyons,R.H., Garg,M.,
Duan,D.R., Xing,L., Gentz,R., Ni,J. and Dixit,V.M.
TITLE Signal transduction by DR3, a death domain-containing receptor
related to TNF-R-1 and CD95
JOURNAL Science 274 (5289), 990-992 (1996)
MEDLINE 97081063
PUBMED 8875942
REFERENCE
2 (bases 1 to 1254)
AUTHORS Chinaiyan,A.M., O'Rourke,K., Yu,G.-L., Lyons,R.H., Garg,M.,
Duan,R., Xing,L., Gentz,R., Ni,J. and Dixit,V.M.
TITLE Direct Submission
JOURNAL Submitted (29-SEP-1996) Pathology, University of Michigan Medical
School, 1301 Catherine St., Box 0602, Ann Arbor, MI 48109, USA
FEATURES
source 1..1254
location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
gene 1..1254
/gene="DR3"
1..1254
CDS 1..1254
/gene="DR3"

TLTYTYRHCMPLVTADAGMEALTTPPATHLSPLDSAHLLAPDSEKICIVOL
VNSWTPGYPETOEALCPQYTWSDQLPSRALGPAAPTLSPESPAGPAMLOPQPO
LYDMDAVPARRWKEFVRTILGLREAEIEAVEVEIGRFDOQYEMLKRWROQOPAGLGA
VYALERMGLDGCVEDLRSLRQRP"
BASE COUNT 201 a 420 c 407 g 226 t
ORIGIN

Alignment Scores:
Pred. No.: 2.64e-114 Length: 1254
Score: 2323.00 Matches: 417
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-993-234-6 (1-417) x HSU94501 (1-1254)

OY 1 MetGluGlnArgProArgGlyCysAlaAlaValAlaAlaLeuLeuValLeu 20
Db 1 ATGGAGCAGCGCGCGGGGCTGCGGGGTGGCGCGCGCTCCCTGCTGCTG 60
OY 21 GlyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHis 40
Db 61 GGGGCCCGCGCCAGGGCGGCACTCGTAGCCCCAGGTGTGACTGTGCCGGTGAAGTCCAC 120
OY 41 LysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaPro 60
Db 121 AAGAAGATGGTCTGTTTGTGTGCAGAGGCTGCCAGCGGGGCACATACCTGAAGCCCCCT 180
OY 61 CysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAla 80
Db 181 TGCACGGAGCCCTGCGGCACTCCACCTGCTGTGTGTCCCAAGACACTTCTTGGCC 240
OY 81 TrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSer 100
Db 241 TGGAGAACCACTAATTCTGAATGTGCCCTGCCAGGCTGTGATGAGCAGGCCCTCC 300
OY 101 GlnValAlaLeuGlnAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGly 120
Db 301 CAGGTGGCGCTGAGAACTGTTACAGCAGTGGCCGACACCCGCTGTGGCTGAAGCCAGGC 360
OY 121 TrpPheValGluCysGlnValSerGlnCysValSerSerSerProPheTyrCysGlnPro 140
Db 361 TGGTTGTGAGTGCAGGTACGCCAATGTGTACAGTTCACCCCTTACTGCCAACCA 420
OY 141 CysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThr 160
Db 421 TGCCTAGACTGGGGGGCCCTGCACCCGCCACACAGGGCTACTCTGTCCCGCAGAGATACT 480
OY 161 AspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysPro 180
Db 481 GACTGTGGGACCTGCCCTGCTGCTTATGAACATGGCGATGGCTGCTGCTGCCCC 540
OY 181 ThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTyrParGlnMet 200
Db 541 ACGAGCACCTGGGGAGCTGTCCAGAGCCTGTGCGCTGTGTGCTGAGGAGCATG 600
OY 201 PheTyrValGlnValLeuAlaGlyLeuValAlaProLeuLeuLeuGlyAlaThrLeu 220
Db 601 TTCTGGGTCCAGGTGCTCTGCTGGCTGTGCTGCCCTCTGCTGGGGCCACCCCTG 660
OY 221 ThrTyrThrTyrArgHisCysTyrProHisLysProLeuValThrAlaAspGluAlaGly 240
Db 661 ACCTACACATACCGCCACTGCTGGCTGCACAAGCCCTGTACTGCAGATGAAGCTGGG 720
OY 241 MetGluAlaLeuThrProProAlaThrHisLeuSerProLeuAspSerAlaHisThr 260
Db 721 ATGAGGCTCTGACCCACACACCGGCCCACTCTGTACCCCTTGAGACGCCACACACC 780
OY 261 LeuLeuAlaProProAspSerSerGluLysIleCysThrValGlnLeuValGlyAsnSer 280
Db 781 CTCTAGCACTCTCTGACAGCAGTGAAGATCTGCACCGTCCAGTTGGTGGGTAAACAGC 840

OY 281 TrpThrProGlyTyrProGluThrGlnGluAlaLeuCysProGlnValThrTrpSerTrp 300
Db 841 TGGACCCCTGGCTACCCCGAGACCAGAGAGCGCTGTGCCCGAGGTGACTGTCTGG 900
OY 301 AspGlnLeuProSerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGlnSer 320
Db 901 GACCAGTTGCCACAGCAGACTCTTGGCCCCCGCTGTGCGCCACACTCTGCCAGAGTCC 960
OY 321 ProAlaGlySerProAlaMetMetLeuGlnProGlyProGlnLeuTyrAspValMetAsp 340
Db 961 CCAGCCGGCTGCCAGCCATGATGCTGCAGCCGCCGCCAGCTCTACGACGTATGGAC 1020
OY 341 AlaValProAlaArgArgTyrLysGluPheValArgThrLeuGlyLeuArgGluAlaGlu 360
Db 1021 GCGGTCCAGCGCGCGCTGGAAGAGTTCTGTGCGCACGCTGGGGCTGCCGAGGCAGAG 1080
OY 361 IleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGluMetLeuLys 380
Db 1081 ATCGAAGCCGTGAGGTGAGATCGCCGCTTCGAGACAGCAGTACGAGATGCTCAAG 1140
OY 381 ArgTyrArgGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMet 400
Db 1141 CGCTGGCGCAGCAGACGCCCGCGGCTCGAGCCGTTTACGCGGCCCTGAGCCCATG 1200
OY 401 GlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 417
Db 1201 GGGCTGACGGCTGGTGAAGACTTGCGCAGCGCCCTGCAGCGCGGCCG 1251

RESULT 5
HSU74611 1634 bp mRNA linear PRI 02-JAN-1997
LOCUS
DEFINITION Human Apo-3 mRNA, complete cds.
ACCESSION U74611
VERSION U74611.1 GI:1763292
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1634)
REFERENCE
AUTHORS Marsters,S.A., Sheridan,J.P., Donahue,C.J., Pittl,R.M., Gray,C.L.,
Goddard,A.D., Bauer,K.D. and Ashkenazi,A.
Apo-3, a new member of the tumor necrosis factor receptor family,
contains a death domain and activates apoptosis and NF-kB
Curr. Biol. (1996) In press
2 (bases 1 to 1634)
JOURNAL
REFERENCE Marsters,S.A., Sheridan,J.P., Donahue,C.J., Pittl,R.M., Gray,C.L.,
Goddard,A.D., Bauer,K.D. and Ashkenazi,A.
Direct Submission
JOURNAL Submitted (15-OCT-1996) Molecular Oncology, Genentech, 460 Pt. San
Bruno Blvd., South San Francisco, CA 94080, USA
FEATURES
source Location/Qualifiers
1. 1634
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/map="1p36.3"
/tissue_type="heart"
/dev_stage="fetal"
89. 1342
/note="contains death domain, activates apoptosis and
NF-kB; TNF receptor family member"
/codon_start=1
/product="Apo-3"
/protein_id="AAB39714.1"
/db_xref="GI:1763293"
/translation="MEQRPRGCAVAVALLLVLLGARAGGTRSPRCDAAGDFHRTKIG
LRCRCGPAGHYLKAPCTEPCGNSTLCVCPDFTFLAWENHNSECARCOACDEQASOV
ALENCSAVADTRCGCKPGWFVECOVSQCVSSSPFYCPCLDCGALHRHTRLCSKRDPT
DCGTCILPGFEYEHGDGCVSCPSTLGSCEPERCAAVCGWROMWVOVLLAGLVPLILGA
TLTYTYRHCMPLVTADAGMEALTTPPATHLSPLDSAHLLAPDSEKICIVOL
VNSWTPGYPETOEALCPQYTWSDQLPSRALGPAAPTLSPESPAGPAMLOPQPO
LYDMDAVPARRWKEFVRTILGLREAEIEAVEVEIGRFDOQYEMLKRWROQOPAGLGA

	300 a	528 c	519 g	287 t
BASE COUNT				
ORIGIN				

Alignment Scores:

Pred. No.:	3,51e-114	Length:	1634
Score:	2323.00	Matches:	417
Best Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-993-234-6 (1-417) x HSU74611 (1-1634)

QY	1	MetGluGlnArgProArgGlyCysAlaAlaValAlaAlaLeuLeuValLeu	20
Db	89	ATGGAGCAGCGCGCGCGCGCTGCCGGCGGTGGCGCGCGCTCTCTGGTGTGCTG	148
QY	21	GlyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHis	40
Db	149	GGGGCCCCGGCCAGGGCGGCACCTGTAACCCCAAGTGTGACTGTGCCGGTGAATTCCAC	208
QY	41	LysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlnHisTyrLeuLysAlaPro	60
Db	209	AAGAAGATTGGTCTGTTTGTGTGCAGAGGCTGCCAGCGGGGCACTACCTGAAGGCCCT	268
QY	61	CysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAla	80
Db	269	TGCACGAGCCCTCGCGCAACTCCACCTGCCCTGTGTCTCCCAAGACACCTTCTTGCC	328
QY	81	TrpGluAsnHisAsnSerGlyCysAlaArgCysGlnAlaCysAspGluGlnAlaSer	100
Db	329	TGGGAGAACCACCATATATTCTGAATGTGCCCGCTGCCAGGCCGTGTATGAGCAGGCTCC	388
QY	101	GlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGly	120
Db	389	CAGGTGGCGCTGGAGAAGTGTTCAGCAGTGGCCGACACCCGGCTGTGGCTGTAAAGCAGGC	448
QY	121	TrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCysGlnPro	140
Db	449	TGGTTTGTGAGTCCAGGTCAGGCAATGTCTCAGCAGTTCAACCTTCTACTGCCAACCA	508
QY	141	CysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThr	160
Db	509	TGCCTAGACTGGCGGGCCCTGCACCGCCACACACAGGCTACTCTGTCCCGCAGAGATACT	568
QY	161	AspCysGlyThrCysLeuProGlyPheTyrGlnHisGlyAspGlyCysValSerCysPro	180
Db	569	GACTGTGGACCTGCCCTGGCTGTATGAACATGGCGATGGCTGCCGTCTCTGCCCC	628
QY	181	ThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTyrPargGlnMet	200
Db	629	ACGAGCACCCCTGGGAGCTGTCCAGACGCGCTGTGCCGCTGTCTGTGGCTGGAGGCAGATG	688
QY	201	PheTrpValGlnValLeuLeuAlaGlyLeuValValProLeuLeuGlyAlaThrLeu	220
Db	689	TTCTGGGTCAGGTGCTCTGGCTGGCTTGTGTGTCCTCTCTGCTGGGGCCACCCCTG	748
QY	221	ThrTyrThrTyrArgHisCysTrpProHisLysProLeuValThrAlaAspGluAlaGly	240
Db	749	ACCTACACATACCGCCACTGTGGCTTCACAAGCCCTGTACTGCAGATGAAGCTGGG	808
QY	241	MetGluAlaLeuThrProProProAlaThrHisLeuSerProLeuAspSerAlaHisThr	260
Db	809	ATGGAGGCTCTGACCCCAACCAACCGGCCACCATCTGTACACCTTGGACAGCGCCACACC	868
QY	261	LeuLeuAlaProProAspSerSerGlyLysIleCysThrValGlnLeuValGlyAsnSer	280
Db	869	CTTCTAGCACCTCCTGACAGCAGTGAAGAAGATCTGCACCCGTTCAGCTTGGGTAACAGC	928
QY	281	TrpThrProGlyTyrProGluThrGlnGluAlaLeuCysProGlnValThrTrpSerTyr	300
Db	929	TGGACCCCTGGCTACCCCGAAGACCAAGAGGCGCTCTGCCCGCAGGTGACATGGTCTGG	988

QY 301 AspGlnIeuProSerAArgAlaIeuGlyProAlaAlaIaIaProThrLeuSerProGluSer 320
 |||||
 989 GACCACTTGGCCAGACAGAGACTCTTGGCCCCGCTGCTGCGCCACACTCTCGCCAGAGTCC 1048
 Db

QY 321 ProLacIySerProAlaMetMetLeuGlnProGlyProGlnLeuTyrAspValMetasp 340

Db 1049 CCAGCCGGCTCGCCAGCCATGATGCTGCAGCCGGGCCCGCAGCTCTACGACGTGATGGAC 1108

QY 341 AAlaValProAlaArgArgTrrPLysGluPheValArgThrLeuGlyLeuArgGluAlaGlu 360

Db 1109 GCGGTCCAGCGCGGCTGGAGGAGTTCGTGCCACGCTGGGCTGCCGAGGCAGAG 1168

QY 361 IIEGLUALaValGluIleGlyArgPheArgAspGlnGlnTyrGluMetLeuLys 380

Db 1169 ATCGAAGCCGTGGAGGTGGAGATCGGCCGCTTCCGAGACCAGCAGTACGAGATGCTCAAG 122

381 ArgTTPArgGInGInProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMet 400

LD 1229 CGCTGGCCAGCAGCCCGCGGGCTTCGGAGCCGTTACGGCGCCCTGAGCGCATG 128

401 GILYLeuAspGlyCysValGIuAspLeuArgSerArgLeuGlnArgGlyPro 417

DB 1289 GGGCTGGACGGCTGGCTGGAGACTTGGCGCAGCCGCCCTGCAGCGCGGCCG 1339

RESULT: 6
AX055442

AX055442

LOCUS	AX055442	1662 bp	DNA	linear	PAT 13-JAN-2001
DEFINITION	Sequence 72 from Patent WO0073452.				

DEFINITION Sequence 72 from Patent W00073452.

AX055442.1 GI:12228713

KEYWORDS
VENDOR
ha050442.1 01:12228/13

DOORCE
ORGANISM

ORGANISM

REFERENCE 1. Bates 1 to 1959, Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.

AUTHORS Asinkehazi, A. J., Baker, K. P., Chan, B., Goddard, A., Godowski, C., Gurney, A. I., Hebert, C., Hwang, J. H., Kozlowski, J. T., Lachy, M. R.,

TTTIF
Tomas, D., Watanabe, C.K. and Wood, W.I.
Compositions and methods for the

Journal of Diseases
Patent: WO 0073453-A 73 07 255 2000

General Tech, Inc. (US)
Location/Overview

source
I, :100Z
/organism="Homo sapiens"

```
BASE COUNT      302 a      540 c      531 a      289 +
```

Pred.

Alignment Scores:	
Pred. No.:	3.57e-114
Score:	2323.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	6
	Gaps: 0
	Length: 1662
	Matches: 417
	Conservative: 0
	Mismatches: 0
	Indels: 0

US-09-993-234-6 (1-417) X AX055442 (1-1662)

QY	1	MetGluGlnArgProArgGlyCysAlaAlaValAlaAlaLeuLeuValLeuLeu	20
Db	103	ATGAGACAGCGCGCGCGGCTCGCGCGGCGGTGGCGCGCGCTCTCTGCTGCTG	162
QY	21	GlyAlaArgAlaGlnGlyThrArgSerProArgCysAspCysAlaGlyAspPheHis	40
Db	163	GGGGCCCCGGCCCCAGGGCGGCACTGTAGCCCCAGGTGTGACTGTGCCGGTGACTTCCAC	222
QY	41	LysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlnHisTyrLeuLysAlaPro	60
Db	223	AAGAGATTTGCTGTTTGTGTCAGAGGCTGCCACGCGGGCACTACTGTAAGGCCCT	282

QY 61 CysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAla 80
Db 283 TGCACGAGAGCCCCCTGGGCAACTCCACCCTGTGTGTCTCCCAAGACACCTTCTTGGCC 342
QY 81 TrpGluAsnHisHisAsnSergLcysAlaIaArgCysGlnAlaCysAspGluGlnAlaSer 100
Db 343 TGGAGAACCACTAATTTCTGAATGTGCCCCCTGCCAGGCTGTGATGACAGAGGCTTCC 402
QY 101 GlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGly 120
Db 403 CAGGTGGCGCTGGAGAAGCTGTTTCAGCAGTGGCGACACCCGCTGTGGCTGTAGCCAGGC 462
QY 121 TrpPheValGluCysGlnValSergLcysValSergSerProPheTyrCysGlnPro 140
Db 463 TGGTTGTGAGTGCAGAGTCCAGCCAAATGTGTACAGTTACCCCTTCTACTGCCAACCA 522
QY 141 CysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThr 160
Db 523 TGCCTAGACTGGGGGCCCTGCACCGCCACACAGGCTACTCTGTCCCGCAGAGATACT 582
QY 161 AspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSergCysPro 180
Db 583 GACTGTGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 642
QY 181 ThrSerThrLeuGlySerCysProGlyIaArgCysAlaAlaValCysGlyTyrPargGlnMet 200
Db 643 ACGAGCACCTGGGGAGCTGTCCAGAGCGCTGTCCGCTGTGTGGCTGGAGGCAGATG 702
QY 201 PheTyrValGlnValLeuLeuAlaGlyLeuValValProLeuLeuGlyAlaThrLeu 220
Db 703 TTCTGGGTCCAGGTCTCTGCTGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTG 762
QY 221 ThrTyrThrTyrArgHisCysTyrProHisLysProLeuValThrAlaAspGluAlaGly 240
Db 763 ACCTACACATACGCCCACTGCTGGCTCACAAGCCCTGGTTACTGCAGATGAAGCTGGG 822
QY 241 MetGluAlaLeuThrProProProAlaThrHisLeuSerProLeuAspSerAlaHisThr 260
Db 823 ATGGAGGCTGTGACCCCAACACCCGCGCCACCATCTGTACCCCTGGACAGCCGCCACACC 882
QY 261 LeuLeuAlaProProAspSerSergLcysLysIleCysThrValGlnLeuValGlyAsnSer 280
Db 883 CTCTAGCACTCTCTGACAGCAGTAGAGATCTGCACCGTCCAGTTGGTGGTAAACAGC 942
QY 281 TyrThrProGlyTyrProGlyLcysGlnGluAlaLeuCysProGlnValThrTrpSerTrp 300
Db 943 TGCACCCCTGGCTACCCGAGACCCAGAGGCGCTGCGCCAGAGTGCATGTCTCTGG 1002
QY 301 AspGlnLeuProSerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSer 320
Db 1003 GACCAAGTGGCCAGCAGAGCTTGGCCCCGCTGTGCCCCACACACTGCGCCACAGATCC 1062
QY 321 ProAlaGlySerProAlaMetMetLeuGlnProGlyProGlnLeuTyrAspValMetAsp 340
Db 1063 CCAGCCGGCTGGCCAGCCATGATGCTGCAGCCGGGCCCCGAGCTTACGACGTGATGGAC 1122
QY 341 AlaValProAlaIaArgTyrTrpLysGluPheValArgThrLeuGlyLeuArgGluAlaGlu 360
Db 1123 GCGGTCCAGCGCGCGCTGGAAAGAGTTCGTGCGCACGCTGGGGCTGCCGAGGCGAGAG 1182
QY 361 IleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGluMetLeuLys 380
Db 1183 ATCGAAGCCGTGGAGGTGGAGATCGGCGCTTCCGAGACCAGCAGTAGAGATGCTCAAG 1242
QY 381 ArgTyrPargGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMet 400
Db 1243 CGCTGGCGCCAGCAGACCGCGCGCTGGAGCGGTTTACGGCGCTGGAGCGCATG 1302
QY 401 GlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 417
Db 1303 GGGCTGAGAGGCTGCGTGAAGACTTGGCGAGCCGCTGCAGCGCGGCCG 1353
RESULT 7

AX201344
LOCUS AX201344 1662 bp DNA linear PAT 30-AUG-2001
DEFINITION Sequence 23 from patent WO0153486.
ACCESSION AX201344
VERSION AX201344.1 GI:15391165
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1662)
Ashkenazi,A.J., Goddard,A., Godowski,P.J., Gurney,A.L.,
Hillan,K.J., Marsters,S.A., Pan,J., Pittl,R.M., Roy,M.A., Smith,V.,
Stone,D.M., Watanabe,C.K. and Wood,W.I.
Compositions and methods for the treatment of tumour
patent: WO 0153486-A 23 26-JUL-2001;
Genentech, Inc. (US)
FEATURES
source location/Qualifiers
1..1662
BASE COUNT 302 a 540 c 531 g 289 t
ORIGIN
Alignment Scores:
Pred. No.: 3.57e-114 Length: 1662
Score: 2323.00 Matches: 417
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
US-09-993-234-6 (1-417) x AX201344 (1-1662)
QY 1 MetGluGlnIaArgProArgGlyCysAlaAlaValAlaAlaLeuLeuValLeu 20
Db 103 ATGGAGCAGCGCGCGCGCTGCGCGGGGTGGCGCGCGCTCTCTGTGCTGCTG 162
QY 21 GlyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHis 40
Db 163 GGGGCGCGCGCGCGCGCGCACTGCTAGCCCGCAGGTGTGACTGTGCCGGTGACTCCAC 222
QY 41 LysLysIleGlyLeuPheCysArgGlyCysProAlaGlyHisTyrLeuLysAlaPro 60
Db 223 AAGAAGATTGCTGTGTTTGTGACAGAGCTGCCAGCGGGGCACTACCTGAAGGCCCT 282
QY 61 CysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAla 80
Db 283 TGCACGAGCCCTGGGCAACTCCACCTGCTGTGTGTCCCAAGACACCTTCTTGGCC 342
QY 81 TrpGluAsnHisHisAsnSergLcysAlaIaArgCysGlnAlaCysAspGluGlnAlaSer 100
Db 343 TGGGAGAACCACTAATTTCTGAATGTGCCCGCTGCCAGGCTGTGATGAGAGGCTTCC 402
QY 101 GlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGly 120
Db 403 CAGGTGGCGCTGGAGAAGCTGTTTCAGCAGTGGCGACACCCGCTGTGGCTGTAGCCAGGC 462
QY 121 TrpPheValGluCysGlnValSergLcysValSergSerProPheTyrCysGlnPro 140
Db 463 TGGTTGTGAGTGCAGAGTCCAGCCAAATGTGTACAGTTACCCCTTCTACTGCCAACCA 522
QY 141 CysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThr 160
Db 523 TGCCTAGACTGGGGGCCCTGCACCGCCACACAGGCTACTCTGTCCCGCAGAGATACT 582
QY 161 AspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSergCysPro 180
Db 583 GACTGTGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 642
QY 181 ThrSerThrLeuGlySerCysProGlyIaArgCysAlaAlaValCysGlyTyrPargGlnMet 200
Db 643 ACGAGCACCTGGGGAGCTGTCCAGAGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 702

QY	201	PheTrpValGlnValLeuLeuAlaGlyLeuValValProLeuLeuLeuGlyAlaThrLeu	220
Db	703	TTCTGGGTCACAGGTGCTCTCTGGCTGGCTTGTGTCCCCCTCTGCTTGGGGCCACCCCTG	762
QY	221	ThrTrpThrTyraArgHisCysTrpProHisLysProLeuValThrAlaAspGluAlaGly	240
Db	763	ACCTACACATACCGCCACTGTGCTGCACAAAGCCCTGGTTACTGACATGAAGCTGGG	822
QY	241	MetGluAlaLeuThrProProProAlaThrHisLeuSerProLeuAspSeraAlaHisThr	260
Db	823	ATGGAGGCTGTGACCCACACACCAGCCACCCATCTGTACACCTTGGACAGCGCCACACC	882
QY	261	LeuLeuAlaProProAspSerSerGluLysIleCysThrValGlnLeuValGlyAsnSer	280
Db	883	CTTCTAGCACCTCTCTGACAGCAGTGAAGATCTGCACCCTTCAGTTGGTGGTAACAGC	942
QY	281	TrpThrProGlyTyrProGluIuThrGlnGluAlaLeuCysProGlnValThrTrpSerTrp	300
Db	943	TGGACCCCTGGCTACCCCGAGACCCAGAGAGCGCTCTGCCCCGAGGTGACATGGTCTCG	1002
QY	301	AspGlnLeuProSerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSer	320
Db	1003	GACCAGTTGCCACAGCAGAGCTCTGGCCCCGCTGCTGCGCCACACTCTGCCACAGTCC	1062
QY	321	ProAlaGlySerProAlaMetMetLeuGlnProGlyProGlnLeuTyrAspValMetAsp	340
Db	1063	CCAGCCGGCTCGCCACGACCATGATGCTGCAGCCGCGCCGACGCTTACGACGATGAGAC	1122
QY	341	AlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGluAlaGlu	360
Db	1123	GCGGTCCACAGCGCGGCGCTGGAAGAGTTCTGCGCACGCTGGGGCTGCGCGAGGCAGAG	1182
QY	361	IleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGluMetLeuLys	380
Db	1183	ATCGAAGCCGTGAGGTGAGATCGCGCCGCTTCCGAGACACGACGATGAGATGCTCAAG	1242
QY	381	ArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMet	400
Db	1243	CGCTGGCCGCCACGACGACGCCCGCGGCGCTCGGAGCCGTTTACGCGCGCCCTGGAGCGCATG	1302
QY	401	GlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro	417
Db	1303	GGGCTGACGCGCTGCTGGAAAGACTTGGCAGCCGCTGCAGCGCGGCGCCG	1353
RESULT 8			
LOCUS	HSU94502	1257 bp	mRNA
DEFINITION		Human lymphocyte associated receptor of death 1b mRNA,	
ACCESSION	U94502		alternatively spliced, complete cds.
VERSION	U94502.1	GI:2071950	
KEYWORDS			
SOURCE			
ORGANISM			Homo sapiens.
			Homo sapiens
REFERENCE			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS			Mammalia; Eutheria; Primates; Catarrhini; Homiinae; Homo.
			1 (bases 1 to 1257)
TITLE			Screaton,G.R., Xu,X.N., Olsen,A.L., Cowper,A.E., Tan,R.,
			McMichael,A.J. and Bell,J.I.
JOURNAL			LARD: a new lymphoid-specific death domain containing receptor
MEDLINE			regulated by alternative pre-mRNA splicing
PUBMED			Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)
REFERENCE			9114039
AUTHORS			2 (bases 1 to 1257)
TITLE			Screaton,G.R.
JOURNAL			Direct Submission
			Submitted (19-MAR-1997) Molecular Immunology Group, Institute of
			Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3
			9DU, UK
FEATURES			
source			Location/Qualifiers
			1..1257

OY 181 ThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTrpArgGlnMet 200
|||||
Db 541 ACGAGCACCCCTGGGAGCTGTCCAGAGCGCTGTGCCCTGTCTGTGGCTGAGGAGATG 600
OY 201 PheTrpValGlnValLeuLeuAlaGlyLeuValValProLeuLeuLeuGlyAlaThrLeu 220
|||||
Db 601 TTCTGGGTCACAGGTGCTGCTGGCTGGCTGTGGTCCCTCTCTGCTGGGGCCACCCTG 660
OY 221 ThrTrpThrTrpArgHisCysTrpProHisLysProLeuValThr--AlaAspGluAla 239
|||||
Db 661 ACCTACACATACCGCCACTGCTGGCTCACAAGCCCTGCTTACTGCAGCAGATGAAGCT 720
OY 240 GlyMetGluAlaLeuThrProProProAlaThrHisLeuSerProLeuAspSerAlaHis 259
|||||
Db 721 GGGATGAGGCTCTGACCCACACACCGGCCACCATCTGTCAACCTTGGACAGCGCCAC 780
OY 260 ThrLeuLeuAlaProProAspSerSerGluLysIleCysThrValGlnLeuValGlyAsn 279
|||||
Db 781 ACCCTTCTAGCACCTCTGACAGACAGTGAAGAAGATCTGCACCGCTCCAGTTGGGTAAAC 840
OY 280 SerTrpThrProGlyTrpProGluThrGlnGluAlaLeuCysProGlnValThrTrpSer 299
|||||
Db 841 AGCTGAGCCCTGGCTACCCCGAGAGACAGAGGCGCTCTGCCCGCAGGTGACATGCTCC 900
OY 300 TrpAspGlnLeuProSerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGlu 319
|||||
Db 901 TGGGACCAAGTGGCCACAGACAGCTCTTGCGCCCTGCTGCGCCACACACTCTCGCCAGAG 960
OY 320 SerProAlaGlySerProAlaMetMetLeuGlnProGlyProGlnLeuTrpAspValMet 339
|||||
Db 961 TCCCGACCGGCTCGCCAGCATGATGTGTCAGCGCGCGCCGACAGCTCTACGACGTGATG 1020
OY 340 AspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGluAla 359
|||||
Db 1021 GACCGCGTCCAGCGCGCGCTGGAAGAGTTCGTGCGCACGCTGGGGCTGCGCGAGCA 1080
OY 360 GluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTrpGluMetLeu 379
|||||
Db 1081 GAGATCGAAGCCGTGAGGTGAGATCGCGCTGCCGAGACACAGCAGATAGATGCTC 1140
OY 380 LysArgTrpArgGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArg 399
|||||
Db 1141 AAGCGCTGGCCGACGACAGACCCCGGGCGCTCGGAGCCGTTTACGGCGCCCTGGAGCGC 1200
OY 400 MetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 417
|||||
Db 1201 ATGGGGCTGGACGCGCTGCGTGAAGACTTGGCGACCGCTGCAGCGCGGCGCCG 1254
RESULT 9
HSU83597 1528 bp mRNA linear PRI 27-JAN-1997
LOCUS
DEFINITION Human death domain receptor 3 (DDR3) mRNA, partial cds.
ACCESSION U83597
VERSION U83597.1 GI:1800292
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1528)
AUTHORS Chaudhary, P.M. and Hood, L.E.
TITLE Direct Submission
JOURNAL Submitted (03-JAN-1997) Molecular Biotechnology, University of
Washington, 1705 NE Pacific Street, HSB-K360, Seattle, WA 98195,
USA
FEATURES
source
1..1528
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/map="1p36"
1..1528
/gene="DDR3"
gene

CDS
1..1238
/gene="DDR3"
/function="mediates apoptosis when cross-linked"
/note="A TNFRI-related death-domain containing receptor;
DR3, WSL-IR, Apo-3, TRAMP; transmembrane form; similar to
human EST clone 298913, GenBank Accession Number N71143"
/codon_start=3
/product="death domain receptor 3"
/protein_id="AAB41432.1"
/db_xref="GI:1800293"
/translation="GCCAAVAAALLVLGARAQGGTRSPRCDCAGDFHKKIGLFCRCG
CPAGHYLRAPCTEPCGNSTCLVCPODFILAMENHNHNSCARCQACDEQASQVALENC
AVADTRCGCRPGWFEVCOVSQCVSSPFCQPCLDGALHRTLRCSRRDTCGCL
LGFEYEHGDGCVSCPSTSLGSCPERCAVCGWRQMFVQVLLAGLVPLLGATLTITY
RHCWPHKPLVTADAGMEALTPPATFHLSPLDASHLLAPDSSSEKCTVQLVNSWT
PGYPTQELCPQVTVWSWDQLPSRALGPAAAPTLSPESPAGSPAMQLQPGPOLYDMD
AVPARRWKEFVRTLGLREAIEIAVEVEIGFRDQYEMLRWRQDQPAGLGAVYALE
RMGLDGVEDLRSRLQRP"
BASE COUNT 280 a 496 c 470 g 282 t
ORIGIN
Alignment Scores:
Pred. No.: 5.34e-112 Length: 1528
Score: 2281.00 Matches: 410
Percent Similarity: 99.76% Conservative: 0
Best Local Similarity: 99.76% Mismatches: 1
Query Match: 98.19% Indels: 0
DB: 9 Gaps: 0
US-09-993-234-6 (1-417) x HSU83597 (1-1528)
OY 7 GlyCysAlaAlaValAlaAlaAlaLeuLeuValLeuLeuGlyAlaArgAlaGlnGly 26
|||||
Db 3 GGCTGGCGCGCGGTGGCGCGCGCTCCTCTGCTGCTGCTGGGGCGCGCGCGCGCG 62
OY 27 GlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGlyLeuPhe 46
|||||
Db 63 GGCACCTGTAAGCCCGCAGGTGTGACTGTGCCGGTGACTTCACAAAGAAATTGCTGTTT 122
OY 47 CysCysArgGlyCysProAlaGlnHisIleThrLeuLysAlaProCysThrGluProCysGly 66
|||||
Db 123 TGTTCAGAGAGCTGCCAGCGGGGCACTACCTGAAGGCCCTTGACAGAGCCCTGGCGC 182
OY 67 AsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHisAsn 86
|||||
Db 183 AACTCCACCTGCGCTGTGTGTGCCCAAGACACCTTCTTGCCCTGGGAGAACCATTAAT 242
OY 87 SerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeuGluAsn 106
|||||
Db 243 TCTGAATGTGCCCGCTGCCAGGCTGTGATGACAGAGGCTCCAGGTGGCGCTGGAGAAC 302
OY 107 CysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGluCysGln 126
|||||
Db 303 TGTTCAGCAGTGGCCGACACCGCTGTGGCTGTAAAGCCAGGCTGTTGTGAGTGGCAG 362
OY 127 ValSerGlnCysValSerSerSerProPheTyrCysGlnProCysLeuAspCysGlyAla 146
|||||
Db 363 GTACGCCAATGTGTACAGAGTTCACCTTCTACTGCCAACCATGCTAGACTGGGGGCC 422
OY 147 LeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThrCysLeu 166
|||||
Db 423 CTGCACCGGCACACAGCGCTACTGTCTCCCGCAGAGATACTGACTGTGGAGCTGCTG 482
OY 167 ProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeuGlySer 186
|||||
Db 483 CTGGCTTCTATGAACATGGCGATGGCTGCGGTGTCTGCCCCACGAGCACCCCTGGGAGC 542
OY 187 CysProGluArgCysAlaAlaValCysGlyTrpArgGlnMetPheTrpValGlnValLeu 206
|||||
Db 543 TGTTCAGAGCGCTGTGCGCTGTGCTGGCTGGAGGAGATGTTCTGGGTCCAGGTGCTC 602
OY 207 LeuAlaGlyLeuValValProLeuLeuLeuGlyAlaThrLeuThrTrpTrpArgHis 226
|||||

Db 603 CTGGCTGGCCCTGTGTGTCCTCCCTCCCTGCTGTGGGGCCACCCCTGACCTACACATACGCCAC 662

QY 227 CystTrpProHisLysProLeuValThrAlaAspGluAlaGlyMetGluAlaLeuThrPro 246

Db 663 TGCTGGCCCTCACAGCCCTGGTTACTGACAGATGAGCTGGATGAGGCTCTGACCCCA 722

QY 247 ProProAlaThrHisLeuSerProLeuAspSerAlaHisThrLeuLeuAlaProProAsp 266

Db 723 CCACCGGCCACCCATGTGTACCCCTTGACAGCGCCACACCCCTTCTAGCACCCTCTGAC 782

QY 267 SerSerGluLysIleCysThrValGlnLeuValGlyAsnSerTrpThrProGlyTyrPro 286

Db 783 AGCAGTGAGAGATGTGCACCCGTCCAGTTGGTGGTAACAGCTGACCCCTGGCTACCC 842

QY 287 GluThrGlnGluAlaLeuCysProGlnValThrTrpSerTrpAspGlnLeuProSerArg 306

Db 843 GAGACCCAGAGAGCGCTCTGCCCGCAGGTGACATGCTCCTGGACCAGTTGCCCAAGCAGA 902

QY 307 AlaleuGlyProAlaAlaAlaProThrLeuSerProGluSerProAlaGlySerProAla 326

Db 903 GCTCTTGCCCGCTGTGCGCCACACTCTCCGCAAGAGTCCCCAGCGCGCTGCCACAGCC 962

QY 327 MetMetLeuGlnProGlyProGlnLeuTyrAspValMetAspAlaValProAlaArgArg 346

Db 963 ATGATGCTGCAGCCCGCGCCGACGCTTACGACGTATGAGACGCGGTCCAGCGCGCGC 1022

QY 347 TrpLysGluPheValArgThrLeuGlyLeuArgGluAlaGluIleGluAlaValGluVal 366

Db 1023 TGGAGGAGTTCGTGCGCACGCTGGGGCTGCGCGAGGACAGATCGAAGCCGTGGAGGTG 1082

QY 367 GluIleGlyArgPheArgAspGlnGlnTyrGluMetLeuLysArgTrpArgGlnGlnGln 386

Db 1083 GAGATCGGCGCTTCCGAGACGACAGATGAGATGCTCAAGCGCTGGCGCCACAGCAGCAA 1142

QY 387 ProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMetGlyLeuAspGlyCysVal 406

Db 1143 CCGCGCGGCTTCGGAAGCCGTTTACGCGCGCTTGAGCGCATGGGCTGAGACGCGCTG 1202

QY 407 GluAspLeuArgSerArgLeuGlnArgGlyPro 417

Db 1203 GAAGACTTGGCAGCGCGCTGACGCGGCGCG 1235

RESULT 10

LOCUS HSU75380 1557 bp mRNA linear PRI 05-APR-1997

DEFINITION Human apoptosis-mediating receptor TRAMP mRNA, partial cds.

ACCESSION U75380

VERSION U75380.1 GI:1695924

KEYWORDS

SOURCE Homo sapiens.

ORGANISM Homo sapiens.

REFERENCE 1 (bases 1 to 1557)

AUTHORS Bodmer, J.L., Burns, K., Schneider, P., Hofmann, K., Steiner, V., Thome, M., Bornand, T., Hahne, M., Schroter, M., Becker, K., Wilson, A., French, L.E., Browning, J.L., Macdonald, R. and Tschoopp, J.

TITLE TRAMP, a novel apoptosis-mediating receptor with sequence homology to tumor necrosis factor receptor 1 and Fas(Apo-1/CD95)

JOURNAL Immunology 6 (1), 79-88 (1997)

MEDLINE 97205335

PUBMED 9052839

REFERENCE 2 (bases 1 to 1557)

AUTHORS Bodmer, J.L., Burns, K., Schneider, P., Hofmann, K., Steiner, V., Thome, M., Bornand, T., Hahne, M., Schroter, M., Wilson, A., French, L.E., Browning, J.L., Macdonald, R. and Tschoopp, J.

TITLE Direct Submission

JOURNAL Submitted (18-OCT-1996) Institute of Biochemistry, University of Lausanne, 155 Chemin des Boveresses, Epalinges, CH 1066, Switzerland

FEATURES

source location/Qualifiers

1..1557

/organism="Homo sapiens"

CDs

/db_xref="taxon:9606"

/chromosome="1"

/map="1p36.2"

/tissue_type="fetal lung"

<1..1245

/function="activates NF-kB"

/function="mediates apoptosis"

/note="contains a death domain; similar to TNF receptor"

/codon_start=1

/product="apoptosis-mediating receptor TRAMP"

/protein_id="AAC51192.1"

/db_xref="GI:1695925"

/translation="AAAGCAAVAAALLVLGARAQGGTRSPRCDCAGDFHKKIGLFC

CRGCPAGHYLKAPCTEPCGNSTCLVCPDPTFLMHNHNSCARCQACIDQASQVALE

NCSAVADTRCGCKPGMEVECCQVSQCVSSPFYCOPLDCGALHRTLRILCSRDYDCG

TCLLGFYEHDGCVSCTSTLGSCEPCAAVCGWQMFVQVLLAGLVPLLGATLT

YTYRHCPHKLPLVTRADEAGMEALTPPATHTLSPLDSAHTLAPDPDSSEKICTVQLVGN

SWTPGYPETOEALCPQVTWSWDQLPSRALGPAAPTLSPESPAGSPAMLOPGPOLYD

VMDAVPARRMKEFVRRLGLREAIEAVEVEIGRRDQYEMLKRRWQDQDPAGLGAVYA

ALERMGLDGCVEDLRSLQRGP"

BASE COUNT 286 a 508 c 477 g 286 t

ORIGIN

Alignment Scores:

Pred. No.: 5.45e-112 Length: 1557

Score: 2281.00 Matches: 410

Percent Similarity: 99.76% Conservative: 0

Best Local Similarity: 99.76% Mismatches: 1

Query Match: 98.19% Indels: 0

DB: Gaps: 0

US-09-993-234-6 (1-417) x HSU75380 (1-1557)

QY 7 GlyCysAlaAlaValAlaAlaAlaLeuLeuValLeuLeuGlyAlaArgAlaGlnGly 26

Db 10 GCGTCGCGCGCGGTGGCGCGCGCTCTCTCTGCTGCTGCTGGGGCGCGCCAGGCGC 69

QY 27 GlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGlyLeuPhe 46

Db 70 GGCACCTCGTAGCCCCAGGTGTACTGTGCGGTGACTTCCACAGAAGATTGCTGT 129

QY 47 CysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluProCysGly 66

Db 130 TGTTCAGAGAGGCTGCCAGCGGGGCACTACCTGAAGGCCCTTGACAGGAGCCCTGCGGC 189

QY 67 AsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHisAsn 86

Db 190 AACTCCACCTGCTGTGTGTCTCCCAAGACACCTCTTGCCCTGGAGAACCACTAAT 249

QY 87 SerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeuGluAsn 106

Db 250 TCTGAATGTGCCCGCTGCGCAGGCTGTGATGAGCAGGCCCTCCAGGTGGCGTGAAGAAC 309

QY 107 CysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGluCysGln 126

Db 310 TGTTCAGCAGTGGCGCGACACCCGCTGTGCTGTAAAGCCAGGCTGTTGTGAGTGCAG 369

QY 127 ValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCysGlyAla 146

Db 370 GTCAGCCAATGTGTGACAGAGTTACACCTTCTACTGCCAACCATATGCTTACTGCGGGCC 429

QY 147 LeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThrCysLeu 166

Db 430 CTGACACGCGCACACAGGCTACTCTGTTCGCCAGAGATACTGACTGTGGGACCTGCTG 489

QY 167 ProGlyPheTyrGlnHisGlyAspGlyCysValSerCysProThrSerThrLeuGlySer 186

Db 490 CTGCGCTTCTATGAACATGGCGATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 549

QY 187 CysProGluArgCysAlaAlaValCysGlyTrpArgGlnMetPheTrpValGlnValLeu 206

Db 550 TGTCCAGAGCGCTGTGCGCTGTGTGTGCTGAGGACAGATGTCTGCGGTCCAGGTGCTC 609

OY 207 LeuAlaGlyLeuValProLeuLeuGlyAlaThrLeuThrTyrThrArgHis 226
|||||
Db 610 CTGGCTGGCCTGTGTGCTCCCTCTGCTTGGGGCCACCTGACCTACACATACGGCCAC 669
OY 227 CysTrpProHisLysProLeuValThrAlaAspGluAlaGlyMetGluAlaLeuThrPro 246
|||||
Db 670 TGCTGGCCTCACAGCCCTGGTTACTGCAGATGAAGCTGGGATGGAGGCTCTGACCCCA 729
OY 247 ProProAlaThrHisLeuSerProLeuAspSerAlaHisThrLeuLeuAlaProProasp 266
|||||
Db 730 CCACCGGCCACCATCTGTCACTTGACAGCGGCCACACCTTCTAGCACCTCTGAC 789
OY 267 SerSerGluLysIleCysThrValGlnLeuValGlyAsnSerTrpThrProGlyTyrPro 286
|||||
Db 790 AGCAGTGAGAGATCTGCACCGCTCCAGTTGGTGGTACAGCTGGACCCCTGGCTACCCC 849
OY 287 GluThrGlnGluAlaLeuCysProGlnValThrTrpSerTrpAspGlnLeuProSerArg 306
|||||
Db 850 GAGACCCAGAGAGCGCTGCGCCGACAGTACATGCTCCGGGACACAGTGGCCACAGACA 909
OY 307 AlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSerProAlaGlySerProAla 326
|||||
Db 910 GCTCTGGCCCCGCTGCTGCGCCACACTCTCGCCACAGATCCCCAGCGGCTCGCCAGCC 969
OY 327 MetMetLeuGlnProGlyProGlnLeuTyrAspValMetAspAlaValProAlaArgArg 346
|||||
Db 970 ATGATGCTGCAGCCGGCCGCGACGCTTACGACGTGATGAGCGCGGTCCAGCGCGCGCC 1029
OY 347 TrpLysGluPheValArgThrLeuGlyLeuArgGluAlaGluIleGlyAlaValGluVal 366
|||||
Db 1030 TGGAAAGGAGTTCTGCGCAGCGCTGGGGCTGCGCGAGAGATCGAAGCCGTGAGGTG 1089
OY 367 GluIleGlyArgPheArgAspGlnGlnTyrGluMetLeuLysArgTrpArgGlnGln 386
|||||
Db 1090 GAGATCGCGCGCTTCCGAGACCAAGCAGTACGAGATGCTCAAGCGCTGGCGCAGCAGCAG 1149
OY 387 ProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMetGlyLeuAspGlyCysVal 406
|||||
Db 1150 CCGCGGGGCTCGAGCGCTTACGGCGGCTGAGCGCATGGGGCTGGACGGGCTGGCTG 1209
OY 407 GluAspLeuArgSerArgLeuGlnArgGlyPro 417
|||||
Db 1210 GAAGACTTGGCGCAGCCGCTGCAAGCGAGGCCG 1242
RESULT 11
HSU94503 1355 bp mRNA linear PRI 15-MAY-1997
LOCUS
DEFINITION Human lymphocyte associated receptor of death 2 mRNA, alternatively
spliced, complete cds.
ACCESSION U94503
VERSION U94503.1 GI:2071952
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 1355)
AUTHORS Sreaton,G.R., Xu,X.N., Olsen,A.L., Cowper,A.E., Tan,R.,
McMichael,A.J. and Bell,J.I.
TITLE LARD: a new lymphoid-specific death domain containing receptor
regulated by alternative pre-mRNA splicing
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)
MEDLINE 97272273
PUBMED 9114039
REFERENCE 2 (bases 1 to 1355)
AUTHORS Sreaton,G.R.
TITLE Direct Submission
JOURNAL Submitted (19-MAR-1997) Molecular Immunology Group, Institute of
Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3
9DU, UK
FEATURES
source location/Qualifiers
1..1355
/organism="Homo sapiens"

CDS
/db_xref="taxon:9606"
/cell_line="Hela"
/cell_type="lymphocyte"
1..762
/function="mediates apoptosis"
/note="LARD-2; similar to Fas and TNF-R1; possibly
soluble; truncated before the transmembrane domain"
/codon_start=1
/product="lymphocyte associated receptor of death 2"
/protein_id="AAC51308.1"
/db_xref="GI:2071953"
/translation="MEQRPKCAVAALLLVLGARAQGGTRSPKDCAGDFHKKIG
LFCCRGCPAGHYLKAPCTEPCGNSTCLVCPDQDFLAWENHNHSEARQACDEQASQV
ALENCSAVADTRCGCKPGWFEQVSCVSSPFYCQPCLDGALHRTLLCSRDY
DCGTLPGFYEHDGCVSPTSTLIGSCPERAAVCGWRQSRWCAGNASRTGMDRGEA
GEEGNHPTPTSCFQCSGSRCSWLALWSPSLGPP"
599..700
/note="Insertion compared to LARD 1a, deposited in GenBank
Accession Number U94501, probable retained intron leading
to premature transcriptional termination"
BASE COUNT 223 a 441 c 451 g 240 t
ORIGIN
Alignment Scores:
Pred. NO.: 1.49e-111 length: 1355
Score: 2271.50 matches: 416
Percent Similarity: 92.24% conservative: 0
Best Local Similarity: 92.24% mismatches: 1
Query Match: 97.78% indels: 35
DB: 9 gaps: 1
US-09-993-234-6 (1-417) x HSU94503 (1-1355)
OY 1 MetGluGlnArgProArgGlyCysAlaAlaValAlaAlaLeuLeuValLeu 20
|||||
Db 1 ATGAGACAGCGCGCGCGGCTGCGCGGCTGGCGCGGCTCTCTGCTGCTGCTG 60
OY 21 GlyAlaArgAlaGlnGlyThrArgSerProArgCysAspCysAlaGlyAspPheHis 40
|||||
Db 61 GGGGCCCCGGGCCAGAGGGGCGACTCGTAGCCCCAGGTGTAAGTGTGCCGCTGCCAC 120
OY 41 LysLysIleGlyLeuPheCysArgGlyCysProAlaGlnHisTyrLeuLysAlaPro 60
|||||
Db 121 AAGAGATTGGTCTGTTTGTTCAGAGGCTGCCACGGGCGCACTACCTGAAGGCCCT 180
OY 61 CysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAla 80
|||||
Db 181 TGCACGGAGCCCTGCGCAACTCCACTGCTGTGTGTCCCAAGACACACTTCTTGCC 240
OY 81 TrpGluAsnHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluAlaSer 100
|||||
Db 241 TGGAGAAACCAACCATTAATTCTGAATGTGCCCGCTGCAGGCTGTGATGAGCAGGCTCC 300
OY 101 GlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGly 120
|||||
Db 301 CAGGTGGCGCTGGAGAACTGTCAGACAGTGGCCGACACCCGCTGTGCTGAAGCCAGGC 360
OY 121 TrpPheValGluCysGlnValSerGlnCysValSerSerSerProPheTyrCysGlnPro 140
|||||
Db 361 TGGTTTGTGAGAGTGCAGGTGACCAATGTGTACAGCAGATTACACCTTCTACTGCCACCA 420
OY 141 CysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThr 160
|||||
Db 421 TGCCTAGACTGCGGGGCCCTGCACCGCCACACACAGGCTACTGTCTCCGACAGATACT 480
OY 161 AspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysPro 180
|||||
Db 481 GACTGTGGGACCTGCTGCTGCTTCTATGAACATGCGATGCGTGGCTGTGCTGCC 540
OY 181 ThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTyrParg----- 198
|||||
Db 541 ACGAGCACCCCTGGGAGCTGTCCAGAGCGGTGTGCGCTGTGCTGGAGCGCAGAGT 600

QY 198 ----- 198
Db 601 AGGTGGTGTGCTGGAAATGCGAGTGGGAGAACTGGGATGGACCGAGGGGAGGGGGGTGAG 660
QY 199 -----GlnMetPheTrpValGlnValLeu 206
Db 661 GAGGGGGGCAACCAACCAACCAACCAACCAAGCTGCTTTCAGTG-TTCTGGGTCCAGGTGCTC 719
QY 207 LeuAlaGlyLeuValValProLeuLeuGlyAlaThrLeuThrTrpArgHis 226
Db 720 CTGGCTGGCTGTGTGTCCTCCCTGCTGTGGGCCACCTGACCTACACATACCGCCAC 779
QY 227 CysTrpProHisLysProLeuValThrAlaAspGluAlaGlyMetGluAlaLeuThrPro 246
Db 780 TGCTGGCTCACAAGCCCTGCTTACTGAGATGAGCTGGATGAGGCTGTGACCCCA 839
QY 247 ProProAlaThrHisLysSerProLeuAspSerAlaHisThrLeuLeuAlaProProAsp 266
Db 840 CCACCGGCCACCCATCTGTCAACCTTGACAGCGCCACACACCTTCTAGCACTCCTGAC 899
QY 267 SerSerGluLysIleCysThrValGlnLeuValGlyAsnSerTrpThrProGlyTyrPro 286
Db 900 AGCAGTGAAGAAGATGCAACCGTCCAGTGTGGGTAACAGCTGGAACCCCTGGCTACCCC 959
QY 287 GluThrGlnGluAlaLeuCysProGlnValThrTrpSerTrpAspGlnLeuProSerArg 306
Db 960 GAGACCCAGAGAGCGCTCTGCCCGCAGGTGATGCTCTGGGACAGTTGTCACAGCAGA 1019
QY 307 AlaLeuGlyProAlaAlaAlaProThrLysSerProGluSerProAlaGlySerProAla 326
Db 1020 GCTCTTGGCCCCGCTGTCTGCGCCACACATCTGCCAGAGTCCCGCAGCGCTGCCAGCC 1079
QY 327 MetMetLeuGlnProGlyProGlnLeuTyrAspValMetAspAlaValProAlaArgArg 346
Db 1080 ATGATGCTGCAGCGCGCGCCCGCAGCTCTACGACGTGATGACCGCGGTCCACGCGCGC 1139
QY 347 TrpLysGluPheValArgThrLeuGlyLeuArgGluAlaGluIleGluAlaValGluVal 366
Db 1140 TGAAGGAGATTGCTGCGCACGCTGGGGCTGCGCGAGAGATCGAAGCCGTGAGGTG 1199
QY 367 GluIleGlyArgPheArgAspGlnGlnTyrGluMetLeuLysArgTrpArgGlnGln 386
Db 1200 GAGATCGGCCCTTCCAGACCAAGCAGATGCTCAAGCGCTGGCGCCACAGCAGCAG 1259
QY 387 ProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMetGlyLeuAspGlyCysVal 406
Db 1260 CCCGCGGGCTCGGAGCCGTTTACGGCGCCCTGAGCGCATGGGGCTGAGCGGCTGCTG 1319
QY 407 GluAspLeuArgSerArgLeuGlnArgGlyPro 417
Db 1320 GAAGACTTGGCGACGCGCGCTGACGCGCGCCCG 1352

RESULT 12

LOCUS ARI19656 1783 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 1 from patent US 6153402.
ACCESSION ARI19656
VERSION ARI19656.1 GI:14102355
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1783)
AUTHORS Yu,G.-L., Ni,J., Gentz,R.L. and Dillon,P.J.
TITLE Death domain containing receptors
JOURNAL Patent: US 6153402-A 1 28-NOV-2000;
FEATURES
source location/Qualifiers
1..1783

BASE COUNT 330 a 562 c 564 g 327 t
ORIGIN

Alignment Scores:

Pred. No.: 3,45e-111 Length: 1783
Score: 2267.00 Matches: 409
Percent Similarity: 97.39% Conservative: 1
Best Local Similarity: 97.15% Mismatches: 5
Query Match: 97.59% Indels: 6
DB: 6 Gaps: 1
US-09-993-234-6 (1-417) x ARI19656 (1-1783)
QY 3 GlnArgProArgGly-----CysAlaAlaValAlaAlaLeuLeu 16
Db 219 GAGGCCCCACGCTGGCGCAGCTGCGGAGAGTCAAGCAGCACCCTGTCCCCAGCGCTCCTC 278
QY 17 LeuValLeuLeuGlyAlaArgAlaGlnGlyThrArgSerProArgCysAspCysAla 36
Db 279 CTGGTGTGCTGGGGGGCCCGGGCCAGGGGGGCACTGCTAGCCCCAGGTGTGACTGTGCC 338
QY 37 GlyAspPheHisLysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyr 56
Db 339 GGTGACTTCCACAAGAAGATTGGTCTGTGTTGTTGTCAGAGAGCTGCCACGGGGCACTAC 398
QY 57 LeuLysAlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAsp 76
Db 399 CTGAAGGCCCTTGCACAGGAGCCCTGCGGCAACTCCACCTGCTGTGTGTCGCCAAGAC 458
QY 77 ThrPheLeuAlaTrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAsp 96
Db 459 ACCTTCTTGGCTGGGAGAACCAACATATCTGATGTGCCCCGCTGCCAGGCTGTGAT 518
QY 97 GluGlnAlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGly 116
Db 519 GAGCAGGCTTCCACAGGTGGCGCTGGAGAACTGTTACAGCAGTGGCCGACACCCGCTGTGCC 578
QY 117 CysLysProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerProPhe 136
Db 579 TGTAAAGCCAGGCTGGTTTGTGAGTGGCCAGGTACGCCAATGTGTCAAGAGTTCAACCTTTC 638
QY 137 TyrCysGlnProCysLysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSer 156
Db 639 TACTGCCAACCATGCCCTAGACTGCGGGGCCCTGCACCGCCACACAGGCTACTGTGTTCC 698
QY 157 ArgArgAspThrAspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCys 176
Db 699 CGCAGAGATACTGACTGTGGGACTGTGCTGCTGCTTCTATGAACATGGCGATGGCTGTC 758
QY 177 ValSerCysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGly 196
Db 759 GTGTCTGCTCCCCACAGACACCCCTGGGGAGCTGTGCCAGAGCGCTGTGCCGCTGTGTGCC 818
QY 197 TrpArgGlnMetPheTrpValGlnValLeuLeuAlaGlyLeuValProLeuLeu 216
Db 819 TGGAGGCAGATGTTCTGGGTCCAGGTGCTCCTGCTGGCTGTGTGTCCTCCCTCTGCTT 878
QY 217 GlyAlaThrLeuThrTyrThrTyrArgHisCysTrpProHisLysProLeuValThrAla 236
Db 879 GGGGCCACCCCTGACCTACACATACCGCCACTGTGCGCTTCACAAAGCCCTGTACTGCA 938
QY 237 AspGluAlaGlyMetGluAlaLeuThrProProProAlaThrHisLysSerProLeuAsp 256
Db 939 GATGAAGCTGGGATGGAGGCTCTGACCCACACCCAGCCGCCACCATCTGTACCCCTTGGAC 998
QY 257 SerAlaHisThrLeuLeuAlaProProAspSerSerGluLysIleCysThrValGlnLeu 276
Db 999 AGCGCCCAACACCCCTTCTAGACCTCCTGACAGCAGTGAAGAATCTGCACCGTTCAGTTG 1058
QY 277 ValGlyAsnSerTrpThrProGlyTyrProGluThrGlnGluAlaLeuCysProGlnVal 296
Db 1059 GTGGGTAACAGCTGACCCCTGGCTACCCCGAGACCAGGAGCGGCTGTGCCGAGGTG 1118
QY 297 ThrTrpSerTrpAspGlnLeuProSerArgAlaLeuGlyProAlaAlaAlaProThrLeu 316
Db 1119 ACATGCTCTGGGACCACTGCCCAGCAGAGCTCTTGGCCCCGCTGTGCGCCACACACTC 1178

QY 317 SerProgluSerProAlaglySerProAlaMetLeuGlnProglyProGlnLeuTyr 336
|||||
Db 1179 TCGCCAGAGTCCCGACCGGGCTCGCCAGCCATGCTTCAGCCGGGGCCGACCTCTAC 1238
QY 337 AspValMetAspAlaValProAlaArgArgTrrplysGluPheValArgThrLeuGlyLeu 356
|||||
Db 1239 GACGTGATGACCGCGTCCAGCGCGCGCTGGAAGAGTTCTGTCGCCACGCTGGGGCTG 1298
QY 357 ArgGluAlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnTyr 376
|||||
Db 1299 CGCGAGCGAGATCGAAGCCGTGGAGGTGGAGATCGGCCCTTCGAGACCAAGCAGTAC 1358
QY 377 GluMetLeuLysArgTrrPargGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAla 396
|||||
Db 1359 GAGATGCTCAAGCCTGGCGCCAGCAGCAGCCCGCGCTCGAGCCGTTACGGCGCC 1418
QY 397 LeuGluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGly 416
|||||
Db 1419 CTGGAGCGCATGGGGCTGGACGGCTGCTGGAAGACTTGGCAGCCGCGCTGCAGCGCGGC 1478
QY 417 Pro 417
|||
Db 1479 CCG 1481

RESULT 13 AX331947 1743 bp DNA linear PAT 09-JAN-2002
AX331947
LOCUS DEFINITION Sequence 2456 from Patent WO0194629.
ACCESSION AX331947
VERSION AX331947.1 GI:18122581

KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1
AUTHORS Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
Horrigan, S., Soppet, D.R. and Weaver, Z.
TITLE Cancer gene determination and therapeutic screening using signature
gene sets
JOURNAL Patent: WO 0194629-A 2456 13-DEC-2001;
Avalon Pharmaceuticals (US)
FEATURES Location/Qualifiers
source 1..1743

BASE COUNT 347 a 543 c 549 g 304 t
ORIGIN
Alignment Scores:
Pred. No.: 1.53e-110 Length: 1743
Score: 2254.50 Matches: 413
Percent Similarity: 91.57% Conservative: 0
Best Local Similarity: 91.57% Mismatches: 4
Query Match: 97.05% Indels: 35
DB: 6 Gaps: 1

US-09-993-234-6 (1-417) x AX331947 (1-1743)

QY 1 MetGluGlnArgProArgGlyCysAlaAlaValAlaAlaLeuLeuValLeuLeu 20
|||||
Db 69 ATGAGCAGCGCGCGGGGCTGCGCGCGGTGGCGGGCGCTCCCTCTGTGCTGCTG 128
QY 21 GAlaAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHis 40
|||||
Db 129 GGGGGCGGGCGCGCGGCACTCTAGCCCAAGGTGACTGTGCCGGTACTTCCAC 188
QY 41 LysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaPro 60
|||||
Db 189 AAGAAGATTGCTCTTTTGTTCAGAGAGCTGCCCAAGCGGGCACTACTGAAGGCCCT 248
QY 61 CysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAla 80
|||||

Db 249 TGCACGAGCCCTGGGCACTCCACCTGCTGTGTGTCCTCCCAAGACACCTTCTTGCC 308
QY 81 TrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSer 100
|||||
Db 309 TGGGAGAACCACCATATTCTGAATGTGCCCCGCTGCCAGGCCGTGTATGAGCAGCCCTCC 368
QY 101 GlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGly 120
|||||
Db 369 CAGGTGGCGCTGGAGAATCTTCAGCAGTGGCGGACACCCGCTGTGGCTGTAAAGCAGGC 428
QY 121 TrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCysGlnPro 140
|||||
Db 429 TGGTTTGTGAGTGGCAGGTCAAGCAATGTGTCAAGCAGTTACACCTTCTACTGCCAACCA 488
QY 141 CysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThr 160
|||||
Db 489 TGCCCTAGACTGGGGGGCTGCACCGCCACACAGGCTACTCTGTCCCGCAGATACT 548
QY 161 AspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysPro 180
|||||
Db 549 GACTGTGGACCTGCTGCTGCTCTTATGAACATGGCGATGGCTGCGTGTCTGCCCC 608
QY 181 ThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTrrParg----- 198
|||||
Db 609 ACGAGACCCCTGGGAGCTGTCCAGAGCGCTGTGCCGTGTCTGTGGCTGAGCAGAGT 668
QY 198 ----- 198
Db 669 AGGTGTGTGCTGGGAATGCCCGTGGGAGAAGTGGATGACCGAGGAGCGGGGTGAG 728
QY 199 -----GlnMetPheTrrPvalGlnValLeu 206
|||||
Db 729 GAGGGGGGCAACCAACCAACACACAGCTGCTTTCAGTG-TTCTGGGTCCAGGTGCTC 787
QY 207 LeuAlaGlyLeuValValProLeuLeuLeuGlyAlaThrLeuThrTyrTrpArgHis 226
|||||
Db 788 CTGGCTGGCCTGTGTGTGCTCCCTCTCTGCTGGGGCAACCTGACCTACACATACCGCCAC 847
QY 227 CysTrrProHisLysProLeuValThrAlaAspGluAlaGlyMetGluAlaLeuThrPro 246
|||||
Db 848 TGCTGGCTCACAAAGCCCTGTACTGCAGATGAAGCTGGAGTGAGGCTGTGACCCCA 907
QY 247 ProProAlaThrHisLeuSerProLeuAspSerAlaHisThrLeuLeuAlaProAsp 266
|||||
Db 908 CCACCGGCAACCATCTGTACACCTTGACAGCGGCCACACCTTCTAGCACCTCTGAC 967
QY 267 SerSerGluLysIleCysThrValGlnLeuValGlyAsnSerTrrThrProGlyTyrPro 286
|||||
Db 968 AGCAGTGAGAAGATCTGCACCGCTCCAGTTGGTGGGTAAACAGCTGGACCCCTGGCTACCCC 1027
QY 287 GluThrGlnGluAlaLeuCysProGlnValThrTrrSerTrrPargGlnLeuProSerArg 306
|||||
Db 1028 GAGACCCAGAGAGCGCTCTGCCCGCAGGTGACATGTTCTGGGACCAAGTTGCCACAGAGA 1087
QY 307 AlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSerProAlaGlySerProAla 326
|||||
Db 1088 GCTCTTGGCCCGCTGCTGCGCCACACTCTCGCCAGAGTCCCGCAGCGGCTGCGCAGCC 1147
QY 327 MetMetLeuGlnProGlyProGlnLeuTyrAspValMetAspAlaValProAlaArgArg 346
|||||
Db 1148 ATGATGCTGACGCGCGCGCGCAGCTCTACGACGTGATGACGCGGTGCCAGCGGGCGC 1207
QY 347 TrpLysGluPheValArgThrLeuGlyLeuArgGluAlaGluIleGluAlaValGluVal 366
|||||
Db 1208 TGGAAAGAGTTCGTGGCAGCGCTGGGGCTGCGCGAGCAGAGATCGAAGCCGTGGAGGTG 1267
QY 367 GluIleGlyArgPheArgAspGlnGlnTyrGluMetLeuLysArgTrrPargGlnGln 386
|||||
Db 1268 GAGATCGGTCTCTCCGAGACCAAGCAGATGATGATGCTCAAGCACTGGCGCCAGCAGCAG 1327
QY 387 ProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMetGlyLeuAspGlyCysVal 406
|||||
Db 1328 CCCGGGGCGCTCGGAGCGCTTTACGCGGGCCCTGAGCGCATGGGGCTGAGCGGCTGCGTG 1387

```

QY      407   GIUASpleuAArgSerArGLeuglInArgGlyPro 417
          |||
Db       1388 GAAGACTTGCGCAGCCGCCCTGCACGCTGGCCCCG 1420

RESULT 14
HMSWLSL1
LOCUS    HMSWLSL1
DEFINITION H.SWSL1                                1743 bp mRNA linear PRI 16-DEC-1996
ACCESSION Y093392
VERSION   Y093392.1 GI:1669690
KEYWORDS  wsl-1 gene; WSL-1R protein; WSL-S1 protein; WSL-S2 protein.
SOURCE    Homo sapiens.
ORGANISM  Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS   Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE     1 (bases 1 to 1743)
JOURNAL   Kitson,J., Raven,T., Jiang,Y.P., Goeddel,D.V., Giles,K.M.,
MEDLINE   Pun,K.T., Grinham,C.J., Brown,R. and Farrow,S.N.
PUBMED    A death-domain-containing receptor that mediates apoptosis
           Nature 384 (6607), 372-375 (1996)
           97088617
FEATURES
source    1..1743
           /organism="Homo sapiens"
           /db_xref="taxon:9606"
           /cell_type="T-lymphocyte"
           /tissue_type="lymphoid"
           1..1742
           /gene="wsl-1"
           1..610
           /gene="wsl-1"
           /number=1
           join(69..666,768..1423)
           /gene="wsl-1"
           /codon_start=1
           /product="WSL-1R protein"
           /protein_id="CAA70561.1"
           /db_xref="GI:1669693"
           /db_xref="SWISS-PROT:Q93038"
           /translation="MEQRPRGCAAVAAALLLVLLGARAOGTSPRCDCAGDFHKKIG
LFCCRGPAGHYLKAPCTEPCGNSTCLVCPDPTFLAMENHNSECARCOACDEOASQY
ALENCSAVADTRCGCKPGWFVEQCYSQCVSSPFYCQPLDCGALHRTRLCSRRDT
DCGTCLPGFYEHGDCGVSCPTSLGSCPERRCAAVCGWRMFVVYVLLIGA
TLTYTRYHCWPHKPLVTADAEAMEALTPPPATHLSPLDSAHTLIAPPDSSEKICTVOL
VGNSWTPGYPETOEALCPQYTWSMDQLPSRALGPAPAPILSPESPASPAMMLQPGPO
LYDVMAIVPARRWKEFYRTLGLREAIEAVEVEIGLEFRDOQYEMLKHWROQPAGIGA
VVAALERMGIDGVEDRLSRLOGRP"
           join(69..610,768..882)
           /gene="wsl-1"
           /codon_start=1
           /product="WSL-S1 protein"
           /protein_id="CAA70560.1"
           /db_xref="GI:1669692"
           /db_xref="SWISS-PROT:Q93038"
           /translation="MEQRPRGCAAVAAALLLVLLGARAOGTSPRCDCAGDFHKKIG
LFCCRGPAGHYLKAPCTEPCGNSTCLVCPDPTFLAMENHNSECARCOACDEOASQY
ALENCSAVADTRCGCKPGWFVEQCYSQCVSSPFYCQPLDCGALHRTRLCSRRDT
DCGTCLPGFYEHGDCGVSCPTVLGPGAPGWPCGPPPAWGHPDLHIPLLASQAPGYCR
"
CDS
           69..830
           /gene="wsl-1"
           /codon_start=1
           /product="WSL-S2 protein"
           /protein_id="CAA70559.1"
           /db_xref="GI:1669691"
           /db_xref="SWISS-PROT:Q93038"

```

```

exon
    /gene="ws1-1"
    /number=2
    667. .767
exon
    /gene="ws1-1"
    /number=3
    768. .1742
exon
    /gene="ws1-1"
    /number=4
    611. .666

BASE COUNT      347 a      543 c      549 g      304 t
ORIGIN

Alignment Scores:
Pred. No.:      1.53e-110      Length:      1743
Score:          2254.50      Matches:      413
Percent Similarity: 91.57%      Conservative: 0
Best Local Similarity: 91.57%      Mismatches: 4
Query Match:      97.05%      Indels:      35
DB:                9      Gaps:      1

US-09-993-234-6 (1-417) x HSNL1 (1-1743)

QY      1 MetGluGlnArgProArgGlyCysAlaAlaValAlaAlaLeuLeuValLeuLeu 20
      |||
Db      69 ATGGAGCAGCGCGCGGCGCTGCGCGGCGGCGGCGCTCTCTGTCGCTG 128

QY      21 GlyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHis 40
      |||
Db      129 GGGGGCCGGGCCAGGCGGCACCTCGTAGCCCAAGTGTGACTGTGCCGCTTCCAC 188

QY      41 LysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaPro 60
      |||
Db      189 AAGAAGATTGGTCTGTTTGTTCAGAGGCTGCCAGCGGGGACACTACTGAAGCCCT 248

QY      61 CysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAla 80
      |||
Db      249 TGCACGGAGCCCTGGGGAACCTCCACCTGCTGTGTGTCCCAAGACACTTCTTGCC 308

QY      81 TrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSer 100
      |||
Db      309 TGGGAGAACACCACCATATTTCTGAATGTGCCCGCTGCCAGGCTGTGATGACAGGCCCTCC 368

QY      101 GlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGly 120
      |||
Db      369 CAGGTGGCGCTGGAGAACTGTTCAAGCAGTGGCCGACACCCGCTGTGCTGTAAAGCCAGGC 428

QY      121 TrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCysGlnPro 140
      |||
Db      429 TGGTTGTGAGTGCAGGTCAGCCAAATGTTCAGATTCAACCCTTACTGCCAACCA 488

QY      141 CysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThr 160
      |||
Db      489 TGCCTAGACTGGGGGCCCTGCACCGCCACACAGGCTACTCTGTCCCGCAGAGATACT 548

QY      161 AspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysPro 180
      |||
Db      549 GACTGTGGGACCTGGCTTCTTAATGAACATGGCGATGGCTGCTCTGCCCC 608

QY      181 ThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTyrParg----- 198
      |||
Db      609 ACGAGCACCCCTGGGAGAGCTGTCCAGAGCCCTGTGCCGCTGTCTGTGGCTGAGGACAGAGT 668

QY      198 ----- 198

Db      669 AGGTGTGTGCTGGGAATGCGCGTGGAGAACTGGGATGACCGAGGAGCGGCTGAG 728

QY      199 -----GlnMetPheTrpValGlnValLeu 206
      |||

```


Db 729 GAGGGGCAACCAACACACCACAGCTCTTCAGTG-TTCTGGGTCCAGGTGCTC 787

QY 207 LeuAlaGlyLeuValValProLeuLeuGlyAlaThrLeuThrTyrThrArgHis 226

Db 788 CTGGCTGGCTTGGTGGTCCCTCTCTGCTGGGGCCACCTGACCTACACATACGGCCAC 847

QY 227 CysTrpProHisLysProLeuValThrAlaAspGluAlaGlyMetGluAlaLeuThrPro 246

Db 848 TGCTGGCTCACAAGCCCCCTGGTTACTGACATGAAGCTGGGATGGAGGCTCTGACCCCA 907

QY 247 ProProAlaThrHisLeuSerProLeuAspSerAlaHisThrLeuLeuAlaProProAsp 266

Db 908 CCACCGGCGCACCATCTGTACACCTTGGACAGCGCCACACCCCTTCTAGCACTCTCTGAC 967

QY 267 SerSerGluLysIleCysThrValGlnLeuValGlyAsnSerTrpThrProGlyTyrPro 286

Db 968 AGCAGTGAAGATCTGCACCGCTCCAGTTGGTGGTAAACAGCTGACCCCTGGCTACCCC 1027

QY 287 GluThrGlnGluAlaLeuCysProGlnValThrTrpSerTrpAspGlnLeuProSerArg 306

Db 1028 GAGACCCAGAGGGCTCTGCCCCGAGGTGACATGGTCTCTGGGACCAGTTGCCCAACAGA 1087

QY 307 AlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSerProAlaGlySerProAla 326

Db 1088 GCTCTGGCCCCGCTGCTGCGCCACACTCTGCCACAGAGTCCCCAGCGGCTCGCCAGCC 1147

QY 327 MetMetLeuGlnProGlyProGlnLeuTyrAspValMetAspAlaValProAlaArgArg 346

Db 1148 ATGATGCTGCAGCGGGGCCCGCAGCTCTACGACGTGATGGACGCGGTCCACGCGGCGC 1207

QY 347 TrpLysGluPheValArgThrLeuGlyLeuArgGluAlaGluIleGluAlaValGluVal 366

Db 1208 TGGAAAGAGTCTGCGCACAGCTGGGGCTGGCGGAGGACAGATGGAAGCCGTGAGGTG 1267

QY 367 GluIleGlyArgPheArgAspGlnGlnIntyrgluMetLeuLysArgTrpArgGlnGln 386

Db 1268 GAGATCGGTCTCTCCGAGACAGACAGTACGATGCTCAAGCACTGGCGCCACAGACAG 1327

QY 387 ProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMetGlyLeuAspGlyCysVal 406

Db 1328 CCGCGGGGCTCGGACCGCTTACGCGGGCCCTGGAGCGCATGGGGCTGGAGGGCTGCGTG 1387

QY 407 GluAspLeuArgSerArgLeuGlnArgGlyPro 417

Db 1388 GAAGACTTGGCGACCGCTGCAGCGTGCCCG 1420

RESULT 15

AF026070 1669 bp mRNA linear PRI 28-JAN-1998

LOCUS Homo sapiens death receptor 3 beta (DR3) mRNA, complete cds.

DEFINITION AF026070

ACCESSION AF026070

VERSION AF026070.1 GI:2570830

KEYWORDS

SOURCE

ORGANISM

Homo sapiens.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS

1 (bases 1 to 1669)

Warzocha,K., Ribeiro,P., Charlot,C., Renard,N., Colffier,B. and

Salles,G.

TITLE

A new death receptor 3 isoform: expression in human lymphoid cell

lines and non-Hodgkin's lymphomas

JOURNAL

Biochem. Biophys. Res. Commun. 242 (2), 376-379 (1998)

MEDLINE

98113360

PubMed

9446802

REFERENCE

2 (bases 1 to 1669)

Warzocha,K., Ribeiro,P., Renard,N., Charlot,C., Colffier,B. and

Salles,G.

TITLE

Direct Submission

JOURNAL

Submitted (19-SEP-1997) Hematology, CTRE Hospitalier Lyon-Sud,

Chemn du Grand Revoyet, Pierre Benite 69495, France

FEATURES

Location/Qualifiers

1..1669

source

gene

CDS

/organism="Homo sapiens"

/db_xref="taxon:9606"

/cell_line="Mieliki"

/note="Identified in human pre-B cell line Mieliki and in

patients with non-Hodgkin's lymphoma"

1..1669

/gene="DR3"

/note="Apo-3; TRAMP; LARD"

69..1349

/gene="DR3"

/note="DR3 beta; TNF receptor family member; alternatively

spliced product; contains 28 amino-acid extension to the

extracellular domain of the ordinary DR3 molecule"

/codon_start=1

/product="death receptor 3 beta"

/protein_id="AAC39556.1"

/db_xref="GI:2570831"

/translation="MEQRPFGCAVAALLLVLGARAOGGTRSPRCDCAGDFHKKIG

LFCCRGPAGHYLKAAPCTEPCCNSTCLVCPQDTFLAWENHNHSEARCAQACDEQASQV

ALENCSAVADTRCGCKPGWFVECOYSQVSSPFYCPCLDGAHLRHTRLCSRRDT

DCGTCLPGFEYEHGDGCVSCTPPPSLAGAPWGAQSAVPLSYAGRVGFVQVLLAG

LVPPLLGATLTYTYRHWCWPHKPLTYADEAGMEALTPPATHTSPDLSAHTLLAPDS

SEKITYQLVGNSTWPTGYPETQALCPQVTWSMDQLPSRALGPAPAPTLSPSPAGSP

AMMLQPGPOLYDMDAVPARMKERYTLGLREAEIIEAVEVEIGLFRDQYEMLKHW

QQQPAQDGAVVAALERMGLDCEVEDLSRLQRCP"

BASE COUNT 329 a 532 c 513 g 295 t

ORIGIN

Alignment Scores:

Pred. No.: 6.68e-110 Length: 1669

Score: 2242.00 Matches: 412

Percent Similarity: 96.72% Conservative: 1

Best Local Similarity: 96.49% Mismatches: 4

Query Match: 96.51% Indels: 11

DB: Gaps: 2

US-09-993-234-6 (1-417) x AF026070 (1-1669)

QY 1 MetGluGlnArgProArgGlyCysAlaAlaValAlaAlaLeuLeuValLeu 20

Db 69 ATGAGACAGCGGGCGGGGCTGCGGGGCTGGCGGGCGGGCTCTCTCTGCTGCTG 128

QY 21 GlyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHis 40

Db 129 GGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGG 188

QY 41 LysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaPro 60

Db 189 AAGAAGATTGCTGTTTGTGTCAGAGGCTGCCACGGGGGCACTACCTGAAGCCCCCT 248

QY 61 CysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAla 80

Db 249 TGCACGGAGCCCTGCCCAACTCCACCTGCTGTGTGTCGCCCAAGACACCTTCTGGGCC 308

QY 81 TrpGluAsnHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSer 100

Db 309 TGGAGAACCAACATTAATCTGAATGTGCCCGCTGCCAGGCTGTGATGAGAGGCTCC 368

QY 101 GlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGly 120

Db 369 CAGGTGGCGCTGAGAACTGTTACAGCAGTGGCGGACACCCGCTGTGGCTGTAGCCAGGC 428

QY 121 TrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCysGlnPro 140

Db 429 TGGTTTGTGAGTGCAGGTCAAGCAATGTGTACAGATTACACCTTCTACTGCCAACCA 488

QY 141 CysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThr 160

Db 489 TGCCTAGACTGCGGGGCTGCACCGCCACACACCGGCTACTCTGTTCGGCAGATACT 548

QY 161 AspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysPro 180

Db 549 GACTGTGGACCTGCTGCTGCTTCTATGAACATGGCGATGGCTGCTGCTGCTGCTGCTG 608

QY 181 ThrSer-----ThrLeuGlySerCysProGluArgCysAlaAla 193
|||
Db 609 ACCGC-ACCCCGCTCCCTTGACAGAGACACCTGGGGAGCTGTCCAGAGCGCTGTGCCGCT 667
QY 194 ValCysGlyTrpArgGln-----MetPheTrpValGlnValLeuAlaGlyLeuVa 211
|||||
Db 668 GTCTGTGGTGGAGGACAGTAGGTGTGTCTGGGTCACAGGTGCTCTGGCTGGCTTGT 727
QY 211 ValProLeuLeuLeuGlyAlaThrLeuThrTrpThrTyrrArgHisCysTrpProHisLy 231
|||||
Db 728 GGTCCCCCTCTGCTTGGGGCCACCCCTGACCTACACATACCCGCTGCTGGCTCACAA 787
QY 231 sProLeuValThrAlaAspGluAlaGlyMetGluAlaLeuThrProProAlaThrHi 251
|||||
Db 788 GCCCCGTGGTACTGACAGATGAAGCTGGGATGAGGCTCTGACCCCAACCCGACCCCA 847
QY 251 sLeuSerProLeuAspSerAlaHisThrLeuLeuAlaProProAspSerSerGluLysIl 271
|||||
Db 848 TCTGTACCCCTTGACAGCGCCACACCTTCTAGCACCTCTGACACAGAGTGAAGAT 907
QY 271 eCysThrValGlnLeuValGlyAsnSerTrpThrProGlyTrpProGluThrGlnGluAl 291
|||||
Db 908 CTGCACCGTCCAGTGGTGGTAAACAGTGAACCCCTGGCTACCCGAGACCCAGAGAGC 967
QY 291 aLeuCysProGlnValThrTrpSerTrpAspGlnLeuProSerArgAlaLeuGlyProAl 311
|||||
Db 968 GCTCTGCCCGCAGGTGACATGCTCTGGGACCAAGTGGCCAGAGAGCTCTGGCCCCGC 1027
QY 311 aAlaAlaProThrLeuSerProGluSerProAlaGlySerProAlaMetMetLeuGlnPr 331
||
Db 1028 TCGTGGCCCACTCTCGCCAGAGTCCCAAGCCGCTCGCCAGCATGATGTCAGACC 1087
QY 331 oGlyProGlnLeuTyrrAspValMetAspAlaValProAlaArgArgTrpLysGluPheVa 351
|||||
Db 1088 GGGCCCGCAGCTCTACGACGTGATGACGGCTGCCAGCGCGGCTGGAAGAGTTCTGT 1147
QY 351 LArgThrLeuGlyLeuArgGluAlaGluIleGluAlaValGluValGluIleGlyArgPh 371
|||||
Db 1148 GCGCAGCTGGGGCTGCGCGAGGACAGATCGAAGCCGTGAGGTGAGATCGGTCTCTT 1207
QY 371 eArgAspGlnGlnIntyrrGluMetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGl 391
|||||
Db 1208 CCGAGACCAAGATGATGATCAAGCACTGGCGCCAGCAGCAGCCCGCGGCTCGG 1267
QY 391 yAlaValTyrrAlaAlaLeuGluArgMetGlyLeuAspGlyCysValGluAspLeuArgSe 411
|||||
Db 1268 AGCCGTTTACGGCGGCTGGAGCGATGGGGCTGGACGGCTGCGTGGAAAGACTTGGCGCAG 1327
QY 411 rArgLeuGlnArgGlyPro 417
|||||
Db 1328 CCGCTTGCAGCGTGGCCCG 1346

Search completed: April 6, 2003, 21:07:27
Job time : 4876.17 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 6, 2003, 15:33:09 ; Search time 388.274 Seconds
(without alignments)
2418.610 Million cell updates/sec

Title: US-09-993-234-6
Perfect score: 2323
Sequence: 1 MEQRPRGCAVAALLLVLL.....ERMGLDGCVEDLRSLQRG 417

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2185239 segs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-O=/cgn2_1/USPTO.spool/US09993234/runat_27032003_115454_15312/app_query.fasta_1.2346
-DB=N_Geneseq_101002 -QFMT=fastap -SUFFIX=tns -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdl
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09993234_@CGN_1.1_660_@runat_27032003_115454_15312 -NCPU=6 -ICPU=3
-NO_XLPRXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_101002: *
1: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT: *
2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT: *
3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT: *
4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT: *
5: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT: *
6: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT: *
7: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT: *
8: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT: *
9: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT: *
10: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT: *
11: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT: *
12: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT: *
13: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT: *
14: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT: *
15: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT: *
16: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT: *
17: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT: *
18: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT: *
19: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT: *
20: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT: *
21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT: *
22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT: *
23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT: *
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2323	100.0	1254	18	AAT89427	Death domain conta
2	2323	100.0	1254	20	AAK00925	Death domain conta
3	2323	100.0	1254	21	AAC68777	Human death domain
4	2323	100.0	1634	18	AAT91180	Human apoptosis pr
5	2323	100.0	1634	22	AAH27782	Human genomic DNA
6	2323	100.0	1634	24	AAL47186	Human rheumatoid a
7	2323	100.0	1662	22	AAC91477	Human PRO779 cDNA.
8	2323	100.0	1662	24	ABK40265	cDNA encoding huma
9	2323	100.0	1847	19	AAV28700	Human apoptosis in
10	2267	97.6	1783	18	AAT89426	Death domain conta
11	2267	97.6	1783	20	AAK00924	Death domain conta
12	2267	97.6	1783	21	AAC68776	Human death domain
13	2254.5	97.1	1743	24	ABL64119	Breast cancer rela
14	2208	95.0	1250	22	AAF83770	Nucleotide sequenc
15	1556.5	67.0	4825	24	AAL47185	Human DR3 gene ass
16	1556.5	67.0	10797	23	ABK42690	Genomic sequence #
17	1404	60.4	1251	19	AAV28701	Mouse apoptosis in
18	1066	45.9	1438	18	AAT91179	Human apoptosis pr
19	1051	45.2	787	24	AAL47187	Human rheumatoid a
20	1039.5	44.7	816	24	ABL67258	Thyroid cancer rel
21	394.5	17.0	2130	24	ABK63694	Rat sequence differe
22	378.5	16.3	2173	11	AAQ06284	Rat Tumour Necrosi
23	374	16.1	1368	14	AAQ49332	Lambda-derived TNF
24	374	16.1	1368	21	AAA95105	Human TNFR1 coding
25	374	16.1	2062	13	AAQ20973	TNF-alpha binding
26	374	16.1	2062	13	AAQ24440	Encodes TNF-alpha
27	374	16.1	2088	12	AAQ10883	30kD TNF inhibitor
28	374	16.1	2088	22	AAC83946	Human 30 kDa TNF 1
29	374	16.1	2111	20	AAZ09170	Human tumour necro
30	374	16.1	2111	22	AAH48859	Human TNFBR-associ
31	374	16.1	2111	24	ABK84039	Human cDNA differe
32	374	16.1	2111	24	ABN95862	Gene #2360 used to
33	374	16.1	2161	21	AAZ48475	Human tumour necro
34	374	16.1	2161	24	ABK13194	Human tumour necro
35	374	16.1	2175	16	AAQ90513	p55 TNF-R gene. H
36	373	16.1	2170	14	AAQ50870	p55 Tumour necrosi
37	371	16.0	2111	12	AAQ10955	Encodes human 55kD
38	370	15.9	2176	12	AAQ12215	Type I TNF recepto
39	369	15.9	2141	11	AAQ06285	Human Tumour Necro
40	320	13.8	511	24	ABQ47530	Oligonucleotide fo
41	320	13.8	511	24	ABQ47531	Oligonucleotide fo
42	261	11.2	1334	11	ABQ06282	Plasmid Tumour Nec
43	253	10.9	511	24	ABQ47532	Oligonucleotide fo
44	253	10.9	511	24	ABQ47533	Oligonucleotide fo
45	233	10.0	1704	19	AAV34509	Human TNF receptor

ALIGNMENTS

RESULT 1	
AAT89427	
ID	AAT89427 standard; cDNA; 1254 BP.
AC	AAT89427;
DT	
XX	02-MAR-1998 (first entry)
DE	Death domain containing receptor DR3 cDNA.
XX	
KW	Death domain containing receptor; DR3; human; apoptosis;
KM	Inflammation; NF-kappaB; ds.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	sig_peptide
FT	Location/Qualifiers
FT	1..72
FT	/*tag- a

FT mat_peptide 73..1251
/*tag= b
PN WO9733904-A1.
XX 18-SEP-1997.
PD 17-OCT-1996; 96WO-US16849.
XX 12-MAR-1996; 96US-0013285.
PR (HUMA-) HUMAN GENOME SCI INC.
PA (UNMT) UNIV MICHIGAN.
PI Dillon PJ, Dixit VM, Gentz RL, Ni J, Yu G;
XX WPI, 1997-470812/43.
DR P-PSDB; AAW31517.
XX
PT Death domain containing receptor polypeptide(s) DR3 and DR3-V1
PT for activation of apoptosis and NF-kappab, antagonists can be used
PT to treat inflammatory diseases
PS Claim 6; Page 75-77; 108pp; English.
XX
CC This cDNA clone codes for human death domain containing receptor
CC DR3 (see AAW31517), a novel member of the tumour necrosis factor
CC receptor family. It was isolated from a HUVEC cDNA library.
CC Related death domain containing receptor DR3-V1 cDNA (see AAT89426)
CC was isolated from a human testis tumour cDNA library. The genes
CC have also been identified in cDNA libraries of foetal liver,
CC foetal brain, tonsil and leukocyte. Nucleic acids encoding full-
CC length or mature DR3, or the extracellular, transmembrane,
CC intracellular or especially the death domain of DR3, can be used to
CC produce recombinant polypeptides in transformed host cells. These
CC polypeptides can be used to treat diseases and disorders associated
CC with the inhibition of apoptosis. Antagonists can be used to treat
CC diseases and disorders associated with increased apoptosis and for
CC treating inflammatory diseases and disorders.
XX
SQ Sequence 1254 BP; 201 A; 420 C; 407 G; 226 T; 0 other;

Alignment Scores:
Pred. No.: 5.32e-122 Length: 1254
Score: 2323.00 Matches: 417
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-09-993-234-6 (1-417) x AAT89427 (1-1254)
QY 1 MetGluGlnArgProArgGlyCysAlaAlaValAlaAlaLeuLeuValLeu 20
DB 1 ATGAGAGCAGCGCGCGGGCTGCCGCGGGTGGCGGGCGGCTCTCTGCTGCTG 60
QY 21 GlyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHis 40
DB 61 GGGGCCCCGGCCAGGGCGGCACTGCTAGCCCCAGGTGTGACTGTGCCGCTGACTTCCAC 120
QY 41 LysLysIleGlyLeuPheCysArgGlyCysProAlaGlyHisTyrLeuLysAlaPro 60
DB 121 AAGAGATTGCTCTTTTGTTCAGAGGCTGCCAGCGGGGCACTAAGAGAGCCCT 180
QY 61 CysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAla 80
DB 181 TGCACGAGACCCCTGCGGCACTCCACTGCTGTGTGTCTCCCAAGACACCTTCTTGCC 240
QY 81 TrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSer 100
DB 241 TGGGAGAACACCATATATCTGAAATGTGCCCGCTGCCAGGCGCTGTGATGAGCAGGCTCC 300
QY 101 GlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGly 120

DB 301 CAGGTGGCGCTGGAGACTGTTTCAGCAGTGGCGCACACCGCTGTGGCTGTAAAGCCAGGC 360
QY 121 TrpPheValGluCysGlnValSerGlnCysValSerSerProPheThrCysGlnPro 140
DB 361 TGGTTTGTGAGTGGCAGGTTCAGCCAAATGTGTGACAGAGTTCACCCCTTCTACTGCCAACCA 420
QY 141 CysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThr 160
DB 421 TGCCCTAGACTGGCGGGCCCTGCACCGCCACACAGGCTACTCTGTTCGCCGACAGATACT 480
QY 161 AspCysGlyThrCysLeuProGlyPheTyrGlnHisGlyAspGlyCysValSerCysPro 180
DB 481 GACTGTGGAGACTGGCCCTGCCCTGGCTTCTATGAACATGGCGATGGCTGCTCTGCCCC 540
QY 181 ThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTrpArgGlnMet 200
DB 541 ACGAGCACCCCTGGGAGAGCTGTCCAGAGCGCTGTGCCGTGTCTGTGGCTGGAGGAGATG 600
QY 201 PheTrpValGlnValLeuLeuAlaGlyLeuValValProLeuLeuGlyAlaThrLeu 220
DB 601 TTCTGGGTCCAGGTGCTCTCTGGCTGGCTTGTGTGCCCTCTCTGTGGGGCCACCCCTG 660
QY 221 ThrTyrThrTyrArgHisCysTrpProHisLysProLeuValThrAlaAspGluAlaGly 240
DB 661 ACCTACACATACCGCCACTGCTGGCTGCACAAAGCCCTGTGTACTGCAGATGAAGTGGG 720
QY 241 MetGluAlaLeuThrProProProAlaThrHisLeuSerProLeuAspSerAlaHisThr 260
DB 721 ATGAGAGCTGTGACCCACACACCGGCCACCATCTGTACACCTTGAGACAGCGCCACACC 780
QY 261 LeuLeuAlaProProAspSerSerGluLysIleCysThrValGlnLeuValGlyAsnSer 280
DB 781 CTTCTAGCACTCTCTGACAGACAGTGAAGAATCTGCACCGCTCAGTGTGGTAAACAGC 840
QY 281 TrpThrProGlyTyrProGluThrGlnGluAlaLeuCysProGlnValThrTrpSerTrp 300
DB 841 TGGACCCCTGGCTACCCCGAGAGACCAGAGCGGCTCTGCCGACAGTGTGCTGTGG 900
QY 301 AspGlnLeuProSerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSer 320
DB 901 GACCAGTTGCCACAGACAGAGCTCTTGGCCCCGCTGCTGCCGCCACACTCTGCCAGAGTCC 960
QY 321 ProAlaGlySerProAlaMetMetLeuGlnProGlyProGlnLeuTyrAspValMetAsp 340
DB 961 CCAGCCGCTGCCACAGCCATGATGCTGCACCGGGCCCGGAGCTCTACGACGTGATGAGAC 1020
QY 341 AlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGluAlaGln 360
DB 1021 GCGGTCCACAGCGCGGCTGTGAAGAGTTCGTGCGCACGCTGGGGCTGGCGAGGACAG 1080
QY 361 IleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGluMetLeuLys 380
DB 1081 ATCGAAGCCGTGGAGGTGAGATCGCCGCTTCCGAGACCAAGATAGATGCTCAAG 1140
QY 381 ArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMet 400
DB 1141 CGCTGGCGCCAGACAGACCGCGGCGCTCGAGAGCCGTTTACGGCGCCCTGGAGCCCATG 1200
QY 401 GlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 417
DB 1201 GGGCTGAGAGCGGCTGCTGAAGACTTGGCGAGCCGCTGCAGCGGCGCCG 1251

RESULT 2
AAAX00925
ID AAAX00925 standard; cDNA; 1254 BP.
XX
AC AAAX00925;
XX
DT 25-MAR-1999 (first entry)
XX
DE Death domain containing receptor polypeptide (DR3) encoding cDNA.
XX

```
KW Death domain; receptor; DR3-V1; DR3; recombinant; ds.
XX Homo sapiens.
XX Key 1..1254
FH CDS Location/Qualifiers
FT sig_peptide /tag- a
FT mat_peptide /product- "Death domain containing receptor DR3"
FT /tag- b
FT /tag- c
PN JP11000170-A.
XX 06-JAN-1999.
XX 12-MAR-1997; 97JP-0057503.
XX 06-FEB-1997; 97US-0037341.
PR 12-MAR-1996; 96US-0013285.
PR 17-OCT-1996; 96US-0028711.
XX (HOMA-) HUMAN GENOME SCI INC.
PA (UNMI ) UNIV MICHIGAN.
XX
DR WP1; 1999-124390/11.
DR P-PSDB; AAW95538.
XX
PT New death domain containing receptor and recombinant vector -
PT optionally comprising leader sequence
XX
PS Claim 6; Fig 3; 50pp; Japanese.
XX
CC The invention provides nucleotide sequences encoding death domain
CC containing receptor polypeptides DR3-V1 and DR3. The DR3-V1 cDNA clone
CC is contained in ATCC deposition No. 97456 and the DR3 cDNA clone is
CC contained in ATCC deposition No. 97757. Recombinant vectors comprising
CC the nucleic acid sequences and optionally the leader sequences are
CC used for the recombinant production of the proteins. The present
CC sequence represents a cDNA encoding the death domain containing
CC receptor polypeptide (DR3).
XX
SQ Sequence 1254 BP; 201 A; 420 C; 407 G; 226 T; 0 other;
XX
Alignment Scores:
Pred. No.: 5.32e-122 Length: 1254
Score: 2323.00 Matches: 417
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 20 Gaps: 0
US-09-993-234-6 (1-417) x AAX00925 (1-1254)
QY 1 MetGluGlnArgProArgGlyCysAlaAlaValAlaAlaLeuLeuValLeuLeu 20
DB 1 ATGAGACAGCGCGCGCGCGCGCGCGCGCGCGCGCTCCTCGTGTGCTGCTG 60
QY 21 GlyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHis 40
DB 61 GGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
QY 41 LysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaPro 60
DB 121 AAGAAGATGTGTGTTGTTCAGAGAGCTGCCAGCGGGGACACTACCTGAAGCCCT 180
QY 61 CysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAla 80
DB 181 TGCACGAGCCCTGCGGCACTCACCTGCTGTGTCTCCCAAGACACCTTTCTTGCC 240
QY 81 TrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSer 100
```

```
DB 241 TGGAGAACACCATTAATTCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGCCCTCC 300
QY 101 GlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGly 120
DB 301 CAGGTGGCGCTGGAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGGCTGTAAAGCCAGGC 360
QY 121 TrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCysGlnPro 140
DB 361 TGGTTTGTGAGTGCAGGTCAGCCAAATGTGTACAGCAGTTACCCCTTACTGCAACCA 420
QY 141 CysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThr 160
DB 421 TGCTTAGACTGGGGGCGCTGCACCGCCACACAGCGCTACTCTGTCCCGCAGATACT 480
QY 161 AspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysPro 180
DB 481 GACTGTGGACCTGCTGCTGCTGCTTCTATGAACAATGGCGATGGCTGCTGCTGCC 540
QY 181 ThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTrpArgGlnMet 200
DB 541 ACGAGCACCCCTGGGAGCTGTCCAGAGCGCTGTGCCCTGTCTGTGGCTGAGCAGATG 600
QY 201 PheTrpValGlnValLeuLeuAlaGlyLeuValValProLeuLeuGlyAlaThrLeu 220
DB 601 TTCTGGGTCCAGGTGTCTCTGCTGCTGCTGCTGCTGTGTGCTGCTGCTGCTGCTGCTG 660
QY 221 ThrTyrThrTyrArgHisCysTrpProHisLysProLeuValThrAlaAspGluAlaGly 240
DB 661 ACCTACACATACCGCCAGCTGCTGCGCTCACAAGCCCTGTGTACTGCAGATGAAGCTGGG 720
QY 241 MetGluAlaLeuThrProProProAlaThrHisLeuSerProLeuAspSerAlaHisThr 260
DB 721 ATGAGAGCTGTGACCCACACACCGGCCACCAATCTGTACACCTTGACAGCGCCACAC 780
QY 261 LeuLeuAlaProProAspSerSerGluLysIleCysThrValGlnLeuValGlyAsnSer 280
DB 781 CTCTTAGACACCTCCTGTGACAGCAGTGAAGATCTGCACCGCTCCAGTTGGTGGTAACAGC 840
QY 281 TrpThrProGlyTyrProGluThrGlnGluAlaLeuCysProGlnValThrTrpSerTrp 300
DB 841 TGGACCCCTGGCTACCCCGAGACCCAGAGAGCGGCTCTGCCCGCAGGTGACATGCTCTGG 900
QY 301 AspGlnLeuProSerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSer 320
DB 901 GACCAGTTGCCAGCAGAGCTCTTGCGCCCGCTGTGCGCCACACTCTGCCAGAGTCC 960
QY 321 ProAlaGlySerProAlaMetMetLeuGlnProGlyProGlnLeuTyrAspValMetAsp 340
DB 961 CCAAGCGGCTGCGCAGCATGATGCTGCAGCGCGGCCCGCAGCTTACGACGATGATGAC 1020
QY 341 AlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGluAlaGlu 360
DB 1021 GCGGTCCAGCGCGCGCTGGAAGAGTTCGTGCGCAGCGCTGGGGCTGCCGAGCAGAG 1080
QY 361 IleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGluMetLeuLys 380
DB 1081 ATCGAAGCCGTGGAGTGAAGATCGGCCGCTTCCGAGACACAGCAGTACGAGATGCTCAAG 1140
QY 381 ArgTrpArgGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMet 400
DB 1141 CGCTGGCGCAGCAGACAGCCCGCGGCGCTGAGCGCTTTCACGCGGCGCTGAGCGCATG 1200
QY 401 GlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 417
DB 1201 GGGCTGAGCGGCTGCTGGAAGACTTGCGCAGCGCCTGACGCGGCGGCCG 1251
RESULT 3
AAC68777
ID AAC68777 standard; cDNA; 1254 BP.
XX AAC68777;
AC
XX 20-FEB-2001 (first entry)
DT
```


XX Human death domain containing receptor DR3 coding sequence.
XX
KW Human; death domain containing receptor; DR3; cancer;
KW autoimmune disorder; inflammation; cardiovascular disorder; infection;
KW neurodegenerative disease; angiogenesis; ss.
OS Homo sapiens.
XX
PN WO200064465-A1.
XX
PD 02-NOV-2000.
XX
PF 21-APR-2000; 2000MO-US10741.
XX
PR 22-APR-1999; 99US-0130488.
PR 28-MAY-1999; 99US-0136741.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (UNMI) UNIV MICHIGAN.
PA (YUGG/) YU G.
PA (NIJJ/) NI J.
PA (GENT/) GENTZ R L.
PA (DILL/) DILLON P J.
PA (DIXI/) DIXIT V M.
XX
PI YU G, NI J, Gentz RL, Dillon PJ, Dixit VM;
XX
DR WPI; 2000-687263/67.
DR P-PSDB; AAB36265.
XX
PT Treating graft-versus-host disease, cancer, immunodeficiency or an
PT autoimmune disease comprising administering an antibody to Death Domain
PT Containing Receptor proteins and a second therapeutic agent -
XX
PS Example 2B; Fig 2; 273pp; English.
XX
CC The present invention provides the protein and coding sequences for two
CC death domain containing receptors, designated DR3 and DR3-V1. These
CC receptors are involved in apoptosis, and the sequences given can be used
CC in the treatment of cancers, infections, cardiovascular disorders such as
CC arrhythmias, ischaemia, aneurysms, arterial occlusive diseases, embolisms
CC and congenital heart defects, neurodegenerative diseases including
CC Alzheimer's and Parkinson's diseases, autoimmune disease such as multiple
CC sclerosis, arthritis, diabetes, Graves' disease, asthma and psoriasis,
CC and to promote angiogenesis and wound healing.
XX
SQ Sequence 1254 BP; 201 A; 420 C; 407 G; 226 T; 0 other;

Alignment Scores:
Pred. No.: 5.32e-122 Length: 1254
Score: 2323.00 Matches: 417
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-09-993-234-6 (1-417) x AAC68777 (1-1254)
QY 1 MetGluGlnArgProArgGlyCysAlaAlaValAlaAlaAlaLeuLeuValLeuLeu 20
Db 1 ATGGAGCAGCGCGCGCGGCTGCGCGCGGCTGCGCGCGGCTCCTCTGCTGCTG 60
QY 21 GlyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHis 40
Db 61 GGGGCCCCGGCCAGGGGCGACTGCTAGCCCCCAGGTGTGACTGTGCCGTTCAC 120
QY 41 LysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuYsAlaPro 60
Db 121 AAGAAGATTGCTGTTTGTTCAGAGGCTGCCCGGGGCACTACCTGAAGCCCCCT 180
QY 61 CysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAla 80
|||||

Db 181 TGCACGAGCCCTGCGGCACTCCACCTGCTGTGTGTCCCAAGACACCTTCTGGCC 240
QY 81 TrpGluAsnHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluAlaSer 100
Db 241 TGGAGAACCAACCAATAATTCTGAATGTGCCCGCTGCCAGGCTGTGATGACAGGCTCC 300
QY 101 GlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysProGly 120
Db 301 CAGGTGGCGCTGGAGAAGTGTTCAGCAGTGGCCGACACCCCGCTGTGGCTGTAAGCCAGGC 360
QY 121 TrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCysGlnPro 140
Db 361 TGGTTGTGGAGTGCACAGGTCCAGCAATGTGTACAGCAGTTCACTTACTGCCAACCA 420
QY 141 CysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgAspThr 160
Db 421 TGCCTAGACTGCGGGCCCTGCACCGCCACACAGCGCTACTCTGTCCCGCAGAGTACT 480
QY 161 AspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysPro 180
Db 481 GACTGTGGAGACTCCCTGCTGCTCTATGAACATGGCGATGGCTGCTCTGCCCC 540
QY 181 ThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTyrArgGlnMet 200
Db 541 ACGAGCACCTGGGGAGCTGTCCAGAGCGCTGTGCCGCTGTCTGTGGCTGAGGCGCATG 600
QY 201 PheTrpValGlnValLeuLeuAlaGlyLeuValValProLeuLeuGluAlaThrLeu 220
Db 601 TTCTGGGTCCAGGTGCTCTGCTGGGCTGTGTGTCCTCCCTCTGCTGGGGCCACCCTG 660
QY 221 ThrTyrThrTyrArgHisCysTrpProHisLysProLeuValThrAlaAspGluAlaGly 240
Db 661 ACCTACACATACCGCCACTGCTGGCTTCAACAAGCCCTGCTTACTGCAGATGAAGCTGGG 720
QY 241 MetGluAlaLeuThrProProAlaThrHisLeuSerProLeuAspSerAlaHisThr 260
Db 721 ATGGAGGCTCTGACCCACCCAGCGGCCACCATCTGTACCTTGGACAGCGCCACACC 780
QY 261 LeuLeuAlaProProAspSerSerGluLysIleCysThrValGlnLeuValGlyAsnSer 280
Db 781 CTTCCTAGCACCTCTGTACAGAGTGAAGAATCTGCACCGTCCAGTTGGTGGTAAACAGC 840
QY 281 TrpThrProGlyTyrProGluThrGlnGluAlaLeuCysProGlnValThrTrpSerTrp 300
Db 841 TGGACCCCTGGTACCCTGAGACCCAGAGGCGCTGTGCCCGCAGGTGACATGCTCCTGG 900
QY 301 AspGlnLeuProSerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSer 320
Db 901 GACCAGTTGCCACAGAGACTCTTGGCCCCGCTGTGCGCCACACTCTCGCCAGAGTCC 960
QY 321 ProAlaGlySerProAlaMetMetLeuGlnProGlyProGlnLeuTyrAspValMetAsp 340
Db 961 CCAGCCGGCTCGCCAGCCATGATGCTGCAGCCGGGGCCCGCAGCTCTACGACGTGATGGAC 1020
QY 341 AlaValProAlaArgArgTyrPlyGluPheValArgThrLeuGlyLeuArgGluAlaGlu 360
Db 1021 GCGGTCCAGCGCGGCTGGAAGAGTTCGTGCGCACCGCTGGGGCTGCGGAGGCGAGAG 1080
QY 361 IleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGluMetLeuLys 380
Db 1081 ATCGAAGCCGTGAGGTGAGATCGGCGCTTCGAGACACAGCAGTACGATGCTCAAG 1140
QY 381 ArgTrpArgGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMet 400
Db 1141 CGCTGGCGCCAGCAGACGCCCGGGCTCGGAGCCGTTTACGCGGCCCTGGAGCGCATG 1200
QY 401 GlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 417
Db 1201 GGGCTGAGCGGCTGGTGAAGACTTGGCAGCGCCCTGCAGCGCGGCCG 1251
RESULT 4
AAT91180
ID AAT91180 standard; cDNA; 1634 BP.

XX AAT91180;
AC 14-APR-1998 (first entry)
XX
DE Human apoptosis protein Apo-3 cDNA clone FH20.57.
XX
KW Apo-3; apoptosis; human; therapy; drug screening; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 89..1342
FT sig_peptide 89..160
FT /*tag- b
FT /*tag- determined by hydropathy analysis
FT mat_peptide 161..1339
FT /*tag- c
XX
PN W09737020-A1.
XX
PD 09-OCT-1997.
XX
PF 31-MAR-1997; 97WO-US05230.
XX
PR 23-SEP-1996; 96US-0710802.
PR 01-APR-1996; 96US-0625328.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ;
XX
DR WPI: 1997-503105/46.
XX
PT Polypeptide(s) Apo-3 and Apo-2LI - useful for regulating apoptosis
PT in mammalian cells
XX
PS Example 1; Page 45-46; 70pp; English.
XX
CC cDNA clone FH20.57 (ATCC 55820) codes for a novel polypeptide (see
CC W26709), designated Apo-3, that stimulates or induces apoptotic
CC activity in mammalian cells. It was isolated from a human foetal
CC heart cDNA library by screening with probes (see T91183-84) based
CC on an EST sequence (Genbank locus W71984) that showed homology to
CC the intracellular domain of human TNFR1 and CD95. Amino acid
CC residues 1-181 of Apo-3 are identical to another novel apoptosis
CC polypeptide, Apo-2LI (see W26708). Nucleic acids encoding Apo-3
CC can be used diagnostically for tissue-specific typing and to
CC produce recombinant Apo-3 polypeptides, especially the
CC extracellular domain (amino acids 1-198) or death domain (amino
CC acids 338-417). Apo-3 can be used to induce apoptosis or
CC NF-kappa-N- or JNK-mediated gene expression for therapeutic
CC purposes. Non-human transgenic animals containing cells that
CC express Apo-3 nucleic acid, and knockout animals containing
CC cells that have an altered Apo-3 gene, can be used in drug
CC screening and development.
XX
SQ Sequence 1634 BP; 300 A; 528 C; 519 G; 287 T; 0 other;
XX
Alignment Scores:
Pred. No.: 7.06e-122 Length: 1634
Score: 2323.00 Matches: 417
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0
US-09-993-234-6 (1-417) x AAT91180 (1-1634)
QY 1 MetGluGlnArgProArgGlyCysAlaAlaValAlaAlaAlaLeuLeuValLeuLeu 20
Db 89 ATGAGACAGCGCGCGCGCTGCGCGCGGTGGCGCGGCTCTCTGCTGCTG 148

QY 21 GlyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHis 40
Db 149 GGGGCCCCGGCCAGGGCGGCACTGAGCCCCAGGTGACTGTGCGGTACTTCCAC 208
QY 41 LysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlnHisTyrLeuLysAlaPro 60
Db 209 AAGAAGATTGGTCTGTTTGTTCAGAGGCTGCCAGCGGGGCACTACCTGAGAGCCCT 268
QY 61 CysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAla 80
Db 269 TGCACGGAGCCCTGCGGCACTCCACCTGCTGTGTGCCCAAGACACCTTCTTGCC 328
QY 81 TrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluAlaSer 100
Db 329 TGGAGAACCCACCATTAATTCGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCTCC 388
QY 101 GlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGly 120
Db 389 CAGGTGGCGCTGAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGGCTGTAAGCCAGCC 448
QY 121 TrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCysGlnPro 140
Db 449 TGGTTTGTGAGTGCACAGTCCAGCCAAATGTGTACAGACTTACCTTACTGCCAACCA 508
QY 141 CysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThr 160
Db 509 TGCCTAGACTGCGGGGCGCCGTGACCCGACACACGCGTACTCTGTCCCGCAGAGATACT 568
QY 161 AspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysPro 180
Db 569 GACTGTGGGACCTGCTGCTGCTTCTATGAAACATGGCGATGGCTGCTGCTGCTGCC 628
QY 181 ThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTyrPargGlnMet 200
Db 629 ACGAGCACCCCTGGGAGCTGTCCAGAGCGCTGTGCCGTGTGTGGCTGAGGACAGATG 688
QY 201 PheTrpValGlnValLeuLeuAlaGlyLeuValProLeuLeuGluAlaThrLeu 220
Db 689 TTCTGGGTCCAGGTGCTCTGCTGGCTGTGTGTCCTCTGCTGGGGCCACCTG 748
QY 221 ThrTyrThrTyrArgHisCysTyrProHisLysProLeuValThrAlaAspGluAlaGly 240
Db 749 ACCTACACATACCGCCACTGTGCTGCTCACAAGCCCTGTGTTACTGCAGATGAAGCTGG 808
QY 241 MetGluAlaLeuThrProProProAlaThrHisLysSerProLeuAspSerAlaHisThr 260
Db 809 ATGAGAGCTCTGACCCACCCAGCCGCGCCACCATCTGTGACCTTGGACAGCGGCCACACC 868
QY 261 LeuLeuAlaProProAspSerSerGluLysIleCysThrValGlnLeuValGlyAsnSer 280
Db 869 CTCTAGACACTCTCTGACAGAGTGAAGAATCTGCACCGTCCAGTTGGTGAACAGC 928
QY 281 TrpThrProGlyTyrProGluThrGlnGluAlaLeuCysProGlnValThrTyrSerTyr 300
Db 929 TGGACCCCTGGCTACCCCGAGACCCAGAGGCGCTGTGCCCGCAGGTGACATGTCTGG 988
QY 301 AspGlnLeuProSerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGlnSer 320
Db 989 GACCAAGTTGCCACAGACAGACTTGGCCCCCGCTGCTGCGCCACACTCTGCCACAGATCC 1048
QY 321 ProAlaGlySerProAlaMetMetLeuGlnProGlyProGlnLeuTyrAspValMetAsp 340
Db 1049 CCAGCGGGCTGCGCCAGCCATGATGCTGCAGCGGGGCCCCAGCTTACGACGTGATGAC 1108
QY 341 AlaValProAlaArgArgTyrPlyGluPheValArgThrLeuGlyLeuArgGluAlaGlu 360
Db 1109 GCGGTCCAGCGCGCGCTGGAAGAGTTCGTGCGCACGCTGGGGCTGCGCGAGGACAG 1168
QY 361 IleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGluMetLeuLys 380
Db 1169 ATCGAAAGCCGTGAGGTGAGATCGCGCGCTTCCGAGACACAGCATGAGATGCTCAAG 1228

QY 381 ArgTrpArgGlnGlnInProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMet 400
Db 1229 CGCTGGCGCCAGACAGACAGCCCGGGCTCGGAGCCGTTTACGCGCGCTGAGCGCATG 1288
QY 401 GlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 417
Db 1289 GGGCTGGACGCGCTCGTGAAGACTTGCAGAGCCGCTGCAGCGCGGCCG 1339

RESULT 5
AAH27782

ID AAH27782 standard; DNA; 1634 BP.

AC AAH27782;

DT 15-AUG-2001 (first entry)

DE Human genomic DNA encoding a rheumatoid arthritis associated protein.

KW Rheumatoid arthritis; transmembrane protein; human; ds.

OS Homo sapiens.

FT Key Location/Qualifiers

FT CDS 89..1342

FT /*tag= a

FT /product= "Rheumatoid arthritis associated protein"

PN WO200132921-A2.

PD 10-MAY-2001.

PF 01-NOV-2000; 2000WO-JP07690.

PR 01-NOV-1999; 99JP-0310805.

PA (SHIO/) SHIOZAWA S.

PI Shiozawa S, Konishi Y;

DR WPI; 2001-308750/32.

DR P-PSDB; AAB97370.

PT Diagnosing rheumatoid arthritis by probing digested human genomic DNA
PT or comparing expression of mRNA or polypeptide of a region of
PT transmembrane protein

PS Claim 1; Page 14-18; 21pp; Japanese.

CC This invention relates to a method of diagnosing chronic rheumatoid
CC arthritis by digesting human genomic DNA with EcoRI and hybridizing it
CC with a probe containing a fragment of the present sequence which
CC represents DNA encoding a transmembrane protein. The method is used for
CC the diagnosis of chronic rheumatoid arthritis, and for developing new
CC treatments.

SQ Sequence 1634 BP; 300 A; 528 C; 519 G; 287 T; 0 other;

Alignment Scores:

Pred. No.: 7.06e-122

Score: 2323.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 100.00%

DB: 22

Length: 1634

Matches: 417

Conservative: 0

Mismatches: 0

Indels: 0

Gaps: 0

US-09-993-234-6 (1-417) x AAH27782 (1-1634)

QY 1 MetGluGlnArgProArgGlyCysAlaAlaValAlaAlaLeuLeuValLeu 20
Db 89 ATGGAAGCAGCGCGCGGCTGCGCGGCTGCGCGCGCTCTCTGCTGCTG 148
QY 21 GlyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHis 40

Db 149 GGGGGCCGGCCAGGGCCGACCTGCTAGCCCAAGGTGTGACTGTGCCGTGACTTCCAC 208
QY 41 LysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaPro 60
Db 209 AAGAAGATTGGTCTGTTTGTGTGACAGAGGCTGCCAGCGGGGACACTTGAAGGCCCT 268
QY 61 CysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAla 80
Db 269 TGCACGAGAGCCCTGCCGCAACTCCACCTGCTGTGTGTCCCAAGACACCTTCTTGCC 328
QY 81 TrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSer 100
Db 329 TGGAGAACCAACATTAATTGAAATGTGCCCTGCCAGGCTGTGATGAGCAGGCTCC 388
QY 101 GlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGly 120
Db 389 CAGTGGCGCTGGAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGGCTGAAGCCAGGC 448
QY 121 TrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCysGlnPro 140
Db 449 TGGTTTGTGAGTGCACAGGTGCAGCCATGTGTACAGCAGTTCACTTCTTACTGCCAACCA 508
QY 141 CysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThr 160
Db 509 TGCCTAGACTGCGGGGCCCTGCACCGCCACACAGCGCTACTCTGTTCGCCAGAGTACT 568
QY 161 AspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysPro 180
Db 569 GACTGTGGACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 628
QY 181 ThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTyrPargGlnMet 200
Db 629 ACGAGACCTTGGGAGGCTGTCCAGAGCGCTGTGCGCTGTGTGCTGTGAGGCGATG 688
QY 201 PheTyrValGlnValLeuLeuAlaGlyLeuValValProLeuLeuGlyAlaThrLeu 220
Db 689 TTCTGGGTCCAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 748
QY 221 ThrTyrThrTyrArgHisCysTyrProHisLysProLeuValThrAlaAspGluAlaGly 240
Db 749 ACCTACACATACCGCCACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 808
QY 241 MetGluAlaLeuThrProProAlaThrHisLeuSerProLeuAspSerAlaHisThr 260
Db 809 ATGGAGGCTGTGACCCCAACCCAGCCCATCTGCACCTTGACACAGCCGCCACACACC 868
QY 261 LeuLeuAlaProProAspSerSerGluLysIleCysThrValGlnLeuValGlyAsnSer 280
Db 869 CTCTACAGCAGCTCTGACAGCAGTGAAGAAGATGTGACCCGTCAGTGTGGGTAAACAGC 928
QY 281 TrpThrProGlyTyrProGluThrGlnGluAlaLeuCysProGlnValThrTyrPserTrp 300
Db 929 TGGACCCCTGGCTACCCGAGAGACCCAGAGGCGCTCTGCCCGCAGGTTGACATGTCTCTGG 988
QY 301 AspGlnLeuProSerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSer 320
Db 989 GACCAGTTGCCAGCAGAGCTCTTGGCCCGCTGCTGCGCCACACACTTCTGCCAGAGTCC 1048
QY 321 ProAlaGlySerProAlaMetLeuGlnProGlyProGlnLeuTyrAspValMetAsp 340
Db 1049 CCAGCCGCTGCGCAGCCATGATGTGTGAGCGGGGCCGAGCTCTACGACGTGATGAGC 1108
QY 341 AlaValProAlaArgArgTyrPlyGluPheValArgThrLeuGlyLeuArgGluAlaGlu 360
Db 1109 GCGGTCCAGCGCGGCTGGAAGAGTGTGCGCACGCTGGGCTGCCGAGCAGCAGAG 1168
QY 361 IleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGluMetLeuLys 380
Db 1169 ATCGAAGCCGTGAGGTGAGATGCGCCGCTTCCGAGACCAAGCAGATGATGCTCAAG 1228
QY 381 ArgTrpArgGlnGlnInProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMet 400
Db 1229 CGCTGGCGCCAGACAGACAGCCCGGGCTCGGAGCCGTTTACGCGCGCTGAGCGCATG 1288

```

OY 401 G1yLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 417
      |||||||
Db 1289 GGGCTGCAGCGGCTGCGTGGAGACTTGGCGACCGCGCTGCAGCGGCCCCG 1339

RESULT 6
AAL47186
ID AAL47186 standard; cDNA; 1634 BP.
XX
XX AAL47186;
XX
DT 22-AUG-2002 (first entry)
XX
DE Human rheumatoid arthritis associated DR3 gene related cDNA #1.
XX
KW Human; DR3; rheumatoid arthritis; anti-rheumatic; antiarthritic;
KW gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FH CDS 89..1342
FT /*tag= a
FT /product= "AAO17879"

WO200234912-A1.
XX
PD 02-MAY-2002.
XX
PF 24-OCT-2001; 2001WO-JP09313.
XX
XX 24-OCT-2000; 2000JP-0324296.
PR 27-MAR-2001; 2001JP-0090546.
PR 30-MAR-2001; 2001JP-0099990.
XX
PA (NEWI-) NEW IND RES ORG.
PA (SHIO/) SHIOZAWA S.
XX
PI Shiozawa S, Konishi Y;
XX
DR WPI: 2002-417132/44.
DR P-PSDB; AAO17879.
XX
PT Genomes, particularly DR3 genomic DNA, participating in rheumatoid
PT arthritis via mutation, useful in evaluating disease onset and its
PT possibility and providing therapy and remedies -
XX
PS Example 1; Page 66-69; 84pp; Japanese.
XX
CC The present invention relates to the human DR3 gene, which is associated
CC with rheumatoid arthritis. Certain mutations in the gene can be linked to
CC the disease. The sequences can be used to evaluate disease onset and its
CC possibility and to provide therapy and remedies. The present sequence is
CC a coding sequence described in the exemplification of the invention.
XX
SQ Sequence 1634 BP; 300 A; 528 C; 519 G; 287 T; 0 other;

Alignment Scores:
Pred. No.: 7.06e-122 Length: 1634
Score: 2323.00 Matches: 417
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 24 Gaps: 0

US-09-993-234-6 (1-417) x AAL47186 (1-1634)

OY 1 MetGluGlnArgProArgGlyCysAlaAlaValAlaAlaLeuLeuValLeu 20
      |||||||
Db 89 ATGAGACAGCGCGCGGCTGCGCGCGTGGCGGCGGCGCTCCTCGTGTGCTG 148
      |||||||
OY 21 GlyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHis 40
      |||||||

```

Db	149	GGGGCCCCGGGGCCAGGGGGGAC	CTCGTAGCCCCAGGTGTGACTGTGCCGGTGACTTCCAC	208
QY	41	LysLysIleGlyLeuPheCysCysArgGlyCysProIleGlnHisTyrLeuLysAlaPro		60
Db	209	AAGAAGATTGGTCTGTATTGTGTGCAGAGGCTGCCACAGCGGGCACTACTGAAGGCCCT		268
QY	61	CysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAla		80
Db	269	TGCACGGAGCCCTGGGGCACTCCACCTGCCCTTGTGTGTCCCAAGACACCTTCTGGCC		328
QY	81	TrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluAlaSer		100
Db	329	TGGGAGAACCACTAATTTCTGAATGTGCCCGCTGCCAGCGCTGTGATGACAGGCGCTCC		388
QY	101	GlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGly		120
Db	389	CAGGTGGCGCTGGAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGGCTGTAAAGCCAGGC		448
QY	121	TrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCysGlnPro		140
Db	449	TGGTTTGTGAGTGCACGCTCAGCCAAATGTGTACAGCAGTTCACCTTCTACTGCCAACCA		508
QY	141	CysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThr		160
Db	509	TGCCTAGACTGGGGGGGCTGCACCGCCACACACAGGCTACTGTGCCGAGAGATACT		568
QY	161	AspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysPro		180
Db	569	GACTGTGGGACCTGCTGCTGCTGCTTCTATGAACATGGCGATGGCTGCTGCTGCCCC		628
QY	181	ThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTyrParGlnMet		200
Db	629	ACGAGCACCTGGGGAGCTGTCCAGAGCGTGTGCCGCTGTCTGTGGCTGGAGGCAGATG		688
QY	201	PheTrpValGlnValLeuLeuAlaGlyLeuValValProLeuLeuLeuGlyAlaThrLeu		220
Db	689	TTCCTGGGTCCAGGTGTCTCTGGCTGGCTTGTGTGTCCCTCTGCTTGGGGCACCTTG		748
QY	221	ThrTyrThrTyrArgHisCysTrrProHisLysProLeuValThrAlaAspGluAlaGly		240
Db	749	ACCTACACATACCGCCACTGTGGCTCACAAGCCCTGTACTGCAGATGAAGCTGGG		808
QY	241	MetGluAlaLeuThrProProProAlaThrHisLeuSerProLeuAspSerAlaHisThr		260
Db	809	ATGGAGGCTCTGACCCCAACCGGGCCACCATCTGTACACCTTGGACAGCGCCACACC		868
QY	261	LeuLeuAlaProProAspSerSerGluLysIleCysThrValGlnLeuValGlyAsnSer		280
Db	869	CTTCTAGCACCTCTCTGACAGCAGTGAGAGATCTGCACCGCTCCAGTTGGTGGTAAACAGC		928
QY	281	TrpThrProGlyTyrTrpProGluThrGlnGluAlaLeuCysProGlnValThrTrrSerTrp		300
Db	929	TGGACCCCTGGCTTACCCCGAGACCACGAGGCGCTCTGCCCGCAGGTGACATGTCTCTGG		988
QY	301	AspGlnLeuProSerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSer		320
Db	989	GACCAGTTGCCACGACGAGCTTGTGGCCCCGCTGTCGCCCCACACTCTGCCAGAGTCC		1048
QY	321	ProAlaGlySerProAlaMetMetLeuGlnProGlyProGlnLeuTyrAspValMetAsp		340
Db	1049	CCAGCCGGCTCGCCACGCAATGATGCTGCAGCCGGGGCCCGCAGCTTACGACGTATGGAC		1108
QY	341	AlaValProAlaArgArgTrrPlyGluPheValArgThrLeuGlyLeuArgGluAlaGlu		360
Db	1109	GCGGTCCACAGCGCGGCTGGAAGGAGTTCGTGCCGACACCTGGGGGCTGCGGAGGCAGAG		1168
QY	361	IleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGluMetLeuLys		380
Db	1169	ATCGAAGCCGTGGAGGTGGAGATCGGCCGCTTCCGAGACCAGCAGTACGAGATGCTCAAG		1228
QY	381	ArgTrrParGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMet		400
Db	1229	CGCTGGCGCCAGCAGCAGCCCCGGGGGCTCGAGGCGGTATACGGGGCCCTGGAGCGCTTG		1288

QY 401 GlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 417
|||||
DB 1289 GGGCTGGACGGCTGCTGGAGACTTGGCGACGCCGCTGCAGCGGCCG 1339
RESULT 7
AAC91477
ID AAC91477 standard; cDNA; 1662 BP.
XX AAC91477;
AC AAC91477;
XX
DT 21-MAR-2001 (first entry)
XX
DE Human PRO779 cDNA.
XX
KW Human; PRO; antiinflammatory; dermatological; antiarthritic;
KW antirheumatic; cardiant; antihaemic; immunosuppressive; antithyroid;
KW antidiabetic; nootropic; neuroprotective; hepatotropic; virucide;
KW antiallergic; antiasthmatic; immune related disorder;
KW hepatobiliary disease; autoimmune disease; allergy; ss.
XX
OS Homo sapiens.
XX
PN WO200073452-A2.
XX
PD 07-DEC-2000.
XX
PF 02-JUN-2000; 2000WO-US15264.
XX
PR 02-JUN-1999; 99WO-US12252.
PR 20-JUL-1999; 99US-0144732.
PR 20-JUL-1999; 99US-0144758.
PR 28-JUL-1999; 99US-0146222.
PR 01-SEP-1999; 99WO-US20111.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 29-OCT-1999; 99US-0162506.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28634.
PR 09-DEC-1999; 99US-0170262.
PR 20-DEC-1999; 99WO-US30911.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Chan B, Goddard A, Godowski PJ, Gurney AL;
PI Hebert C, Henzel W, Kabakoff RC, Shelton DL, Tumas D, Watanabe CK;
PI Wood WI;
XX
DR WPI; 2001-025253/03.
DR P-PSDB; AAB50918.
XX
PT Thirty three nucleic acids encoding PRO polypeptides which are useful
PT in the diagnosis and treatment of immune related disorders, e.g.
PT systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
PT thyroiditis and diabetes mellitus -
XX
PS Claim 48; Fig 33; 218pp; English.
XX
CC The present sequence is one of thirty three nucleic acids encoding PRO
CC polypeptides. The PRO polypeptides, anti-PRO antibodies, agonists and

CC antagonists are useful for treating and diagnosing immune related
CC disorders such as systemic lupus erythematosus, rheumatoid arthritis,
CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,
CC immune-mediated renal disease, demyelinating diseases of the central
CC and peripheral nervous systems (such as multiple sclerosis, idiopathic
CC demyelinating polyneuropathy or Guillain-Barre syndrome, and chronic
CC inflammatory demyelinating polyneuropathy), hepatobiliary diseases
CC (such as infectious, autoimmune chronic active hepatitis, primary
CC biliary cirrhosis, granulomatous hepatitis and sclerosing cholangitis),
CC inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's
CC disease, autoimmune or immune-mediated skin diseases (such as bullous
CC skin diseases, erythema multiforme, contact dermatitis, psoriasis),
CC allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,
CC food hypersensitivity and urticaria), immunological diseases of the
CC lung (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis
CC and hypersensitivity pneumonitis), transplantation associated diseases
CC including graft rejection and graft-versus-host diseases.
XX
SQ Sequence 1662 BP; 302 A; 540 C; 531 G; 289 T; 0 other;

Alignment Scores:
Pred. No.: 7.19e-122 Length: 1662
Score: 2323.00 Matches: 417
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0

US-09-993-234-6 (1-417) x AAC91477 (1-1662)

QY 1 MetGluGlnArgProArgGlyCysAlaAlaValAlaAlaLeuLeuValLeu 20
DB 103 ATGAGCAGCGCGCGCGGCGCGCGGCGGTGGCGCGCGCTCCTCTGCTGCTG 162

QY 21 GlyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHis 40
DB 163 GGGGCGCGCGCGCGCGCGCGCTGAGCCCGAGGTGACTGTGCCGGTACTCCAC 222

QY 41 LysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaPro 60
DB 223 AAGAAGATTGGTCTGTTTGTTCAGAGGCTGCCCGCGGCGCACTACCTGAAGGCCCT 282

QY 61 CysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAla 80
DB 283 TGCACGGAGCCCTCGCGCACTCCACCTGCTGTGTGCCCAAGACACACTTCTGGCC 342

QY 81 TrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSer 100
DB 343 TGGGAGAACCAACATAATTCTGAATGTGCCCGCTGCCAGCGCTGTGATGAGCGCCCTC 402

QY 101 GlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGly 120
DB 403 CAGGTGGCGCTGAGAACTGTTCAAGCAGTGGCGCGACACCGCTGTGGCTGAAGCCAGGC 462

QY 121 TrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCysGlnPro 140
DB 463 TGGTTTGTGAGTGGCAGGTCCAGCCAAATGTGTACAGTTCACCCCTTCTACTGCCAACCA 522

QY 141 CysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThr 160
DB 523 TGCCTAGACTGGCGGCGCTGCACCGCCACACACAGGCTACTCTGTTCGCCGAGATACT 582

QY 161 AspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysPro 180
DB 583 GACTGTGGGACCTGCCTGCCTGCTTATGACATGGCATGGATGGCTGCTGCTGCCCC 642

QY 181 ThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTrpArgGlnMet 200
DB 643 ACGAGCACCTGGGAGCTGTCCAGAGCGCTGTGCCGCTGTCTGTGCTGGAGGACAGATG 702

QY 201 PheTrrpValGlnValLeuLeuAlaGlyLeuValValProLeuLeuLeuGlyAlaThrLeu 220
Db 703 TTCTGGGTCAGGTGCTCGTGGTGGCCCTTGTGGTCCCCCTCTGCTGGGGCCACCCCTG 762
QY 221 ThrTyrThrTyrArgHisCysTrrProHisLysProLeuValThrAlaAspGluAlaGly 240
Db 763 ACCTACACATACCGCCACTGCTGCTCACAAGCCCCCTGTTACTGCAGATGAAGCTGGG 822
QY 241 MetGluAlaLeuThrProProProAlaThrHisLeuSerProLeuAspSerAlaHisThr 260
Db 823 ATGGAGGCTCTGACCCCAACCCAGCCACCCATCTGTACCCCTTGGACAGCGCCACACAC 882
QY 261 LeuLeuAlaProProAspSerSerGlnLysIleCysThrValGlnLeuValGlyAsnSer 280
Db 883 CTTCAGACACCTCCTGACAGACAGTGAAGAATCTGCACCCGTCACAGTTGGTGAACAGC 942
QY 281 TrrPrrProGlyTyrProGluThrGlnGluAlaLeuCysProGlnValThrTrrSerTrr 300
Db 943 TGGACCCCTGGCTACCCCGAGACCCAGAGGCGCTCTGCCCGCAGGTGACATGCTCTGG 1002
QY 301 AspGlnLeuProSerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSer 320
Db 1003 GACCAAGTGGCCACAGACAGAGCTCTGGCCCCCGCTGCTGCCCCACACTCTCGCCAGAGTCC 1062,
QY 321 ProAlaGlySerProAlaMetMetLeuGlnProGlyProGlnLeuTyrAspValMetasp 340
Db 1063 CCAGCCGGCTCGCCAGCCATGATGCTGCAGCCGGCCCGCAGCTCTACGACGTGATGAC 1122
QY 341 AlaValProAlaArgArgTrrPrrGluPheValArgThrLeuGlyLeuArgGluAlaGlu 360
Db 1123 GCGGTCCAGCGCGCGCTGGAAGAGTTCGTGCGCACGCTCGCGCTGCGGAGGACAGC 1182
QY 361 IleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGluMetLeuLys 380
Db 1183 ATCGAAGCCGTGAGGTGAGATCGGCCGCTTCGAGACCAAGCAGATGATGCTCAAG 1242
QY 381 ArgTrrPrrGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMet 400
Db 1243 CGCTGGCGCCAGCAGCAGCCCGCGGCTCGGAGCCGTTTACGCGGCGCTGGAGCGCATG 1302
QY 401 GlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 417
Db 1303 GGGCTGGACGGCTCGCTGGAAGACTTCCGACGCCGCTGCACGCGGCGCCG 1353
RESULT 8
ABK40265
ID ABK40265 standard; cDNA; 1662 BP.
XX
AC ABK40265;
XX
DT 15-JUL-2002 (first entry)
XX
DE cDNA encoding human PRO779 polypeptide.
XX
KW Human; PRO; benign tumour; malignant tumour; lymphoid malignancy;
KW leukaemia; neuronal disorder; stromal disorder; blastocoealic disorder;
KW inflammatory disorder; immune disorder; angiogenic disorder;
KW gene therapy; cytostatic; neuroprotective; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200153486-A1.
XX
PD 26-JUL-2001.
XX
PF 11-FEB-2000; 2000WO-US03565.
XX
PR 08-MAR-1999; 99WO-US05028.
PR 11-MAR-1999; 99US-123972P.
PR 11-MAY-1999; 99US-133459P.
PR 02-JUN-1999; 99WO-US12252.
PR 22-JUN-1999; 99US-140650P.
PR 22-JUN-1999; 99US-140653P.

PR 20-JUL-1999; 99US-144758P.
PR 26-JUL-1999; 99US-145698P.
PR 28-JUL-1999; 99US-146222P.
PR 17-AUG-1999; 99US-149395P.
PR 31-AUG-1999; 99US-151689P.
PR 01-SEP-1999; 99WO-US20111.
PR 15-SEP-1999; 99WO-US21090.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.
PR 05-JAN-2000; 2000WO-US00219.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL, Hillan KJ;
PI Marsters SA, Pan J, Pittl RM, Roy MA, Smith V, Stone DM;
PI Watanabe CK, Wood WI;
XX
DR WPI; 2002-205567/26.
DR P-PSDB; AAU86139.
XX
PT Thirty five nucleic acids encoding PRO polypeptides, useful for
PT treating benign or malignant tumours, leukaemias and lymphoid
PT malignancies, inflammatory, angiogenic and immunologic disorders -
PS Claim 50; Fig 23; 302bp; English.
XX
CC The present invention relates to the isolation of novel human PRO
CC polypeptides and the polynucleotide sequences encoding them. The
CC PRO polypeptides, agonists, antagonists or anti-PRO antibodies are
CC useful for treating benign or malignant tumours (e.g. renal, kidney,
CC bladder, breast, etc), leukaemias and lymphoid malignancies, other
CC disorders such as neuronal, glial, astrocytal, hypothalamic, glandular,
CC macrophagal, stromal and blastocoealic disorders, inflammatory, immune
CC and angiogenic disorders. The polynucleotide sequences are also
CC useful in gene therapy. ABK40254-ABK40288 encode for the human PRO
CC polypeptides of the invention.
XX
SQ Sequence 1662 BP; 302 A; 540 C; 531 G; 289 T; 0 other;

Alignment Scores:
Pred. No.: 7.19e-122 Length: 1662
Score: 2323.00 Matches: 417
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 24 Gaps: 0

US-09-993-234-6 (1-417) x ABK40265 (1-1662)
QY 1 MetGluGlnArgProArgGlyCysAlaAlaValAlaAlaLeuLeuValLeu 20
Db 103 ATGAGCAGCGCGCGCGGCTGCGCGGCGGTGGCGGCGGCGCTCTCTGCTGCTG 162
QY 21 GlyAlaArgAlaGlnGlnGlyTrrArgSerProArgCysAspCysAlaGlyAspPheHis 40
Db 163 GGGGCGCGGCGCCAGGGCGGCGGCTGTAAGCCCCAGGTGTGACTGTGCGGTGACTTCCAC 222
QY 41 LysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlnHisTyrLeuLysAlaPro 60
Db 223 AAGAAGATTGCTGTGTTGTTGTCAGAGGCTGCCACAGCGGCGGCACTGTAAGGCCCT 282
QY 61 CysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAla 80
Db 283 TGCACGAGCCCTGCGCAACTCACTGCTGTGTGTCCCAAGACACCTTCTTGCC 342
QY 81 TrrGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSer 100
Db 343 TGGAGAACCAACCATATATCTGAATGTGCCCGCTGCCAGGCCCTGTGATGACAGGCTCC 402
QY 101 GlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGly 120
Db 403 CAGGTGGCGCTGGAGAAGTGTTCAGACAGTGGCGGACACCCCGCTGTGTGCTGAAGCCAGGC 462

OY 121 TrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCysGlnPro 140
Db 463 TGGTTTGTGGAGTCCAGGCTCAGCAATGTGTGACAGATTCAACCTTCTACTGCCAACCA 522
OY 141 CysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThr 160
Db 523 TGCCTAGACTGCGGGCCCTGCACCGCCACACAGCGCTACTCTGTCTCCCGCAGAGATACT 582
OY 161 AspCysGlyThrCysLeuProGlyPheTyrGlnHisGlyAspGlyCysValSerCysPro 180
Db 583 GACTGTGGACCTGCTGCTGCTGCTTCTATGACATGGCGATGGCTGCGGTGCTGCCCC 642
OY 181 ThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTyrParglnMet 200
Db 643 ACGAGCACCCCTGGGAGCTGTCCAGAGCGCTGTGCCGCTGTCTGTGGCTGAGGCAAGATG 702
OY 201 PheTyrValGlnValLeuLeuAlaGlyLeuValValProLeuLeuGlyAlaThrLeu 220
Db 703 TTCTGGGTCCAGGTGCTCTGCTGGCTGGCTGTGTGCTCCCTCTGCTTGGGCCACCCCTG 762
OY 221 ThrTyrThrTyrArgHisCysTyrProHisLysProLeuValThrAlaAspGluAlaGly 240
Db 763 ACCTACACATACCGCCACTGTGCTGGCTCACAAGCCCTGTACTGTACAGATGAAGCTGGG 822
OY 241 MetGluAlaLeuThrProProProAlaThrHisLeuSerProLeuAspSerAlaHisThr 260
Db 823 ATGGAGGCTGTGACCCACACACCGGCCACCACTGTACACCTTGACACAGCGCCACACAC 882
OY 261 LeuLeuAlaProProAspSerSerGlnLysIleCysThrValGlnLeuValGlyAsnSer 280
Db 883 CTTCTAGCACCTCTGTGACAGCAGTAGAAGATCTGCACCGTCCAGTTGGTGGTAACAGC 942
OY 281 TrpThrProGlyTyrProGluThrGlnGlnAlaLeuCysProGlnValThrTrpSerTrp 300
Db 943 TGGACCCCTGGCTACCCCGAGAGACCCAGAGAGCGCTCTGCCCGCAGGTGACATGCTCTGG 1002
OY 301 AspGlnLeuProSerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSer 320
Db 1003 GACCAAGTGGCCACAGAGACTCTTGCGCCCGCTGCTGCCCCACACTCTCGCCACAGAGTCC 1062
OY 321 ProAlaGlySerProAlaMetMetLeuGlnProGlyProGlnLeuTyrAspValMetAsp 340
Db 1063 CCAGCCGGCTCGCCACGCAATGATGCTGCAGCGCGGGCCCGCAGCTCTACGACGTGATGAC 1122
OY 341 AlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGluAlaGlu 360
Db 1123 GCGGTCCAGCGCGCGCTGGAAGAGTTCGTGCGCACGCTGGGGCTGCGCGAGGCAAG 1182
OY 361 IleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGluMetLeuLys 380
Db 1183 ATCGAAGCCGTGAGGTTGAGATCGCGCTTCCGAGACAGACAGATGATGCTCAAG 1242
OY 381 ArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMet 400
Db 1243 CGCTGGCGCCAGCAGACGCGCGCGCTCGGAGCGCTTACGCGCGCTGGAAGCGCATG 1302
OY 401 GlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 417
Db 1303 GGGCTGAGCGGCTGCTGGAAGACTTGGCGCAGCGCGCTGACGCGCGCGCCG 1353
RESULT 9
ID AAV28700 standard; cDNA; 1847 BP.
XX AAV28700;
AC AAV28700;
XX 20-AUG-1998 (first entry)
DT Human apoptosis inducing receptor coding sequence.
DE Apoptosis inducing receptor; AIR protein; human; cell death regulator;
XX Type I transmembrane protein; tumour cell death; autoimmune disease;
KW

KW therapy; ss.
XX OS Homo sapiens.
XX Key CDS Location/Qualifiers
FT 236..1489
FT /*tag= a
FT /product= AIR
XX
PN WO9814565-A1.
XX
PD 09-APR-1998.
XX
PF 03-OCT-1997; 97WO-US17876.
XX
PR 04-OCT-1996; 96US-0044456.
XX
PA (IMMV) IMMUNEX CORP.
XX Perkins PA;
PI
XX
DR WPI; 1998-240077/21.
DR P-PSDB; AAW57045.
XX
PT DNA encoding apoptosis inducing receptor - which is Type I
PT transmembrane protein, useful for regulating cell death
XX
PS Claim 2; Page 28-30; 45pp; English.
XX
CC This sequence encodes the human apoptosis inducing receptor (AIR) of the
CC invention. AIR is a Type I transmembrane protein, soluble forms of which
CC can be used to regulate cell death in a therapeutic setting. Soluble AIR
CC can also be used in vitro to block apoptosis or AIR-expressing cells, or
CC to screen agonists or antagonists of AIR activity. The cytoplasmic domain
CC of AIR can be used to develop assays for inhibitors of AIR-induced cell
CC death, which is useful to regulate cell death in a therapeutic setting as
CC well as in vitro. Agonists of AIR activity can be used to kill tumour
CC cells that express AIR, or T cells expressing AIR in autoimmune diseases.
XX
SQ Sequence 1847 BP; 316 A; 605 C; 579 G; 347 T; 0 other;
Alignment Scores:
Pred. No.: 8.05e-122 Length: 1847
Score: 2323.00 Matches: 417
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 19 Gaps: 0
US-09-993-234-6 (1-417) x AAV28700 (1-1847)
OY 1 MetGluGlnArgProArgGlyCysAlaAlaValAlaAlaLeuLeuValLeu 20
Db 236 ATGAGCAGCGCGCGCGGCTGCGCGCGGCTGCGCGCGCTCTGCTGCTGCTG 295
OY 21 GlyAlaArgAlaGlnGlyThrArgSerProArgCysAspCysAlaGlyAspPheHis 40
Db 296 GGGGCGCGCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 355
OY 41 LysLysIleGlyLeuPheCysArgGlyCysProAlaGlyHisTyrLeuLysAlaPro 60
Db 356 AAGAGATTGCTGCTGTTTGTGCAAGAGCTGCCAGCGGGGCACTACCTGAAGGCCCT 415
OY 61 CysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAla 80
Db 416 TGCACGGAAGCCCTGCGGCACTCCACCTGCTGTGTGTTCCCAAGACACCTTCTGGCC 475
OY 81 TrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSer 100
Db 476 TGGGAGAACCAACCATATTTCTGAATGTGCCCGCTGCCAGCGCTGTGATGAGCAGGCTCC 535
OY 101 GlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGly 120

Db 536 CAGGTGGCGCTGGAGAACTGTTACAGACAGTGGCCGACACCCGCTGTGGCTGTAAACCCAGGC 595

QY 121 TrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCysGlnPro 140

Db 596 TGGTTGTGGAGTGCACAGGTCACCAATGTGTACAGAGTTACACCTTCTACTGCCAACCA 655

QY 141 CysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThr 160

Db 656 TGCCTAGACTGGGGGCCCTGCACCCGACACAGGCTACTCTGTCCCGCAGAGATACT 715

QY 161 AspCysGlyThrCysLeuProGlyPheTyrGlnHisGlyAspGlyCysValSerCysPro 180

Db 716 GACTGTGGAGACCTGCCTGCCTGCTTATGAAATGGGATGGCTGCGTGTCTGCC 775

QY 181 ThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTyrPargLmet 200

Db 776 ACGAGCACCCGTGGGAGCTGTCCAGAGCGGTGTGCCGTGTGTGGCTGGAGCAGATG 835

QY 201 PheTrpValGlnValLeuLeuAlaGlyLeuValValProLeuLeuGlyAlaThrLeu 220

Db 836 TTCTGGGTCCAGGTGCTCTGGCTGGCTGTGTGCTCCCTCTCTGCTGGGGCCACCTG 895

QY 221 ThrTyrThrTyrArgHisCysTrpProHisLysProLeuValThrAlaAspGluAlaGly 240

Db 896 ACCTACACATACCCGACACTGTGCTGCTCACAAAGCCCTGTTACTGACAGATGAAGCTGG 955

QY 241 MetGluAlaLeuThrProProProAlaThrHisLeuSerProLeuAspSerAlaHisThr 260

Db 956 ATGGAGGCTGTACCCACACACCCGACCCACCTGTCTACACCTTGACAGCCGCCACACC 1015

QY 261 LeuLeuAlaProProAspSerSerGluLysIleCysThrValGlnLeuValGlyAsnSer 280

Db 1016 CTTCTAGCACCTCTGCAGACAGCAGTAGAAGATGTGCACCGTCCAGTGTGGGTAAACAGC 1075

QY 281 TrpThrProGlyTyrProGluThrGlnGluAlaLeuCysProGlnValThrTyrSerTrp 300

Db 1076 TGGACCCCTGGCTACCCCGAGACCCAGAGGCGCTCTGCCCGCAGGTGACATGTCTCTGG 1135

QY 301 AspGlnLeuProSerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSer 320

Db 1136 GACCAGTGGCCAGCAGAGCTCTTGGCCCCGCTGCTGCGCCACACACTCTCGCAGAGTCC 1195

QY 321 ProAlaGlySerProAlaMetMetLeuGlnProGlyProGlnLeuTyrAspValMetAsp 340

Db 1196 CCAGCCGGCTGCCAGCCATGATGTGACGCCGGCCCGCAGCTCTACGACGTGATGGAC 1255

QY 341 AlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGluAlaGlu 360

Db 1256 GCGGTCCAGCGCGCGCTGGAAAGAGTTCGTGGCAGCTGGGCTGGCGGAGCAGAG 1315

QY 361 IleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGluMetLeuLys 380

Db 1316 ATCGAAGCCGTGGAGGTGAGATCGGCCGCTTCGAGACAGCAGAGTACGAGATGCTCAAG 1375

QY 381 ArgTrpArgGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMet 400

Db 1376 CGCTGGCGCCAGCAGACGCCCGCGGCTCGGAGCCGTTTACGGCGGCCCTGGAGCGCATG 1435

QY 401 GlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 417

Db 1436 GGGCTGGACGGCTGGAAAGACTTGGCAGCGCCCTGCAGCGGCGCCG 1486

RESULT 10

AAT89426

ID AAT89426 standard; cDNA; 1783 BP.

XX AAT89426;

AC AAT89426;

XX 02-MAR-1998 (first entry)

DT 02-MAR-1998 (first entry)

XX Death domain containing receptor DR3-V1 cDNA.

DE Death domain containing receptor; DR3-V1; human; apoptosis;

XX

KW Death domain containing receptor; DR3-V1; human; apoptosis;

KW Inflammation; NF-kappaB; ds.

XX

OS Homo sapiens.

XX

PH Key

FT CDS

FT sig_peptide

FT mat_peptide

FT

XX

PN W09733904-A1.

XX

PD 18-SEP-1997.

XX

PF 17-OCT-1996; 96WO-US16849.

XX

PR 12-MAR-1996; 96US-0013285.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

PA (UNMI) UNIV MICHIGAN.

PI Dillon PJ, Dixit VM, Gentz RL, Ni J, Yu G;

XX

DR WPI; 1997-470812/43.

DR P-PSDB; AAW31516.

XX

PT Death domain containing receptor polypeptide(s) DR3 and DR3-V1 -

PT for activation of apoptosis and NF-kappaB, antagonists can be used

PT to treat inflammatory diseases

XX

PS Claim 2; page 71-73; 108pp; English.

XX

CC This cDNA clone, deposited as ATCC 97456, codes for human death

CC domain containing receptor DR3-V1 (see AAW31516), a novel member of

CC the tumour necrosis factor receptor family. It was isolated from a

CC cDNA library derived from cells of a human testis tumour. Related

CC death domain containing receptor DR3 cDNA (see AAT89427) was isolated

CC from a HUVEC cDNA library. The genes have also been identified in

CC cDNA libraries of foetal liver, foetal brain, tonsil and leukocyte.

CC Nucleic acids encoding full-length or mature DR3-V1 can be used to

CC produce recombinant polypeptides in transformed host cells. These

CC polypeptides can be used to treat diseases and disorders associated

CC with the inhibition of apoptosis. Antagonists, such as antibodies

CC raised against DR3-V1, can be used to treat diseases and disorders

CC associated with increased apoptosis and for treating inflammatory

CC diseases and disorders.

XX

SQ Sequence 1783 BP; 330 A; 562 C; 564 G; 327 T; 0 other;

Alignment Scores:

Pred. No.: 1.08e-118 Length: 1783

Score: 2267.00 Matches: 409

Percent Similarity: 97.39% Conservative: 1

Best Local Similarity: 97.15% Mismatches: 5

Query Match: 97.59% Indels: 6

DB: 18 Gaps: 1

US-09-993-234-6 (1-417) x AAT89426 (1-1783)

QY 3 GlnArgProArgGly-----CysAlaAlaValAlaAlaLeuLeu 16

Db 219 GAGGCCCCACGTGGGACGCTGCCGCGAGAGTACAGACACCTGTCCCCAGCGCTCTC 278

QY 17 LeuValLeuLeuGlyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAla 36

Db 279 CTGCTGTCTGTGGGCGCGGCCAGAGCGGCACATCTGTAGCCAGGTGTGACTGTGCC 338

QY 37 GlyAspPheHisLysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyr 56

Db 339 GGTGACTTCCACAAGAGATGTGTCTGTGTGTTCAGAGAGCTGCCCCAGCGGGGACTAC 398

|||||
Db 279 CTGGTCTGCTGGGGCCCCGGGCCAGGGGGGCACTGTAGCCCCAGGTGTGACTGTGCC 338
OY 37 GLYAspPheHisLysLysILEGLyleuPheCysArgGLYCysProAlaGlyHisTyr 56
|||||
Db 339 GGTGACTTCCACAGAAGATTGGTCTGTTTGTTCAGAGGCTGCCAGCGGGCACTAC 398
OY 57 LeuLysAlaProCysThrGluProCysGLYAsnSerThrCysLeuValCysProGlnAsp 76
|||||
Db 399 CTGAAGGCCCTTGCACGAGAGCCCTGGCGCACTCCACCTGCTGTGTGTCCCAAGAC 458
OY 77 ThrPheLeuAlaTirpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAsp 96
|||||
Db 459 ACCTTCTTGGCCCTGGAGAACCAACCATATCTGAATGTGCCCGCTGCCAGGCTGTGAT 518
OY 97 GluGlnAlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGly 116
|||||
Db 519 GAGCAGGCTCCAGAGTGGCGCTGGAGAACTGTTCAAGTGGCCGACACCGCTGTGGC 578
OY 117 CysLysProGlyTirpPheValGluCysGlnValSerGlnCysValSerSerProPhe 136
|||||
Db 579 TGTAAAGCCAGGCTGTTTGTGAGTGCAGGTCACCAATGTGTACAGAGTTCACCCCTTC 638
OY 137 TyrCysGlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSer 156
|||||
Db 639 TACTGCCAACCAATGCCCTAGACTGCGGGGCCCTGCACCGCCACACAGGCTACTCTGTTC 698
OY 157 ArgArgAspThrAspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCys 176
|||||
Db 699 CGCAGAGATACTGACTGTGGGACCTGCCCTGCTGCTTCTATGAACATGGCGATGGCTGC 758
OY 177 ValSerCysProThrSerThrLeuGlySerCysProGluArgCysAlaValCysGly 196
|||||
Db 759 GTGTCTTGGCCCCAGAGCACCCCTGGGAGCTGTCCAGAGCGCTGTGCCGTGTGTGGC 818
OY 197 TrpArgGlnMetPheTrpValGlnValLeuLeuAlaGlyLeuValProLeuLeu 216
|||||
Db 819 TGGAGGACAGATGTTGTGGTCCAGGTGCTCTGCTGCTGTGTGTCCCTCTGTGCTT 878
OY 217 GLYAlaThrLeuThrTyrThrTyrArgHisCysTrpProHisLysProLeuValThrAla 236
|||||
Db 879 GGGGCCACCCCTGACATACACATACCGCCACCTGCGCTCACAAGCCCCCTGTTACTGCA 938
OY 237 AspGluAlaGlyMetGluAlaLeuThrProProProAlaThrHisLeuSerProLeuAsp 256
|||||
Db 939 GATGAAGCTGGGATGGAGGCTCTGACCCCAACCCAGCCCAATCTGTACCCCTTGAC 998
OY 257 SerAlaHisThrLeuLeuAlaProProAspSerSerGluLysILECysThrValGlnLeu 276
|||||
Db 999 AGCGCCACACCTTCTAGCACCTCTGTACAGCAGTGAGAAGATCTGCACGCTCCAGTTG 1058
OY 277 ValGlyAsnSerTrpThrProGlyTyrProGluThrGlnGluAlaLeuCysProGlnVal 296
|||||
Db 1059 GTGGGTAAACAGCTGGACCCCTGGCTACCCCGAGACCAGAGGCGCTGTGCCCGCAGGTG 1118
OY 297 ThrTrpSerTrpAspGlnLeuProSerArgAlaLeuGlyProAlaAlaAlaProThrLeu 316
|||||
Db 1119 ACATGGTCTGGGACAGTTGCCACAGAGCTTGGCCCCGCTGCGGCCACACTC 1178
OY 317 SerProGluSerProAlaGlySerProAlaMetLeuGlnProGlyProGlnLeuTyr 336
|||||
Db 1179 TCGCCAGAGTCCCAAGCCGGCTGCGCAAGCATGATGCTGCAGCCGGGCCGCACTTAC 1238
OY 337 AspValMetAspAlaValProAlaArgArgTirpLysGluPheValArgThrLeuGlyLeu 356
|||||
Db 1239 GACGTGATGGACCGGCTCCCAAGCGGCGCTGGAAGAGTTGCTGCGCACCTGGGGCTG 1298
OY 357 ArgGluAlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyr 376
|||||
Db 1299 CGCGAGGCGAGAGATCGAAGCCGCTGAGGTGAGATCGGCCCTTCCGAGACCAAGATAC 1358
OY 377 GluMetLeuLysArgTrpArgGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAla 396
|||||

Db 1359 GAGATGCTCAAGCGCTGGCGCCAGACAGACCCCGCGGCTCGGAGCCGTTTACGGGCC 1418
OY 397 LeuGluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGly 416
|||||
Db 1419 CTGAGCGCATGGGGCTGGACGGCTGCTGCGTGAAGACTTGGCGACCGCCCTGCACCGCGC 1478
OY 417 Pro 417
|||
Db 1479 CCG 1481
RESULT 12
AAC68776
ID AAC68776 standard; cDNA; 1783 BP.
XX AAC68776;
AC AAC68776;
XX 20-FEB-2001 (first entry)
DT
XX Human death domain containing receptor DR3-V1 coding sequence.
DE
XX Human; death domain containing receptor; DR3-V1; cancer;
KW autoimmune disorder; inflammation; cardiovascular disorder; infection;
KW neurodegenerative disease; angiogenesis; ss.
XX Homo sapiens.
OS
XX WO200064465-A1.
PN
XX 02-NOV-2000.
PD
XX 21-APR-2000; 2000WO-US10741.
PF
XX 22-APR-1999; 99US-0130488.
PR
XX 28-MAY-1999; 99US-0136741.
PR
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (UNMT) UNIV MICHIGAN.
PA (YUGG/) YU G.
PA (NIJ/) NI J.
PA (GENT/) GENTZ R L.
PA (DILL/) DILLON P J.
PA (DIXI/) DIXIT V M.
XX
PI YU G, NI J, Gentz RL, Dillon PJ, Dixit VM;
XX
DR WPI; 2000-687263/67.
DR P-PSDB; AAB36264.
XX
PT Treating graft-versus-host disease, cancer, immunodeficiency or an
PT autoimmune disease comprising administering an antibody to Death Domain
PT Containing Receptor proteins and a second therapeutic agent -
XX
PS Example 1; Fig 1; 273pp; English.
XX
CC The present invention provides the protein and coding sequences for two
CC death domain containing receptors, designated DR3 and DR3-V1. These
CC receptors are involved in apoptosis, and the sequences given can be used
CC in the treatment of cancers, infections, cardiovascular disorders such as
CC arrhythmias, ischaemia, aneurysms, arterial occlusive diseases including
CC and congenital heart defects, neurodegenerative diseases including
CC Alzheimer's and Parkinson's diseases, autoimmune disease such as multiple
CC sclerosis, arthritis, diabetes, Graves' disease, asthma and psoriasis,
CC and to promote angiogenesis and wound healing.
XX
SQ Sequence 1783 BP; 330 A; 562 C; 564 G; 327 T; 0 other;
Alignment Scores:
Pred. No.: 1.08e-118 Length: 1783
Score: 2267.00 Matches: 409
Percent Similarity: 97.39% Conservative: 1
Best Local Similarity: 97.15% Mismatches: 5
Query Match: 97.59% Indels: 6
DB: 21 Gaps: 1

US-09-993-234-6 (1-417) x AAC68776 (1-1783)

QY 3 GlnArgProArgGly-----CysAlaAlaValAlaAlaLeuLeu 16
Db 219 GAGGCCCCACGTGGCAGCTGCGCGAGAGTCAAGCACACCTGTCCCCAGGGCTCCTC 278
QY 17 LeuValLeuLeuGlyAlaArgAlaGlnGlyThrArgSerProArgCysAspCysAla 36
Db 279 CTGTGCTGTGGGGCCCGGGCCAGGGCGGCACCTCGTAGCCCCAGGTGTGACTGTGCC 338
QY 37 GlyAspPheHisIleGlyLeuPheCysArgGlyCysProAlaGlyHisTyr 56
Db 339 GGTAAGCTCCACAGAGAATGGTCTGTGTTGTGCAGAGGCTGCCACGGGGGCACTAC 398
QY 57 LeuLysAlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAsp 76
Db 399 CTGAAGGCCCTTGACAGGAGCCCTGCGGCACTCCACCTGCTGTGTGCCCAAGAC 458
QY 77 ThrPheLeuAlaTyrGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAsp 96
Db 459 ACCTCTTGGCTGGGAGAGAACCACTAATCTGAATGTGCCCGCTGCCAGCCCTGTGAT 518
QY 97 GluGlnAlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGly 116
Db 519 GAGCAGGCTTCCAGGTGGCGGTGGAGAACTGTTACAGAGTGGCCGACACCCGCTGTGCC 578
QY 117 CysLysProGlyTyrPheValGluCysGlnValSerGlnCysValSerSerProPhe 136
Db 579 TGTAAAGCCAGGCTGTTGTGAGAGTGCAGGTTCAGCCAATGTGTACAGAGTTCACCTTC 638
QY 137 TyrCysGlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSer 156
Db 639 TACTGCCAACCATGCTAGACTGCGGGGCCCTGCACCGCACACAGCGCTACTCTGTGCC 698
QY 157 ArgArgAspThrAspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCys 176
Db 699 CGCAGAGATACTGACTGTGGACCTGCTGCTGCTGTCTATATACATGGCGATGGCTGCC 758
QY 177 ValSerCysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGly 196
Db 759 GTGTCTTGGCCCCACGAGCACCTGGGAGAGCTGTCCAGAGCGCTGTGCCGTGTGTGCC 818
QY 197 TyrArgGlnMetPheTyrValGlnValLeuLeuAlaGlyLeuValValProLeuLeu 216
Db 819 TGGAGGCAGATGTTCTGGGTCCAGGTGCTCTGCTGGCTGTGTGCCCTCTGCTT 878
QY 217 GlyAlaThrLeuThrTyrThrTyrArgHisCysTyrProHisLysProLeuValThrAla 236
Db 879 GGGGCCACCTGACCTACACATACGCCACTGTGGCTGCCTACAAAGCCCTGTACTGCA 938
QY 237 AspGluAlaGlyMetGluAlaLeuThrProProProAlaThrHisLeuSerProLeuAsp 256
Db 939 GATGAAGCTGGAGTGGAGGCTGTGACCCACACCGGCCACCCATCTGTACACCTTGGAC 998
QY 257 SerAlaHisThrLeuLeuAlaProProAspSerSerGlyLysIleCysThrValGlnLeu 276
Db 999 AGCGCCACACACCTTCTAGACCTCTGACAGCAGTGAAGATCTGCACCCGCTCAGTTG 1058
QY 277 ValGlyAsnSerTyrThrProGlyTyrProGluThrGlnAlaLeuCysProGlnVal 296
Db 1059 GTGGGTAAACAGCTGGACCCCTGGCTACCCCGAGAGCCAGGAGCGCTGTGCCCGAGGTG 1118
QY 297 ThrTyrSerTyrAspGlnLeuProSerArgAlaLeuGlyProAlaAlaAlaProThrLeu 316
Db 1119 ACATGGTCTTGGAGCACGTTGCCACAGAGAGCTTGGCCCCGCTGTGCCACACTC 1178
QY 317 SerProGluSerProAlaGlySerProAlaMetLeuGlnProGlyProGlnLeuTyr 336
Db 1179 TCGCCAGAGTCCCGAGCGGCTCGCCAGCCATGATGCTGCAGCCGGCGCGCAGCTCTAC 1238
QY 337 AspValMetAspAlaValProAlaArgArgTyrLysGluPheValArgThrLeuGlyLeu 356
|||||

Db 1239 GACGTGATGACGCGGTCCAGCGCGCGCTGCAAGAGATTCTGTGGCACACGCTGGGGCTG 1298
QY 357 ArgGluAlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyr 376
Db 1299 CGCGAGCGCAGATCGAAGCCGTGGAGGTGAGATCGGCCCTTCCGAGACACAGAGTAC 1358
QY 377 GluMetLeuLysArgTyrParGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAla 396
Db 1359 GAGATGCTCAAGCGCTGGCGCCAGCAGACCCCGCGGCTCGGAGCGCTTTACGGGGCC 1418
QY 397 LeuGluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGly 416
Db 1419 CTGGAAGCGCATGGGGCTGGACGGCTGCTGGAAGACTTGGCGACCGCGCTGCAGCGGGC 1478
QY 417 Pro 417
Db 1479 CCG 1481
RESULT 13
ABL64119
ID ABL64119 standard; DNA; 1743 BP.
XX
AC ABL64119;
XX
DT 15-MAY-2002 (first entry)
XX
DE Breast cancer related gene sequence SEQ ID NO:2456.
XX
KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW cytostatic; gene therapy; antineoplastic; Wilms' tumour; adenocarcinoma;
KW gene; ds.
XX
OS Homo sapiens.
XX
PN WO200194629-A2.
XX
PD 13-DEC-2001.
XX
PE 30-MAY-2001; 2001WO-US10838.
XX
PR 05-JUN-2000; 2000US-209473P.
PR 05-JUN-2000; 2000US-209531P.
PR 18-SEP-2000; 2000US-233133P.
PR 18-SEP-2000; 2000US-233617P.
PR 20-SEP-2000; 2000US-234009P.
PR 20-SEP-2000; 2000US-234034P.
PR 20-SEP-2000; 2000US-234052P.
PR 22-SEP-2000; 2000US-234509P.
PR 22-SEP-2000; 2000US-234567P.
PR 25-SEP-2000; 2000US-234923P.
PR 25-SEP-2000; 2000US-234924P.
PR 25-SEP-2000; 2000US-235077P.
PR 25-SEP-2000; 2000US-235082P.
PR 25-SEP-2000; 2000US-235134P.
PR 25-SEP-2000; 2000US-235280P.
PR 26-SEP-2000; 2000US-235637P.
PR 26-SEP-2000; 2000US-235638P.
PR 27-SEP-2000; 2000US-235711P.
PR 27-SEP-2000; 2000US-235720P.
PR 27-SEP-2000; 2000US-235840P.
PR 27-SEP-2000; 2000US-235863P.
PR 28-SEP-2000; 2000US-236028P.
PR 28-SEP-2000; 2000US-236032P.
PR 28-SEP-2000; 2000US-236033P.
PR 28-SEP-2000; 2000US-236034P.
PR 28-SEP-2000; 2000US-236109P.
PR 28-SEP-2000; 2000US-236111P.
PR 29-SEP-2000; 2000US-236842P.
PR 29-SEP-2000; 2000US-236891P.
PR 02-OCT-2000; 2000US-237172P.
PR 02-OCT-2000; 2000US-237173P.
PR 02-OCT-2000; 2000US-237278P.

PR 02-OCT-2000; 2000US-237294P.
PR 02-OCT-2000; 2000US-237295P.
PR 02-OCT-2000; 2000US-237316P.
PR 03-OCT-2000; 2000US-237425P.
PR 03-OCT-2000; 2000US-237598P.
PR 03-OCT-2000; 2000US-237604P.
PR 03-OCT-2000; 2000US-237606P.
PR 03-OCT-2000; 2000US-237608P.
PR 01-NOV-2000; 2000US-244867P.
PR 01-NOV-2000; 2000US-245084P.
XX
XX (AVAL-) AVALON PHARM.
PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppet DR, Weaver Z;
XX
XX WPI; 2002-188264/24.
DR
XX
XX Screening for anti-neoplastic agent involves exposing cells to a
PT chemical agent to be tested for anti-neoplastic activity, and
PT determining a change in expression of a gene of a signature gene set -
XX
XX
PS Claim 1; SEQ ID 2456; 44pp; English.

CC The present invention describes a method (M1) for screening for an
CC anti-neoplastic agent. The method involves exposing cells to a chemical
CC agent to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening
CC an anti-neoplastic agent, and can be used for producing a product which
CC is the data collected with respect to the anti-neoplastic agent as a
CC result of M1, and the data is sufficient to convey the chemical
CC structure and/or properties of the agent. M1 can be used in the
CC treatment of cancer such as colon, breast, stomach, lung, thyroid,
CC oesophageal, ovarian, kidney, prostate or pancreatic cancer,
CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
CC carcinoma, papillary carcinoma and Wilm's tumour.

XX
SQ Sequence 1743 BP; 347 A; 543 C; 549 G; 304 T; 0 other;

Alignment Scores:

Pred. No.: 5.31e-118 Length: 1743
Score: 2254.50 Matches: 413
Percent Similarity: 91.57% Conservative: 0
Best Local Similarity: 91.57% Mismatches: 4
Query Match: 97.05% Indels: 35
DB: 24 Gaps: 1

US-09-993-234-6 (1-417) x ABL64119 (1-1743)

QY 1 MetCluGlInARgProARgGlyCysAlaAlaValAlaAlaAlaLeuLeuValLeu 20
DB 69 ATGGAGCAGCGCGCGGGCTGCGCGGCGGTGGCGCGCGCTCCTCGTGGTGGCTG 128
QY 21 GlyAlaARgAlaGlnGlyGlyThrArgSerProARgCysAspCysAlaGlyAspPheHis 40
DB 129 GGGGCCCCGGGGCCAGGGCGGCACTGTAAGCCCAAGGTGACTGTGCCGGTGACTTCCAC 188
QY 41 LysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaPro 60
DB 189 AAGAAGATTGGTCTGTTTGTTCAGAGAGGCTGCCACGCGGGGCACTACCTGAAGGCCCT 248
QY 61 CysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAla 80
DB 249 TGCACGGAGCCCTGGCGCACTCCACCTGCTGTGTGTCGCCAAGACACACTTCTTGCC 308
QY 81 TrpGluAsnHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSer 100
DB 309 TGGGAGAACCAACATTAATCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCTCC 368

QY 101 GlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGly 120
DB 369 CAGGTGGCGCTGGAGAACTGTTCAGCAGTGGCCGACACCGCTGTGGCTGTAAGCCAGCC 428
QY 121 TrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCysGlnPro 140
DB 429 TGGTTGTGGAGTGGCAGGTGACCAATGTGTACAGCAGTTACCCCTTCTACTGCCAACCA 488
QY 141 CysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThr 160
DB 489 TGCCTAGACTGGGGGGCCCTGCACCGCCACACAGCGCTACTCTGTCCCGCAGAGATACT 548
QY 161 AspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysPro 180
DB 549 GACTGTGGACCTGCGCTGCTGCTTCTATGAACATGGCGATGGCTGCTGCTGCCCC 608
QY 181 ThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTyrParg----- 198
DB 609 ACGAGCACCCCTGGGAGCTGTCCAGAGCGCTGTGCCGCTGTGTGGCTGAGGCAAGT 668
QY 198 ----- 198
DB 669 AGGTGGTGTGCTGGGAATGGCGGTGGGAGAACTGGGATGGACCGAGGGAGCGGGTGAG 728
QY 199 -----GlnMetPheTrpValGlnValLeu 206
DB 729 GAGGGGGGCAACCAACCAACCAACCAAGCTGCTTTTCAGTG- TTCTGGGTCCAGGTGCTC 787
QY 207 LeuAlaGlyLeuValValProLeuLeuGlyAlaThrLeuThrTyrTrpArgHis 226
DB 788 CTGGCTGGCTTGTGGTCCCTCTCTGCTTGGGGCCACCTGACCTACACATACCGGCAC 847
QY 227 CysTrpProHisLysProLeuValThrAlaAspGluAlaGlyMetGluAlaLeuThrPro 246
DB 848 TGTGGCTTCACAAAGCCCTGTGTTACTGCAGATGAAGCTGGATGAGGCTTGACCCA 907
QY 247 ProProAlaThrHisLeuSerProLeuAspSerAlaHisThrLeuLeuAlaProProAsp 266
DB 908 CCACCGGCACCCATCTGTACCTTGGACAGCGCCACACCTTCTAGCACCTCCTGAC 967
QY 267 SerSerGluLysIleCysThrValGlnLeuValGlyAsnSerTrpThrProGlyTyrPro 286
DB 968 AGCATGAGAAGATCTGCACCGCTCCAGTTGGTGGTAACAGCTGGACCCCTGGCTACCCC 1027
QY 287 GluThrGlnGluAlaLeuCysProGlnValThrTrpSerTrpAspGlnLeuProSerArg 306
DB 1028 GAGACCCAGGAGGCGCTGTGCCCGCAGGTGACATGGTCTTGGGAACCAAGTTGCCACAGA 1087
QY 307 AlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSerProAlaGlySerProAla 326
DB 1088 GCTCTTGGCCCCGCTGCGTGGCCACACTCTGCCAGAGTCCCAAGCCGGCTGCCAGCC 1147
QY 327 MetMetLeuGlnProGlyProGlnLeuTyrAspValMetAspAlaValProAlaArgArg 346
DB 1148 ATGATGCTGCAGCGCGGCCGCACTTACGACGTGATGAGCGCGGTCCAGCGCGCGCC 1207
QY 347 TrpLysGluPheValArgThrLeuGlyLeuArgGluAlaGluIleGluAlaValGluVal 366
DB 1208 TGGAAAGAGTTCTGTGCGCAGCGTGGGGCTGCGCGAGGAGAGATCGAAGCCGTGAGGTG 1267
QY 367 GluIleGlyArgPheArgAspGlnGlnTyrGluMetLeuLysArgTrpArgGlnGlnGln 386
DB 1268 GAGATCGGCTCTCTTCCGAGACCAAGTACGAGATGCTCAACACTGGCGCCAGCAGCAG 1327
QY 387 ProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMetGlyLeuAspGlyCysVal 406
DB 1328 CCGCGGGGCTCGGAGCGCTTTCAGCGGGCCCTGGAAGCGCATGGGGCTGGACGGCTGCGTG 1387
QY 407 GluAspLeuArgSerArgLeuGlnArgGlyPro 417
DB 1388 GAAGACTTGGCGCAGCGCGCTGCAGCGTGGCCG 1420

RESULT 14
ID AAF83770 standard; DNA; 1250 BP.
XX AAF83770;
AC
XX 06-AUG-2001 (first entry)
DT
XX Nucleotide sequence of human TR3 gene.
DE
XX TR3; cell proliferation; leukemia; immunosuppressive; cytostatic;
KW dermatological; antiarthritic; antidiabetic; neuroprotective; cardiant;
XX antithyroid; antiinflammatory; antiallergic; T-cell-inhibitor; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 1..1250
FT /*tag= a
FT /transl_except= "(pos:481..482, aa:Asp)"
FT /note= "this codon has an apparent 1 nucleotide
FT deletion which alters the reading frame"
FT /transl_except= "(pos:558..559, aa:Cys)"
FT /note= "this codon has an apparent 1 nucleotide
FT deletion which alters the reading frame"
FT /transl_except= "(pos:638..639, aa:Leu)"
FT /note= "this codon has an apparent 1 nucleotide
FT deletion which alters the reading frame"
FT /transl_except= "(pos:718..719, aa:Met)"
FT /note= "this codon has an apparent 1 nucleotide
FT deletion which alters the reading frame"
FT sig_peptide 1..72
FT /*tag= b
FT mat_peptide 73..1247
FT /*tag= c
XX
XX WO200135995-A2.
XX
XX 25-MAY-2001.
XX
XX 17-NOV-2000; 2000WO-US31692.
XX
XX 19-NOV-1999; 99US-0166583.
XX
XX (TITT/) TITTLE T V.
XX (WEGM/) WEGMANN K W.
XX
XX Tittle TV, Wegmann KW;
XX
XX WPI; 2001-343711/36.
XX P-PSDB; AAB84941.
XX
XX
XX Composition for treatment of T-cell mediated disease e.g. arthritis,
XX cancer comprises a biologically active TR3-specific binding agent
XX especially a monoclonal antibody -
XX
XX Disclosure; Page 72; 77pp; English.
XX
XX The invention relates to a composition comprising a biologically active
XX TR3-specific binding agent (I) that binds to TR3 and inhibits the
XX proliferation of cells expressing TR3. (I) identified by the methods are
XX useful for treating a subject suspected of having a disease associated
XX with a proliferation of cells expressing TR3 especially leukemias or
XX lymphomas or a T-cell mediated disease especially autoimmune diseases
XX such as myasthenia gravis, systemic lupus erythematosis, rheumatoid
XX arthritis, diabetes, multiple sclerosis, sarcoidosis, myocarditis,
XX thyroiditis and tumours. (I) is also useful for treating a subject
XX suspected of having graft-versus-host disease, rejection of a
XX transplanted organ such as heart, liver, lung, kidney, pancreas, bowel,
XX skin or an appendage, or inflammatory diseases, allergies and contact
XX dermatitis. The present sequence represents the nucleotide sequence of
XX human TR3 gene.

US-09-993-234-6 (1-417) x AAF83770 (1-1250)
SQ Sequence 1250 BP; 201 A; 419 C; 406 G; 224 T; 0 other;
Alignment Scores:
Pred. No.: 1.52e-115 Length: 1250
Score: 2208.00 Matches: 413
Percent Similarity: 99.04% Conservative: 0
Best Local Similarity: 99.04% Mismatches: 4
Query Match: 95.05% Indels: 4
DB: 22 Gaps: 0
QY 1 MetGluGlnArgProArgGlyCysAlaAlaValAlaAlaLeuLeuValLeuLeu 20
Db 1 ATGGAGCAGCGCGCGCGCGCGCTGCGCGCGGTGGCGCGCGCTCTCTGCTGCTG 60
QY 21 GAlAaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHis 40
Db 61 GGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
QY 41 LysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaPro 60
Db 121 AAGAAGATTGGTCTTTTGTGTGACAGAGCTGCCAGCGCGGCGACTACCTGAAGCCCT 180
QY 61 CysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAla 80
Db 181 TGCACGAGCGCTGCGGCACTCCACCTGCTGTGTGTCTCCCAAGACACCTTCTGGCC 240
QY 81 TrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluAlaSer 100
Db 241 TGGAGAGACCAACCATATATCTGATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCTCC 300
QY 101 GlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGly 120
Db 301 CAGGTGGCGCTGGAAGACTGTTCAGCAGTGCGCCGACACCCGCTGTGGCTGAAGCCAGGC 360
QY 121 TrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCysGlnPro 140
Db 361 TGGTTGTGGAGTGCCAGGTCCAGCAATGTGTACAGCAGTTCACCTTCTACTGCCAACCA 420
QY 141 CysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThr 160
Db 421 TGCCTAGACTGCGGGCGCTGCACCGCACACAGGCTACTGTGTCCCGCAGAGATAC- 479
QY 161 AspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysPro 180
Db 480 GACTGTGGGACCTGCGCTGCTGCTTCTATGAACATGGCGATGGCTGCTGCTGCCCC 539
QY 181 ThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTyrParglnMet 200
Db 540 ACGAGCACCTGGGAGCGGT-CCAGAGCGCTGTGCCGCTGTGTGGCTGAGGAGCATG 598
QY 201 PheTyrValGlnValLeuLeuAlaGlyLeuValValProLeuLeuGlnGlyAlaThrLeu 220
Db 599 TTCTGGGTCACAGGTGCTCTGGCTGTGTGT-CCCCCTGTGTGGGCCACCCCTG 657
QY 221 ThrTyrThrTyrArgHisCysTrpProHisLysProLeuValThrAlaAspGluAlaGly 240
Db 658 ACCTACACATACCGCCACTGCTGGCTCACAAGCCCTGTACTGACAGATGAAGCTGA 717
QY 241 MetGluAlaLeuThrProProAlaThrHisLeuSerProLeuAspSerAlaHisThr 260
Db 718 TG-GAGGCTTGACCCCAACCGCGCCACCCATGTTCACCTTGACAGCGGCCACACC 776
QY 261 LeuLeuAlaProProAspSerSerGluLysIleCysThrValGlnLeuValGlyAsnSer 280
Db 777 CTCTTAGCACCTCTGACAGCAGTGAGAGATGTGCACCGTCCAGTTGGTGGTAACAGC 836
QY 281 TrpThrProGlyTyrProGluThrGlnGluAlaLeuCysProGlnValThrTyrSerTrp 300
Db 837 TGGACCCCTGGCTACCCCGAGACCCAGAGGCGCTGTGCCGACAGGTGACATGTGCTGG 896
QY 301 AspGlnLeuProSerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSer 320

|||||
Db 897 GACCAAGTGGCCAGCAGAGCTCTTGGCCCCGCTGCTGCGCCACACTCTCGCAGAGTCC 956
QY 321 ProAlaGlySerProAlaMetMetLeuGlnProGlyProGlnLeuTyrAspValMetAsp 340
Db 957 CCAGCCGCTCGCCAGCATGATGCTGCAGCCGGCCCCGAGCTCTACGACGTGATGAC 1016
QY 341 AlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGluAlaGlu 360
Db 1017 GCGGTCCAGCGCGGCTGGAAGAGATCGTGCCAGCGCTGGGGCTGCGCCAGCAGAG 1076
QY 361 IleGluAlaValGluValIleGlyArgPheArgAspGlnGlnTyrGluMetLeuLys 380
Db 1077 ATCGAAGCCGTGAGGTGAGATCGGCCGCTTCCGAGACCAAGCAGTACGATGCTCAAG 1136
QY 381 ArgTrpArgGlnGlnInProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMet 400
Db 1137 CGCTGGCGCCAGCAGACGCCCGGGCTCGAGCCGTTTACGGCGCCCTGAGCGCATG 1196,
QY 401 GlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 417
Db 1197 GGGCTGACGCGCTCGTGAAGACTTGCGCAGCCGCTGACGCGGCCCG 1247

RESULT 15

AAL47185
ID AAL47185 standard; DNA; 4825 BP.

XX AAL47185;

DT 22-AUG-2002 (first entry)

XX Human DR3 gene associated with rheumatoid arthritis.

XX Human; DR3; rheumatoid arthritis; antirheumatic; antiarthritic;
KW gene therapy; gene; ds.

XX Homo sapiens.

EH Key Location/Qualifiers
FT CDS 1..4825

FT /tag= a
FT /product= "DR3"
FT /note= "this sequence contains introns"
FT 1..127

FT /tag= b
FT /number= 1

FT /tag= c
FT /number= 1

FT /tag= d
FT /number= 2

FT /tag= e
FT /number= 2

FT /tag= f
FT /number= 3

FT /tag= g
FT /number= 3

FT /tag= h
FT /number= 4

FT /tag= i
FT /number= 4

FT /tag= j
FT /number= 5

FT /tag= k
FT /number= 5

FT /tag= l
FT /number= 5

FT /tag= m
FT /number= 6

FT /tag= n
FT /number= 7

FT /tag= o
FT /number= 7

FT /tag= p
FT /number= 8

FT /tag= q
FT /number= 8

FT /tag= r
FT /number= 9

FT exon 3069..3124
FT /tag= 1
FT /number= 6
FT 3125..3225
FT /tag= m
FT /number= 6
FT 3226..3333
FT /tag= n
FT /number= 7
FT 3334..3529
FT /tag= o
FT /number= 7
FT 3530..3577
FT /tag= p
FT /number= 8
FT 3578..4021
FT /tag= q
FT /number= 8
FT 4022..4202
FT /tag= r
FT /number= 9
FT 4203..4433
FT /tag= s
FT /number= 9
FT 4434..4825
FT /tag= t
FT /number= 10

WO200234912-A1.

02-MAY-2002.

24-OCT-2001; 2001WO-JP09313.

24-OCT-2000; 2000JP-0324296.

27-MAR-2001; 2001JP-0090546.

30-MAR-2001; 2001JP-0099990.

(NEWI-) NEW IND RES ORG.

(SHIO/) SHIOZAWA S.

Shiozawa S, Konishi Y;

WPI; 2002-417132/44.

Genomes, particularly DR3 genomic DNA, participating in rheumatoid

arthritis via mutation, useful in evaluating disease onset and its

possibility and providing therapy and remedies -

Claim 1; Page 64-66; 84pp; Japanese.

The present invention relates to the human DR3 gene, which is associated

with rheumatoid arthritis. Certain mutations in the gene can be linked to

the disease. The sequences can be used to evaluate disease onset and its

possibility and to provide therapy and remedies. The present sequence is

the gene of the invention.

Sequence 4825 BP; 921 A; 1378 C; 1521 G; 1005 T; 0 other;

Alignment Scores: 2.42e-78 Length: 4825

Pred. NO.: 1556.50 Matches: 405

Score: 29.10% Conservative: 1

Best Local Similarity: 29.03% Mismatches: 9

Query Match: 67.00% Indels: 984

DB: 24 Gaps: 9

US-09-993-234-6 (1-417) x AAL47185 (1-4825)

QY 3 GlnArgProArgGly-----CysAlaAlaValAlaAlaAlaLeuLeu 16

Db 585 GAGGCCCCACGCTGGCGCTGAGAGTACAGACACCTGTCCCCAGCGCTCCTC 644

QY	17	LeuValLeuLeuGlyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAla	36
Db	645	CTGGTGTCTGGGGGGCCCCGGGCCAGGGGGGCACTGTAGCCCCAGGTGTGACTGTGCC	704
QY	37	GlyAspPheHisIysLysIleGlyLeuPheCysCysArgGlyCysProAla	53
Db	705	GGTGACTTCCACAGAAGATTGGTCTGTGTTGTCAGAGGCTGCCACGGGTAAGTGG	764
QY	53	-----	53
Db	765	CCACAGGGGTGGAGAGGCATGGGGCAGGCAGGGCTGGAGAGGTGGGGGCCAGGGCGG	824
QY	53	-----	53
Db	825	AGGTAAGAGAGAGCTGGCAGGGAGGTAGGGGTAGGCTGACAGAGAAGTAGGAGCTGA	884
QY	53	-----	53
Db	885	GAGAAAGAGGAGGGAGGGCAGGGGTGGGAAGCAGGTGCGGGGTGTGGCCAGCCCTCT	944
QY	54	-----GlyHisTyrLeuLysAlaProCysThrGluPr	64
Db	945	GCCGTGCTGACCCCTGCTGTTCCACAGGGCACTACTGAAGGCCCTTGACAGGAGCC	1004
QY	64	OCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHi	84
Db	1005	CTGGGCACTCCACCTGCTGTGTGTCCCAAGACACCTTCTTGGCTTGGGAGAACCA	1064
QY	84	SHisAsnSerGluCysAlaArgCysGlnAlaCysAspGlu	97
Db	1065	CCATAATTCTGAATGTGCCCCGCTGCCAGGCCCTGTGATGAGCAGGGGTGAGGGCTTCTCAG	1124
QY	97	-----	97
Db	1125	TGCTTGGCAGGGAGTTCCTAAGACAGCCCTTCTGAAGAACTGGCTGGGGCCGA	1184
QY	97	-----	97
Db	1185	AACTTGGGGTGTGAGGTCCTGCACCCACCCTTGCCAGAACCTCCACCCTGATCCTCT	1244
QY	97	-----	97
Db	1245	TCAAGGTGCCCTTGCCCCCTTCTCTCTCTGCTGTGACCTTCCATCTCCATGTGCCCTG	1304
QY	97	-----	97
Db	1305	GCCCTGTGTCGGCCCTTAATCTGTGAGCTTCTCTCTTTTAAAGGTAGCCCTGACCTGTC	1364
QY	97	-----	97
Db	1365	TGCTTTTGGCCTATTCTCTCTCCATTATCTTGGATAATGCCCTTGCCCTGCCATGGGA	1424
QY	98	-----GlnAlaSerGln	101
Db	1425	GCCTTTGGCCCTGACCTAATCTCCACTCCCATCTGCCATCTGCCATGGGA	1483
QY	101	nValAlaLeuGluAsnGlySerAlaValAlaAspThrArgCysGlyCysLysProGlyTr	121
Db	1484	GGTGGCGCTGAGAACTCTTCAGCAGTGGCCGACACCCGCTGTGGCTGTAAGCCAGGCTG	1543
QY	121	pPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCys	141
Db	1544	GTTTGTGAGTGCCAGGTACGCCAATGTGTACAGAGTTACCCCTTACTGCAACCATG	1603
QY	141	sLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSer	156
Db	1604	CCTAGACTGGGGGCTGCACCGCCACACAGGCTACTCTGTGA-GTACCCCAACCCAG	1662
QY	156	-----	156
Db	1663	GGCTCTTACTCCAGAACCCCTTCTCCCTGCTGACCCACTCCTGTCCATGGTGACGC	1722
QY	157	-----ArgArgAspThrAspCysGlyThrCysLeuProGln	168

Db	1723	ATGCTCTCCTGATTCAGGTTCCCGCAGATACTGACTGTGGACCTGCCTGCTGG		1782
QY	168	yphETyGLuHISGLyaspGLyCysValSerCysProThrSer		182
Db	1783	CTTCTATGAACATGGCGATGGCTGCTGCTCTGCCACACGTA-ATTCTAGCTGTCTGG		1841
QY	182	-----	-----	182
Db	1842	GATGGAGGGAAGGGCGCTGGGACGACAGAGGGGCTGGGGTGGGCGAGTCTGCTGG	-----	1901
QY	182	-----	-----	182
Db	1902	TTTCAGGAATAGGAAGAGGGGATAGGAGAGGAGGAGCGCTTGCCCTGTGATGGGTGGGCC	-----	1961
QY	182	-----	-----	182
Db	1962	CACTTCAGGCAAACTTAGATGGCAAAAGACAATCTGATCCGCTTACCCAGATACATA	-----	2021
QY	182	-----	-----	182
Db	2022	AGGGTATTTGCCCTTCACTTTCAGCCACGATTTCCCCCAGCGATCCTAGCCAGATATTACA	-----	2081
QY	182	-----	-----	182
Db	2082	GATGATTTGTCACTTACACAGAGAGTCACATTGATATAGCTTTAAAACTTGGGCTGAAGG	-----	2141
QY	182	-----	-----	182
Db	2142	AGGTGAGGCTGCAGTACGATATGATCGTCCACTGCACCTTCAGCGCTGGGCAACAGAGCG	-----	2201
QY	182	-----	-----	182
Db	2202	AGACCTATTAAATAAATAAATAATTAATCTATTAAATATTAAATATTAAATCTATT	-----	2261
QY	182	-----	-----	182
Db	2262	AAATAAATAAATACAAAGGGCTGAGAGTCAGGACTGTGCTGTAAGTTCTCTAGGGGATCT	-----	2321
QY	182	-----	-----	182
Db	2322	TGGGCAAGTCAGAGAA TTCGCGTCTGTGATGTGTGTGCCCTTCTCAACATGGGATG	-----	2381
QY	182	-----	-----	182
Db	2382	TTAGCAGCTAAATCACAGGCTTTGATCAGAGGTAAGGACTTCTCTAGCTATTCAAGT	-----	2441
QY	182	-----	-----	182
Db	2442	CTTTTTTTTTTTTTTTTTTTTTTTTTTTGAGATGAGACTTGCTCTGTCACCAGGCTG	-----	2501
QY	182	-----	-----	182
Db	2502	GAGTCAGTGGACGATCTTGCGCTCACTACAACTCTGCTGCCCTGGGTTCAAGTATCT	-----	2561
QY	182	-----	-----	182
Db	2562	CCTGCCCTCAGCCTCCCAAGTAGCTGGGACTACAGGAGCCCAACCACCCCGGCTAAAT	-----	2621
QY	182	-----	-----	182
Db	2622	TTTTGTATTTTATAGAGACGGGGTTTACCCGTGTAGCCAAAGATGCTTGATCACCT	-----	2681
QY	182	-----	-----	182
Db	2682	GACCTGATGATCCACCCGCTTGCGCTCCCAAGTGTCTGGGATTACAGGCATGAGCCACC	-----	2741
QY	182	-----	-----	182
Db	2742	GGCGCCGGCCTCCATTCAAGTCTTTATGATAATCTGCTATGTTCTACACACTGTCTAG	-----	2801
QY	182	-----	-----	182

Db 2802 GTGCTGGGATGCAACAGGGGACAAATAGGCAAAATCCCTGTCTTTGGGGTTGACAT 2861
 QY 182 ----- 182
 Db 2862 TCTAGTGA CTTCATGTAGTCTAGAAGAAGCTCAGTGAATAGTGTCTGTGTTACC 2921
 QY 182 ----- 182
 Db 2922 AGGGACACATGACAGAACATTTCTGGGTAGAGTGAGGCCCTGGGAGGGAAGGCTCT 2981
 QY 182 ----- 182
 Db 2982 CTAGGATGGACAGATGCTGGGCAGTCTTAGGGAGCCCCCTCGCATGCAACCCCTCAT 3041
 QY 183 -----ThrLeuGlySerCysProGluArgCysAl 192
 Db 3042 CCCTCAGGCCACCCCGTCCTTGACAGAGCACCCCTGGGGAGCTGTCCAGAGCGCTGTGC 3101
 QY 192 aAlaValCysGlyTTPArg----- 198
 Db 3102 CGCTGTCTGTGGCTGGAGCAGAGTAGTGTGTGCTGGGAATGCGAGTGGAGAACTGG 3161
 QY 198 ----- 198
 Db 3162 GATGGACCGAGGGAGGGGTGAGGAGGGGGCAACCAACCAACCCACAGCTGCTT 3221
 QY 199 -GlnMetPheTrpValGlnValLeuLeuAlaGlyLeuValValProLeuLeuGlyAl 218
 Db 3222 TCAGTG-TTCTGGGTCCAGGTGCTCTCTGGCTGGCTTGTGTGTCCTCCCTGCTTGGGGC 3280
 QY 218 aThrLeuThrTyrThrTyrArgHisCysTrpProHisLysProLeuValThr----- 235
 Db 3281 CACCTGACCTACACATACCGCCACTGTGCGCTCACAAGCCCTGTTACTGTGAAGTA 3340
 QY 235 ----- 235
 Db 3341 CACACACCCACACACGCAACAGAGCCTGGGGTCAGATGGGTAGCCCAGAGTCTACTC 3400
 QY 235 ----- 235
 Db 3401 AACCTGATACAGAAGGGGAAACTGAGGCAGGAGTGTGGGGTGCAGAGGAACCTAGAG 3460
 QY 235 ----- 235
 Db 3461 GAGCTGTACCAGCACCCAGGTCCAGGAGCCTTGCTGTGGCTGACCCGAATCTCTGT 3520
 QY 236 -----AlaAspGluAlaGlyMetGluAlaLeuThrProPro----- 247
 Db 3521 GTCTGTCAAGATGAAGCTGGATGAGGCTGTGACCCCAACCGGTAAAGAACTCAC 3580
 QY 247 ----- 247
 Db 3581 TGTGTGATTTCTGGGCTGCTTCTGAGCTGGAAGATCAAGCCTTACTATGATCCCTGGAG 3640
 QY 247 ----- 247
 Db 3641 CTTGGCAGCGCGGCAGACCCGGGTAGCCCTAGTGACAGAGGTGTGGGAGAGAGTCA 3700
 QY 247 ----- 247
 Db 3701 CAGTGGATGAGACCAAGCAGTGCCTGCCCTCAAGGGGTCTCAGTCAAGCTGAGTTCA 3760
 QY 247 ----- 247
 Db 3761 ATTGCTACACAGAGCTAACAGTTCAATGGAAGAGAGCCCATGTGCTGGGGACAAG 3820
 QY 247 ----- 247
 Db 3821 AGGAAGGAGCGGGGCAAGGGAAGTCAAGGACAGAAAGAGTTCTGCTGGGCTACAGTG 3880
 QY 247 ----- 247
 Db 3881 AGAGCAGGGCAACTGTGGGAGGTGTATTTGGGGGTGTCTGCTGACTGAACGAGGAC 3940

QY 247 ----- 247
 Db 3941 TGTCCCTCTCTGAGAGGCACTGCGGGTAAAGGGGCTTACTTGGCAAGCAGGGCTGACCT 4000
 QY 248 -----Pro-AlaThrHisLeuSerProLeuAspSerAlaHisThrLeu 261
 Db 4001 GGGGCCCTCTTGGCTTCCAGGCCACCCATCTGTACACCTTGACAGCGCCACACCTT 4060
 QY 262 LeuAlaProProAspSerSerGluLysIleCysThrValGlnLeuValGlyAsnSerTrp 281
 Db 4061 CTAGCACTCTGTACAGACAGTGAAGATCTGCACCGTCCAGTTGGGTAAACAGCTGG 4120
 QY 282 ThrProGlyTyrProGluThrGlnGluAlaLeuCysProGlnValThrTrpSerTrpAsp 301
 Db 4121 ACCCTGGCTACCCCGAGACCCAGAGGCGCTCTGCCCGCAGGTACATGTTCTGGGAC 4180
 QY 302 GlnLeuProSerArgAlaLeu----- 308
 Db 4181 CAGTTGCCAGACAGAGCTCTTGGTAAAGGACATCAGTGGCCTGAGGCCCTGACCCATTC 4240
 QY 308 ----- 308
 Db 4241 TCCTGTCTGCGGTGGAAAGTTGTGGTTTCACAACGTGTTCCCTTCTGCCCCCTACTGA 4300
 QY 308 ----- 308
 Db 4301 CGGAGTCCGCCCTATGCCCTGACCCACCGGATCCAGCGGCTTCAGCCCTGGGGTACCCG 4360
 QY 308 ----- 308
 Db 4361 CACGAACGCCCTGACTCTGCTCTCCGACCGCGGGCCAGGTACCCCAATTGGCTCTCTCT 4420
 QY 309 -----GlyProAlaAlaAlaProThrLeuSerProGluSerProAlaGlySer 324
 Db 4421 GGCCCTGCCAGGCGCCGCTGTGCTGCGCCACACTCTGCCAGAGTCCCAAGCGGCTCG 4480
 QY 325 ProAlaMetLeuGlnProGlyProGlnLeuTyrAspValMetAspAlaValProAla 344
 Db 4481 CCAGCATGATGCTGACCGCGGGCCCGCAGCTCTACGACGTGATGAGCGGCTCCACGG 4540
 QY 345 ArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGluAlaGluIleGluAlaVal 364
 Db 4541 CGGCGCTGGAAGAGTTCTGTGCGCACGCTGGGGCTGCGGAGGACAGATCGAAGCGGTG 4600
 QY 365 GluValGluIleGlyArgPheArgAspGlnGlnTyrGluMetLeuLysArgTrpArgGln 384
 Db 4601 GAGGTGAGATCGGCGGCTTCCGAGACCAAGACAGATGCTCAAGCGCTGGCCAG 4660
 QY 385 GlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMetGlyLeuAspGly 404
 Db 4661 CAGCAGCCCGCGGGCTCGAGCGCTTTACGCGGCGCTTGAAGCGCATGGGGCTGACGGC 4720
 QY 405 CysValGluAspLeuArgSerArgLeuGlnArgGlyPro 417
 Db 4721 TGCGTGAAGACTTGCAGCGCGCTGACGCGGCGCG 4759

Search completed: April 6, 2003, 16:51:19
 Job time : 420.274 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 6, 2003, 21:08:18 ; Search time 158.782 Seconds
(without alignments)
2303.655 Million cell updates/sec

Title: US-09-993-234-6
Perfect score: 2323
Sequence: 1 MEGRPRGCAVAALLLVL.....ERMGLDGCVEDLRSRLQGP 417

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 593429 seqs, 438583890 residues

Total number of hits satisfying chosen parameters: 1186858

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-O=/cgn2_1/USPTO.spool/US0993234/runat_27032003_115459_15466/app_query.fasta.1.2346
-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=biosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US0993234 @CGN_1_1_249 @runat_27032003_115459_15466
-NCPU=6 -ICPU=3 -NO_XLPXY -NO_MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2323	100.0	1254	10	US-09-333-966-3 Sequence 3, Appl1
2	2323	100.0	1634	9	US-10-081-280-9 Sequence 9, Appl1
3	2323	100.0	1634	9	US-10-112-793-9 Sequence 9, Appl1
4	2323	100.0	1634	9	US-10-112-193-11 Sequence 11, Appl1

5	2323	100.0	1634	10	US-09-993-234-9	Sequence 9, Appl1
6	2267	97.6	1783	10	US-09-333-966-1	Sequence 1, Appl1
7	2254.5	97.1	1743	9	US-09-954-531-1389	Sequence 1389, Ap
8	1556.5	67.0	10797	9	US-10-092-154-1577	Sequence 1577, Ap
9	1556.5	67.0	10797	10	US-09-764-847-1577	Sequence 1577, Ap
10	1066	45.9	1438	9	US-10-081-280-5	Sequence 5, Appl1
11	1066	45.9	1438	9	US-10-112-793-5	Sequence 5, Appl1
12	1066	45.9	1438	9	US-10-112-193-5	Sequence 5, Appl1
13	1066	45.9	1438	10	US-09-884-733-5	Sequence 5, Appl1
14	1066	45.9	1438	10	US-09-993-234-5	Sequence 5, Appl1
15	1039.5	44.7	816	10	US-09-964-824A-292	Sequence 292, App
16	692	29.8	433	9	US-10-081-280-2	Sequence 2, Appl1
17	692	29.8	433	9	US-10-112-793-2	Sequence 2, Appl1
18	692	29.8	433	9	US-10-112-193-2	Sequence 2, Appl1
19	692	29.8	433	10	US-09-884-733-2	Sequence 2, Appl1
20	692	29.8	433	10	US-09-993-234-2	Sequence 2, Appl1
21	394.5	17.0	2130	10	US-09-917-800A-1601	Sequence 1601, Ap
22	387.5	16.7	2440	10	US-09-970-532-1	Sequence 1, Appl1
23	380.5	16.4	2173	9	US-09-898-234-14	Sequence 14, Appl1
24	380.5	16.4	2173	9	US-09-899-429A-24	Sequence 24, Appl1
25	380.5	16.4	2173	9	US-09-792-356-14	Sequence 14, Appl1
26	380.5	16.4	2173	10	US-09-899-422-14	Sequence 14, Appl1
27	374	16.1	1368	9	US-09-898-234-1	Sequence 1, Appl1
28	374	16.1	1368	9	US-09-899-429A-1	Sequence 1, Appl1
29	374	16.1	1368	9	US-09-792-356-1	Sequence 1, Appl1
30	374	16.1	1368	10	US-09-899-422-1	Sequence 1, Appl1
31	374	16.1	2111	10	US-09-880-107-2360	Sequence 2360, Ap
32	374	16.1	2141	9	US-09-898-234-16	Sequence 16, Appl1
33	374	16.1	2141	9	US-09-899-429A-26	Sequence 26, Appl1
34	374	16.1	2141	9	US-09-792-356-16	Sequence 16, Appl1
35	374	16.1	2141	10	US-09-899-422-16	Sequence 16, Appl1
36	374	16.1	2175	12	US-10-120-397-1	Sequence 1, Appl1
37	330	14.2	191	9	US-09-796-692-2549	Sequence 2549, Ap
38	261	11.2	1334	9	US-09-898-234-11	Sequence 11, Appl1
39	261	11.2	1334	9	US-09-792-356-11	Sequence 11, Appl1
40	261	11.2	1334	10	US-09-899-422-11	Sequence 11, Appl1
41	256	11.0	1334	9	US-09-899-429A-21	Sequence 21, Appl1
42	233	10.0	1704	12	US-10-020-787-1	Sequence 1, Appl1
43	230.5	9.9	1724	10	US-09-924-231-1	Sequence 1, Appl1
44	230.5	9.9	1724	10	US-09-934-289A-14	Sequence 14, Appl1
45	220.5	9.5	1834	10	US-09-934-289A-41	Sequence 41, Appl1

ALIGNMENTS

RESULT 1
US-09-333-966-3
Sequence 3, Application US/09333966
Patent No. US20020009773A1
GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang
APPLICANT: Ni, Jian
APPLICANT: Dixit, Vishva
APPLICANT: Gentz, Reiner L.
APPLICANT: Dillon, Patrick J.
TITLE OF INVENTION: Death Domain Containing Receptors
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/333,966
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/815,469
FILING DATE:
APPLICATION NUMBER: No. US20020009773A1 Yet Assigned
FILING DATE: 06-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,711
FILING DATE: 17-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,285
FILING DATE: 12-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1254 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1251
US-09-333-966-3

Alignment Scores:
Pred. No.: 1.52e-198 Length: 1254
Score: 2323.00 Matches: 417
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-993-234-6 (1-417) x US-09-333-966-3 (1-1254)

QY 1 MetGluGlnArgProArgGlyCysAlaAlaValAlaAlaLeuLeuValLeu 20
Db 1 ATGACACAGCGCGCGCGGCTCCGCGGCTGGCGGCGGCTCCTGCTGCTG 60
QY 21 GlyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHis 40
Db 61 GGGGCCCCGGGCCCCAGGGCGGCACTGTAGCCCCAGGTGTGACTGTGCGGTGACTCCAC 120
QY 41 LysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaPro 60
Db 121 AAGAAGATTGCTGTGTTGTGTGACAGAGGCTGCCAGCGGGGCACTACTGAGAGCCCT 180
QY 61 CysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAla 80
Db 181 TGCACGAGACCCCTGGCGCACTCCACCTGCTGTGTGCCCAAGACACCTTTTGGCC 240
QY 81 TrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSer 100
Db 241 TGGGAGAACCACCATATTCTGAATGTGCCCCGCTGCCAGCCCTGTGATGAGAGCCCTCC 300
QY 101 GlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGly 120
Db 301 CAGGTGGCGCTGAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGGCTGTAGCCAGGC 360
QY 121 TrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCysGlnPro 140
Db 361 TGGTTGTGAGTGCAGGTTCAGCCAATGTGTACAGTTACCCCTTACTGCCAACCA 420
QY 141 CysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThr 160
Db 421 TGCCTAGACTGCGGGGCTGCACCGCCACACAGCGCTACTCTGTCCCGCAGAGATACT 480
QY 161 AspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysPro 180

Db 481 GACTGTGGACTGCTGCTGCTGGCTTGTATGAACATGGCATGGCTGGCTGCC 540
QY 181 ThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTrpArgGlnMet 200
Db 541 ACAGACACCTGGGGAGCTGTCCAGAGCGCTGTGCCGCTGTCTGGCTGAGGACAGATG 600
QY 201 PheTrpValGlnValLeuLeuAlaGlyLeuValValProLeuLeuGlyAlaThrLeu 220
Db 601 TTCTGGTTCAGGTGCTCTGCTGGCTGTGGCTGTGGTCCCTCTGCTTGGGGCCACCTG 660
QY 221 ThrTyrThrTyrArgHisCysTrpProHisLysProLeuValThrAlaAspGluAlaGly 240
Db 661 ACCTACACATACCGCCACTGCTGGCTCACAAGCCCCCTGGTTACTGCAGATGAAGCTGGG 720
QY 241 MetGluAlaLeuThrProProAlaThrHisLeuSerProLeuAspSerAlaHisThr 260
Db 721 ATGAGGCTCTGACCCACCCACCGGCCACCATCTGTACCCCTTGGACAGCGCCACACC 780
QY 261 LeuLeuAlaProProAspSerSerGluLysIleCysThrValGlnLeuValGlyAsnSer 280
Db 781 CTCTAGACACTCTGTACAGCAGTGAAGAATCTGCACCGCTCCAGTTGGTGGTAACAC 840
QY 281 TrpThrProGlyTyrProGluThrGlnGluAlaLeuCysProGlnValThrTrpSerTrp 300
Db 841 TGGACCCCTGGCTACCCCGAGACCCAGAGGCGCTCTGCCCGCAGGTGACATGCTCTGG 900
QY 301 AspGlnLeuProSerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSer 320
Db 901 GACCACTTCCAGCAGAGAGCTCTGGCCCCGCTGCTGGCCCCACACTCTGCCAGAGTCC 960
QY 321 ProAlaGlySerProAlaMetLeuGlnProGlyProGlnLeuTyrAspValMetAsp 340
Db 961 CCAGCGGCTGCGCAGCAGCATGATGCTGCAGCGGGGCCGAGCTTACGACGTGATGAGAC 1020
QY 341 AlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGluAlaGlu 360
Db 1021 GCGGTCCAGCGCGCGCTGGAAGAGTTCGTGGCAGCGCTGGGCTCGCGCAGCAGAG 1080
QY 361 IleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGluMetLeuLys 380
Db 1081 ATCGAAGCCGTGAGGTGAGATCGGCCGCTTCCGACACACAGCAGTACGATGCTCAAG 1140
QY 381 ArgTrpArgGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMet 400
Db 1141 CGCTGGCGCCAGCAGCAGCCCCGGGCTCGGAGCCGTTTACGGCGCCCTTGAAGCCCATG 1200
QY 401 GlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 417
Db 1201 GGGCTGACGCGCTGCTGGAAGACTTGGCCGACCGCCCTGCAGCGCGGCCG 1251

RESULT 2

US-10-081-280-9
Sequence 9, Application US/10081280
Patent No. US20020165157A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/081,280

FILING DATE: 23-Sep-1996
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1634 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-112-793-9

Alignment Scores:
Pred. No.: 2.07e-198 Length: 1634
Score: 2323.00 Matches: 417
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-993-234-6 (1-417) x US-10-112-793-9 (1-1634)

QY 1 MetGluGlnArgProArgGlyCysAlaAlaValAlaAlaLeuLeuValLeu 20
DB 89 ATGAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 148
QY 21 GAlAAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHis 40
DB 149 GGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 208
QY 41 LysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaPro 60
DB 209 AAGAAGATTGCTGTTGTTGTTGTCAGAGGCTGCCAGCGGGGCACTACCTGAAGGCCCT 268
QY 61 CysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAla 80
DB 269 TGCACGAGCGCCTGCGGCACTCCACCTGCTGTGTGTCGCCAGAGACACCTTCTTGCC 328
QY 81 TrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSer 100
DB 329 TGGGAGAACCAACATAATCTGAATGTGCCCGCTGCCAGGCGCTGTATGAGCAGCGCTCC 388
QY 101 GlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGly 120
DB 389 CAGGTGGCGCTGGAGAACTGTTCAGAGTGGCCGACACCCCGCTGTGCTGAAGCCAGGC 448
QY 121 TrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCysGlnPro 140
DB 449 TGGTTTGTGAGTGCACAGGTCAACCAATGTGTACAGAGTTCAACCTTCTACTGCCAACCA 508
QY 141 CysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThr 160
DB 509 TGCCTAGACTGCGGGCCCTGCACCGCCACACACGCGCTACTCTGTCCCGCAGAGATACT 568
QY 161 AspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysPro 180
DB 569 GACTGTGGACCTGCGCTGCTTCTATGAACATGGCGATGGCTGCTGCTGCTGCTGCTG 628
QY 181 ThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTyrParglnMet 200
DB 629 ACGAGCACCCCTGGGAGCTGTCCAGAGCGCTGTGCTGTGTGCTGTGAGGAGAGATG 688
QY 201 PheTrpValGlnValLeuLeuAlaGlyLeuValValProLeuLeuLeuGlyAlaThrLeu 220
DB 689 TTCTGGGTCCAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 748
QY 221 ThrTyrThrTyrArgHisCysTrpProHisLysProLeuValThrAlaAspGluAlaGly 240
DB 221 ThrTyrThrTyrArgHisCysTrpProHisLysProLeuValThrAlaAspGluAlaGly 240

DB 749 ACCTACACATACCGCCACTGCTGGCCTCACAGCCCTGTTACTGCAGATGAAGCTGGG 808
QY 241 MetGluAlaLeuThrProProProAlaThrHisLeuSerProLeuAspSerAlaHisThr 260
DB 809 ATGAGGCTCTGACCCCAACCAACCGGCGCCACCTGTCTGACCCCTTGACAGCGCCACACC 868
QY 261 LeuLeuAlaProProAspSerSerGluLysIleCysThrValGlnLeuValGlyAsnSer 280
DB 869 CTCTAGACCTCTCTGACAGCAGTGAAGATCTGCACCGCTGCAGTGTGCTGCTGCTGCTG 928
QY 281 TrpThrProGlyTyrProGluThrGlnAlaLeuCysProGlnValThrTrpSerTrp 300
DB 929 TGGACCCCTGGCTACCCCGAGACCCAGAGCGGCTGCGCCGAGGTGACATGCTCTGG 988
QY 301 AspGlnLeuProSerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSer 320
DB 989 GACCAGTTGCCACAGAGAGCTGTGGCCCGCTGCTGCGCCACACTCTCGCCAGAGTCC 1048
QY 321 ProAlaGlySerProAlaMetMetLeuGlnProGlyProGlnLeuTyrAspValMetAsp 340
DB 1049 CCAGCCGGCTCGCCAGCCATGATGCTGTCAGCCGGCGCCGAGCTTACAGCTGATGAC 1108
QY 341 AlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGluAlaGlu 360
DB 1109 GCGGTCCAGCGCGCGCGCTGGAAGAGTTCGTGCGCACGCTGGGGCTGCGGAGCGAGAG 1168
QY 361 IleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGluMetLeuLys 380
DB 1169 ATCGAAGCCGTGAGGTGAGATCGCGCGCTTCCGAGACAGCACTACAGATGCTCAAG 1228
QY 381 ArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMet 400
DB 1229 CGCTGGCGCCAGCAGCAGCAGCCCGCGCGCTCGGAGCGCTTACCGCGCGCTGAGCGCATG 1288
QY 401 GlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 417
DB 1289 GGGGTGACGGCTGCTGTGAAGACTTGGCAGCGCGCTGCAAGCGCGCGCG 1339

RESULT 4
US-10-112-193-11
Sequence 11, Application US/10112193
Publication No. US20030004313A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-3 POLYPEPTIDE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/112,193
FILING DATE: 28-Mar-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/928,069
FILING DATE: 11-Sep-1997
APPLICATION NUMBER: 60/026943
FILING DATE: 23-Sep-1996
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1052R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416


```

; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 1634 base pairs
;   TYPE: Nucleic Acid
;   STRANDEDNESS: Single
;   TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-112-193-11

Alignment Scores:
Pred. No.: 2.07e-198      Length: 1634
Score: 2323.00           Matches: 417
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00%         Indels: 0
DB: 9                       Gaps: 0

US-09-993-234-6 (1-417) x US-10-112-193-11 (1-1634)
QY 1 MetGlulnArgProArgGlyCysAlaAlaValAlaAlaLeuLeuValLeu 20
   |||||||
Db 89 ATGAGACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTCCTCTG 148
QY 21 GlyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHis 40
   |||||||
Db 149 GGGGGCCCGGGCCAGAGGGCGGCGCTGAGCCCGAGGTGTACTGTCCGGTGACTTCAC 208
QY 41 LysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisIleTyrLeuLysAlaPro 60
   |||||||
Db 209 AAGAAGATTGGTCTGTGTGTTCAGAGAGCTGCGCAGCGGGCGCACTACCTGAAGCCCT 268
QY 61 CysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAla 80
   |||||||
Db 269 TGCACGGAGCCCTGGCGCACTCCACCTGCTGTGTGTCCCAAGACACCTTCTGGCC 328
QY 81 TrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluAlaSer 100
   |||||||
Db 329 TGGGAGAACCACCATTAATTCGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCTTC 388
QY 101 GlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGly 120
   |||||||
Db 389 CAGGTGGCGCTGGAGAAGCTGTTACAGAGTGGCGCCAGACCCGCTGTGCTGAAGCCAGGC 448
QY 121 TrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCysGlnPro 140
   |||||||
Db 449 TGGTTGTGAGTGCAGGTCCAGCAATGTGTACAGAGTTCACCTTCTACTGCCAACCA 508
QY 141 CysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThr 160
   |||||||
Db 509 TGCCTAGACTGGGGGGCCCTGCACCGCACACAGGGCTACTGTCCCGCAGAGATACT 568
QY 161 AspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysPro 180
   |||||||
Db 569 GACTGTGGGACCTGCGCTGCGCTTCTATGACATGGCGATGGCTGCTGCTGCC 628
QY 181 ThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTTPArgGlnMet 200
   |||||||
Db 629 ACGAGCACCCCTGGGAGCTGTCCAGAGCGCTGTGCCGTGTGTGGTGAGGAGATG 688
QY 201 PheTrpValGlnValLeuLeuAlaGlyLeuValValProLeuLeuGluGlyAlaThrLeu 220
   |||||||
Db 689 TTCTGGGTCCAGGTGCTGTGGCTGGCTTGTGTGCCCTCTGCTGGGGCACCCTG 748
QY 221 ThrTyrThrTyrArgHisCysTrpProHisLysProLeuValThrAlaAspGluAlaGly 240
   |||||||
Db 749 ACCTACACATACCGCACCTGTGGCTTCACAGCCCTGTACTGCAGATGAAGCTGGG 808
QY 241 MetGluAlaLeuThrProProAlaThrHisLeuSerProLeuAspSerAlaHisThr 260
   |||||||
Db 809 ATGGAGGCTTGACCCACACACAGCGGACCATCTGTCAACCTTGAGACAGCGCCACACC 868
QY 261 LeuLeuAlaProProAspSerSerGluLysIleCysThrValGlnLeuValGlyAsnSer 280
```

```

Db 869 CTTCAGACACCTCCTGCAGACAGTGAAGATCTGCACACCGTCAGTTGGTGAACAGC 928
QY 281 TrpThrProGlyTyrProGluThrGlnGluAlaLeuCysProGlnValThrTrpSerTrp 300
   |||||||
Db 929 TGGACCCCTGGCTACCCCGAGACCCAGAGGCGCTCTGCCCGCAGGTGACATGCTCTGG 988
QY 301 AspGlnLeuProSerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSer 320
   |||||||
Db 989 GACCAAGTTGCCAGACAGAGCTCTTGCGCCCGCTGCTGCGCCACACTCTCCGACAGATCC 1048
QY 321 ProAlaGlySerProAlaMetMetLeuGlnProGlyProGlnLeuTyrAspValMetAsp 340
   |||||||
Db 1049 CCAGCGGCTCGCCAGCCATGATGTCAGCGCGGCGCCGCGCAGCTTACGACGTGATGAC 1108
QY 341 AlaValProAlaArgArgTrrPlyGluPheValArgThrLeuGlyLeuArgGluAlaGlu 360
   |||||||
Db 1109 GCGGTCCACGCGCGCGCTGGAAGAGTTCGTGCGCACGCTGGGGCTGCGGAGCAGAG 1168
QY 361 IleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGluMetLeuLys 380
   |||||||
Db 1169 ATGAAGCCGTGAGAGTGAAGATCGCGCGCTTCCGAGACACAGATACGAGATGCTCAAG 1228
QY 381 ArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMet 400
   |||||||
Db 1229 CGCTGGCGCCAGCAGCAGACCGCGCGCGCTCGAGACCGTTTACCGCGCCCTGAGCGCATG 1288
QY 401 GlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 417
   |||||||
Db 1289 GGGCTGAGCGGCTGCGTGAAGACTTGCAGACCGCGCTGACGCGCGCGCG 1339

RESULT 5
US-09-993-234-9
; Sequence 9, Application US/09993234
; Patent No. US20020146768A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/993,234
; FILING DATE: 19-No. US20020146768A1-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/828,683
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1007P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5416
; TELEFAX: 415/952-9881
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 1634 base pairs
;   TYPE: Nucleic Acid
;   STRANDEDNESS: Single
;   TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
```


STRANDEDNESS: double
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 198..1481
US-09-333-966-1

Alignment Scores:
Pred. No.: 2,27e-193 Length: 1783
Score: 2267.00 Matches: 409
Percent Similarity: 97.39% Conservative: 1
Best Local Similarity: 97.15% Mismatches: 5
Query Match: 97.59% Indels: 6
DB: 10 Gaps: 1

US-09-993-234-6 (1-417) x US-09-333-966-1 (1-1783)

QY 3 GlnArgProArgGly-----CysAlaAlaValAlaAlaLeuLeu 16
Db 219 GAGGCCCCACGTCGGCAGCTGCGGAGAGTCAGCAGCACCTGTCCCCAGCGCTCTC 278
QY 17 LeuValLeuLeuGlyAlaArgAlaGlnGlyThrArgSerProArgCysAspCysAla 36
Db 279 CTGGTCTGTGGGGCCCCGGCCCCAGGGCGGCACTGTAGCCCCAGGTGTGACTGTGCC 338
QY 37 GlyAspPheHisLysLysIleGlyLeuPheCysArgGlyCysProAlaGlnHisTyr 56
Db 339 GGTGACTTCCACAAGAAGATTGCTGTGTTTGTTCAGAGGCTGCCACAGCGGCGACTAC 398
QY 57 LeuLysAlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAsp 76
Db 399 CTGAAGGCCCTTGACAGGAGCCCTGCGGCACTCCACCTGCTGTGTGCCCAAGAC 458
QY 77 ThrPheLeuAlaTrpGluAsnHisAsnSerGluCysAlaArgCysGlnAlaCysAsp 96
Db 459 ACCTTCTGGCCCTGGAGAAACACCATATTCTGAATGTGCCCGCTGCCAGGCTGTGAT 518
QY 97 GluGlnAlaSerGlnValAlaLeuGluAsnGlnSerAlaValAlaAspThrArgCysGly 116
Db 519 GAGCAGGCCCTCCAGGTGGCGCTGGAGAACTGTTCAGCAGTGCCGACACCCGCTGTGCC 578
QY 117 CysLysProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerProPhe 136
Db 579 TGTAAGCCAGGCTGTGTGTGAGTGCACAGTCAATGTGTCAAGCAGTCAACCTTTC 638
QY 137 TyrCysGlnProCysLeuAspCysGlyAlaAlaLeuHisArgHisThrArgLeuLeuCysSer 156
Db 639 TACTGCCAACCATGCTAGACTGCGGGCCCTGCACCGCCACACAGGCTACTGTCTCC 698
QY 157 ArgArgAspThrAspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCys 176
Db 699 CGCAGAGATACGTACTGTGGGACCTGCTGCTGCTATGAACATGGCGATGGCTGC 758
QY 177 ValSerCysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGly 196
Db 759 GTGTCTGCCCCCAGCAGCACCTGGGAGGCTGTCCAGAGCGCTGTGCCGTGTCTGTGCC 818
QY 197 TrpArgGlnMetPheTrpValGlnValLeuLeuAlaGlyLeuValProLeuLeuLeu 216
Db 819 TGGAGGAGATGTCTGGGTCCAGGTGCTCTGCTGTGCTGTGCTGCCCTGTCTGTCTT 878
QY 217 GlyAlaThrLeuThrTyrThrTyrArgHisCysTrpProHisLysProLeuValThrAla 236
Db 879 GGGGCCACCCCTGACTACACATACCGCCACTGTGGCCCTCACAAGCCCCCTGTACTGCA 938
QY 237 AspGluAlaGlyMetGluAlaLeuThrProProProAlaThrHisLeuSerProLeuAsp 256
Db 939 GATGAAGCTGGGATGAGGCTCTGACCCACACCGGCCACCCCATCTGTACCCCTTGAC 998
QY 257 SerAlaHisThrLeuLeuAlaProProAspSerSerGluLysIleCysThrValGlnLeu 276
Db 999 AGCGCCACACCCCTTCTAGCACCTCTCTGACAGCAGTGAAGAATCTGCACCGTCCAGTTG 1058

QY 277 ValGlyAsnSerTrpThrProGlyTyrProGluThrGlnGluAlaLeuCysProGlnVal 296
Db 1059 GTGGTAACAGCTGACCCCTGGCTACCCCGAGACCCAGAGGCGCTCTGCCCGCAGGTG 1118
QY 297 ThrTrpSerTrpAspGlnLeuProSerArgAlaLeuGlyProAlaAlaProThrLeu 316
Db 1119 ACATGGTCTGGGACCACTTGTCCACAGAGAGCTCTTGGCCCCGCTGTGCCGCCACACTC 1178
QY 317 SerProGluSerProAlaGlySerProAlaMetLeuGlnProGlyProGlnLeuTyr 336
Db 1179 TCGCCAGAGTCCCGACGCGCTCGCCAGCCATGATGTCAGCGGGCCGACGCTCTAC 1238
QY 337 AspValMetAspAlaValProAlaArgArgTrrPlyGluPheValArgThrLeuGlyLeu 356
Db 1239 GACGTGATGAGCGCGGTCCACGCGCGGCTGGAAGGAGTTCGTGCGCACGCTGGGCTG 1298
QY 357 ArgGluAlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnIleTyr 376
Db 1299 CGCGAGGCAGAGATCGAAGCCGTGGAGGTGAGATCGGCCGCTTCCGAGACACAGCTAC 1358
QY 377 GluMetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAla 396
Db 1359 GAGATGCTCAAGCGCTGGCGCCACAGCAGACCCCGCGGCTCGGAGCCGTTTACCGGCC 1418
QY 397 LeuGluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGly 416
Db 1419 CTGGAAGCCATGGGCTGGAAGGCTGCGTGAAGACTTGGCAGCCGCTGCAGCGCGGC 1478
QY 417 Pro 417
Db 1479 CCG 1481

RESULT 7

US-09-954-531-1389
; Sequence 1389, Application US/09954531
; Patent No. US20020165180A1
; GENERAL INFORMATION:
; APPLICANT: weaver, Zoe
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C
; TITLE OF INVENTION: Gene Sets
; FILE REFERENCE: 689290-77
; CURRENT APPLICATION NUMBER: US/09/954,531
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: US/60/233,133
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,009
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,034
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,509
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US/60/234,567
; NUMBER OF SEQ ID NOS: 1392
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1389
; LENGTH: 1743
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-531-1389

Alignment Scores:
Pred. No.: 2,88e-192 Length: 1743
Score: 2254.50 Matches: 413
Percent Similarity: 91.57% Conservative: 0
Best Local Similarity: 91.57% Mismatches: 4
Query Match: 97.05% Indels: 35
DB: 9 Gaps: 1

US-09-993-234-6 (1-417) x US-09-954-531-1389 (1-1743)

QY 1 MetGluGlnArgProArgGlyCysAlaAlaValAlaAlaLeuLeuValLeuLeu 20

Db 5544 GCCTGCCTGACCCCTGCTGGTTCACAGGGCAGCTACCTGAAGCCCCCTTGACAGGAGCC 5603
QY 64 oCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnH1 84
Db 5604 CTGGCGCAACTCCACCCTGCTGTGTGTCGCCAAGACACCTTCTTGCCCTGGAGAACCA 5663
QY 84 sHisAsnSerGluCysAlaArgCysGlnAlaCysAspGlu----- 97
Db 5664 CCATTAATTCTGAATGTCCCCGCTGCCAGGCCCTGTGATGAGCAGGGGTGAGGGGCTTCTCAG 5723
QY 97 ----- 97
Db 5724 TGCCTGGCAGGAGTTCCTTAAGGACAGGCCCTTCTGAAGAGTGGCTGGCTGGGCCCA 5783
QY 97 ----- 97
Db 5784 AACCTGGGGGTGTGAGGGTCTGCACACCCTTGCCAGAACCCCTCCACCCTGATCCTCCT 5843
QY 97 ----- 97
Db 5844 TCAGGGTGCCCTTGCCCTTCTCTCTCTGCTGACCTTCCCATCTCTCCATGTGCCCTTG 5903
QY 97 ----- 97
Db 5904 GCCTCTGGTCGGCCTTAATCTCTGAGCTTCTCTCTTTTAAAGGTAAGCCCTGTACCTGTC 5963
QY 97 ----- 97
Db 5964 TGTCTTTCGCCCTATTCTGTCTCCATTAATCTTGGATTAATGCCCTCTGCCCTCTCCATGGGA 6023
QY 98 -----GlnAlaSerG1 101
Db 6024 GCCTTTGGCCCTGACTAATCTTCCACTCCCCCATCTCCCTGCACCCCCACACAGCC-TCCCA 6082
QY 101 nValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTr 121
Db 6083 GGTGGCGCTGGAGAACTGTTCAAGAGTGGCCGACACCCCGCTGTGGCTGTAAGCCAGGCTG 6142
QY 121 pheValGluCysGlnValSerGlnCysValSerSerProPheTyrcysGlnProCy 141
Db 6143 GTTGTGAGAGTCCAGGTCCAGCCAATGTGTACAGCAGTTACCCCTTCTACTGCCAACCATG 6202
QY 141 sLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCySer----- 156
Db 6203 CCTAGACTGGGGGGCCCTGCACCGCACACAGCGCTACTGTGA-GTACCCCAACCCAG 6261
QY 156 ----- 156
Db 6262 GGTCTCTACTCCAGACCCCTTCTCCCTGCTGACCCACTCTGTCATGTTGAGCG 6321
QY 157 -----ArgArgAspThrAspCysGlyThrCysLeuProG1 168
Db 6322 ATGCCTCTCTGATTCAGAGTTCGCCGACAGATACTGACTGTGGGACCTGCCCTGG 6381
QY 168 yPheTyrcGluHisGlyAspGlyCysValSerCysProThrSer----- 182
Db 6382 CTTCATGAACATGGCGATGGCTGCGTGTCTGCCCCACGTA-ATTCTAGCTGTCTGG 6440
QY 182 ----- 182
Db 6441 GATGGAGGGAAGGGGCTGGGAGCAGAGAGGGGCTGGGGTGGGCGAGGTGCTGCTGG 6500
QY 182 ----- 182
Db 6501 TTCAGGAATAGGAAGAGGGGATAGGAGAGGAGCCCTTGGCCCTGTGATGGGTGGGCC 6560
QY 182 ----- 182
Db 6561 CACTTCAGGCAAACTTAGATGGCAAAAGACAATCTGATCCGCCCTTAGCCAGATACATA 6620
QY 182 ----- 182
Db 6621 AGGGTATTTCCTTCACTTTCAGCCAGCATTCGCCCCAGCGATCCTAGCCAGATATTACA 6680

QY 182 ----- 182
Db 6681 GATGATTTGTCACTTACACAGAGAGTCACATTTGATATAGCTTTAAAACTTGGGCTGAAG 6740
QY 182 ----- 182
Db 6741 AGGTGAGGCTGCAGTGAGCTATGATGTCGCCACTGCACCTTCAGCCTGGGCAACAGAGCG 6800
QY 182 ----- 182
Db 6801 AGACCTATTAAATAATTAATAATAATTAATAATCTATTAAATATTAATAATCTATT 6860
QY 182 ----- 182
Db 6861 AAATTAATAATAACAAGGGCTGAGAGTCAAGAGCTGCTGCTGCTAGGGGATCT 6920
QY 182 ----- 182
Db 6921 TGGCAAGTGCAGAGAAATTCGGCTCTGATGTGTGTTGCCCTTCTCAACATGGGATG 6980
QY 182 ----- 182
Db 6981 TTAGCAGCTAATTCACAGGCCCTTGATCAGAGGTAAGGACTTCTGTAGCTATTCAAGT 7040
QY 182 ----- 182
Db 7041 CTTTTTTTTTTTTTTTTTTTTTTTGTGAGATGAGACTTGTCTGTACCCAGGCTG 7100
QY 182 ----- 182
Db 7101 GAGTGAAGTGGACGATCTTGGCTCACTACAACCTCTGCTGCTGGGTCAAGTGATTC 7160
QY 182 ----- 182
Db 7161 CCTGCTCAGCCTCCCAAGTAGCTGGGACTACAGAGCCACACACCCCGGCTAAT 7220
QY 182 ----- 182
Db 7221 TTTTGTATTTTAGTAGAGCGGGTTTCAACCGTGTAGCCAAGATGCTTGTATCACCT 7280
QY 182 ----- 182
Db 7281 GACCTGTGATCCACCGCCTTGGCCTCCCAAGTGCTGGGATTCAGAGCATGAGCCACC 7340
QY 182 ----- 182
Db 7341 GCGCCGGCCTCATTTCAAGTCTTTAATGAATATCTGTATGTTCTACACACTGTTCTAG 7400
QY 182 ----- 182
Db 7401 GTGTGGGATGCAACAGGGGACAAATAAGCAAAATCCCTGTCTTTTGGGTTGACAT 7460
QY 182 ----- 182
Db 7461 TCTAGTACTTTCATGTAGTCTAGAAGAAGCTCAGTGAATAGTGTCTGTGTGTTACC 7520
QY 182 ----- 182
Db 7521 AGGACACAATGACAGGAACATTTTGGGTAGAGTGAGAGGCCCTGGGAGGGAAGGCTCT 7580
QY 182 ----- 182
Db 7581 CTAGATGAGACAGATGCTGGGCACTTTAAGGAGCCCTCTGCGCATGCACCCCTCAT 7640
QY 183 -----ThrLeuGlySerCysProGluArgCysAl 192
Db 7641 CCTCAGGCCACCCCGCTGCCCTTGAGAGAGCACCCCTGGGAGCTGTCCAAGCGCTGTGC 7700
QY 192 aaLaValCysGlyTrpArg----- 198
Db 7701 CGGTGTGTGTGGCTGAGGAGAGTAGGTGTGTGTGTGGAATGCGAGTGGGAAACTGG 7760

QY 198 ----- 198
Db 7761 GATGACCGAGGGAGCGGGGTGAGGAGGGGGGCAACCAACCAACCAACCAAGCTGCTT 7820
QY 199 -GlnMetPheTrpValGlnValLeuLeuAlaGlyLeuValValProLeuLeuGlyAl 218
Db 7821 TCAGTG-TTCTGGGTCAGAGTGTCTCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 7879
QY 218 aThrLeuThrTyrThrTyrArgHisCysTrpProHisLysProLeuValThr----- 235
Db 7880 CACCTGACCTACACATACATACCGCACTGCTGGCTCACAAGCCCTGCTGTAAGTA 7939
QY 235 ----- 235
Db 7940 CACAGACCCACACACGACCCAGAACCTGGGTACAGATGGGTAGCCAGAGTCTACTC 7999
QY 235 ----- 235
Db 8000 AACCTGATACAGAAAGGAAACTGAGGACGAGGTGGGGTGACAGAGAACCTAGAG 8059
QY 235 ----- 235
Db 8060 GAGCTGTACACAGCACCCAGGTCCAGAGGCTTGCCTGGTGGCTGACCCGAATCTCTGT 8119
QY 236 -----AlaAspGluAlaGlyMetGluAlaLeuThrProPro----- 247
Db 8120 GTCTGTACAGATGAGTGGGATGAGGCTGTGACCCCAACCGGTAGAACCTCAG 8179
QY 247 ----- 247
Db 8180 TGTGTATCTGGGCTGCTCTTGAGCTGGAAGATCAAGCCTTACTATGATCCCTGGAG 8239
QY 247 ----- 247
Db 8240 CTTGGCACGCGGCAACCGGGTAGCCCTAGTGGACAGAGGTGTTGGAGACAGTCAAT 8299
QY 247 ----- 247
Db 8300 CAGTGATGAGACACACAGTGCCTGCCCTCAAGGGGTGCTCAGTCACTGAGTTCAAG 8359
QY 247 ----- 247
Db 8360 ATTGTACACAGAGCTAACAGTTCAATGGAAGAGAGCCCAATGCTGGGGACAAG 8419
QY 247 ----- 247
Db 8420 AGGAAGGAGCGGGGGGAGGAGCTCAAGGACAGCAAGAGTCTGCTGGGCTACAGTG 8479
QY 247 ----- 247
Db 8480 AGAGCAGGCGCACTGTGGAGGTGATTCGCGGGGTGCTGCTGACTGAACGAGGAC 8539
QY 247 ----- 247
Db 8540 TGTCCCTCTCTGAGAGGACACTGGCGGGTAAGGGCCTTACTTGGCAAGAGGGCTGACT 8599
QY 248 -----Pro-AlaThrHisLeuSerProLeuAspSerAlaHisThrLeu 261
Db 8600 GGGGCCCTCTTGGCTTCCAGGCGCAACCATCTGTACACCTTGGACAGCGCCACACCTT 8659
QY 262 LeuAlaProProAspSerSerGlyLysIleCysThrValGlnLeuValGlyAsnSerTrp 281
Db 8660 CTAGCAGCTCTGACAGCAGTGAAGATCTGACCCGTCAGTGTGGTAACTGAGCTGG 8719
QY 282 ThrProGlyTyrProGluThrGlnGlnAlaLeuCysProGlnValThrTrpSerTrpasp 301
Db 8720 ACCCTGGCTACCCCGAGACAGGAGCGGCTCTGCCGAGGTGACATGTCTGGGAC 8779
QY 302 GlnLeuProSerArgAlaLeu----- 308
Db 8780 CAGTTGCCACAGCAGAGCTCTTGGTAAGGACATCAGTGGCCTGAGGCTTGAACCCATTC 8839
QY 308 ----- 308

Db 8840 TCCTGTCTCGGTTGGGAAGTTGTGTTTACACAGTGTTCCTTCTGCCCTTAAGTGA 8899
QY 308 ----- 308
Db 8900 CGGAGTCCGCCATATGCCCTGACCCACCGGATCCAGCGGCTTACGCCCTGGGGTACCG 8959
QY 308 ----- 308
Db 8960 CACGAACGCCCTGACTTCCCTCCGACCGCGGCCACGTACCCCAATTGGCTCTCT 9019
QY 309 -----GlyProAlaAlaAlaProThrLeuSerProGluSerProAlaGlySer 324
Db 9020 GGCCCTGCCCGAGCGCCGCTGCTGCGCCACACTCTGCGCAGAGTCCCAAGCGCTCG 9079
QY 325 ProAlaMetLeuGlnProGlyProGlnLeuTyrAspValMetAspAlaValProAla 344
Db 9080 CCAGCATGATGCTGACAGCCGCGCCGCACTCTACAGAGTATGACGCGGCTCCAGCG 9139
QY 345 ArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGluAlaGluIleGluAlaVal 364
Db 9140 CGGCGCTGGAAGAGTTCTGTGCGCACGCTGGGGCTGCGGAGGACAGATCGAACCGGTG 9199
QY 365 GluValGluIleGlyArgPheArgAspGlnIleTyrGluMetLeuLysArgTrpArgGln 384
Db 9200 GAGGTGAGATGCGCCGCTTCCGAGACACAGTACGAGATGCTCAAGCGCTGGCGCCAG 9259
QY 385 GlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMetGlyLeuAspGly 404
Db 9260 CAGCAGCCCGCGGCTCGAGCGCTTACGCGGCCCTGAGCGCATGGGCTGAGCGGC 9319
QY 405 CysValGluAspLeuArgSerArgLeuGlnArgGlyPro 417
Db 9320 TGCGTGAAGACTTGCGCAGCCGCTGCAAGCGGCGCCG 9358
RESULT 9
US-09-764-847-1577
: Sequence 1577, Application US/09764847
: Patent NO. US20020132767A1
: GENERAL INFORMATION:
: APPLICANT: Rosen et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
: FILE REFERENCE: PC009
: CURRENT APPLICATION NUMBER: US/09/764,847
: PRIORITY FILING DATE: 2001-01-17
: Prior application data removed - consult PAM or file wrapper
: NUMBER OF SEQ ID NOS: 2003
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1577
: LENGTH: 10797
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-09-764-847-1577
Alignment Scores:
Pred. No.: 4.34e-129 Length: 10797
Score: 1556.50 Matches: 405
Percent Similarity: 29.10% Conservative: 1
Best Local Similarity: 29.03% Mismatches: 9
Query Match: 67.00% Indels: 984
DB: 10 Gaps: 9
US-09-993-234-6 (1-417) x US-09-764-847-1577 (1-10797)
QY 3 GlnArgProArgGly-----CysAlaAlaValAlaAlaAlaLeuLeu 16
Db 5184 GAGGCCCGACGTGGGCAAGTGGCTGAGAGTACAGCAGCAGTCTGCCCAAGGCTCTC 5243
QY 17 LeuValLeuLeuGlyAlaArgAlaGlnGlyThrArgSerProArgCysAspCysAla 36
Db 5244 CTGGTGTCTGGGGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 5303
QY 37 GlyAspPheHisLysLysIleGlyLeuPheCysCysArgGlyCysProAla----- 53

|||||
Db 5304 GGTGACTTCCACAAGATTGGTCTGTTTGTTCAGAGGCTGCCAGCGGGTAAGTGG 5363
QY 53 ----- 53
Db 5364 CCACAGGGGTGGAGAGCATGGGCGAGCGGCTGAGAGTGGCGGACAGCCCCGG 5423
QY 53 ----- 53
Db 5424 AGGTAAGAGAGGCTGGCAGGGGAGGTAGGGTAGGCTGACAGAGAAGTAGGAGCTGGA 5483
QY 53 ----- 53
Db 5484 GAGAAAGAGGAGGAGGCGCAGGCTGGAAGCAGGTGCGGGGTTCCTGGGCGACCCCTCT 5543
QY 54 -----GlyHisTyrLeuLysAlaProCysThrGluPr 64
Db 5544 GCCTGCCCTGACCCCTGCCCTGGTCCACAGGCGACTACTGAAAGGCCCTTGACGGAGCC 5603
QY 64 ocysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnH 84
Db 5604 CTGCGGCAACTCCACCTGCTTGTGTGTCCCAAGACACTTCTTGCCCTGGGAGAACCA 5663
QY 84 SHisAsnSerGluCysAlaArgCysGlnAlaCysAspGlu----- 97
Db 5664 CCATAATTCTGAATGTGCCCGCTGCCAGGCTGTGATGACGAGGCTGAGGGGCTTCAG 5723
QY 97 ----- 97
Db 5724 TGCTTGGCAGGAGTTCCTAAGACAGGCCCTTCTGAAGAAAGTGCGTGCGGCCCA 5783
QY 97 ----- 97
Db 5784 AACTTGGGTGTGAGGGTCTGCACCCACCCCTTGCCAGAACCTCCACCCGTGATCTCT 5843
QY 97 ----- 97
Db 5844 TCAGGGTCCCTTGCCCTTCTCTCTCTGAGACCTTCCCATCTCTCCATGTGCTTG 5903
QY 97 ----- 97
Db 5904 GCCTCTGGTGGCGCTAACTCTGAGCTTCTCTCTTTTAAAGGTAGCCCTGTACCTGTC 5963
QY 97 ----- 97
Db 5964 TGCTTTTCCGCTATTTCGTCTCCATTATCTTGGGATAAGCCTTGCCCTTCCATGGGA 6023
QY 98 -----GlnAlaSerG 101
Db 6024 GCCTTTGGCCCTGACTAATCTCCACTCCCATCTCCCTGACACCCCGCCAGCC-TCCTCA 6082
QY 101 nValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTr 121
Db 6083 GGTGGCGGTGAGAACTGTTCAGCAGTGGCCGACACCGCTGTGGCTGTAAGCCAGGCTG 6142
QY 121 pHeValGluCysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCy 141
Db 6143 GTTGTGAGTGCAGGTCAAGTAATGTGTACAGAGTTCAACCTTCTACTGCCAACATG 6202
QY 141 sleuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSer----- 156
Db 6203 CCTAGACTGCGGGGCTGCACCGCCACACACGCGTACTGTGTGA-GTACCCCGCCAG 6261
QY 156 ----- 156
Db 6262 GGCTCTTACTCCAGACCCCTTCTCCCTGCCCTGACCCACTCCTGCCATGTGAGCC 6321
QY 157 -----ArgArgAspThrAspCysGlyThrCysLeuProG 168
Db 6322 ATGCCCTCTCCTGATTGAGGTTCCCGCAGAGATACTGACTGTGGACCTGCCCTGCG 6381
QY 168 yPheTyrGluHisGlyAspClyCysValSerCysProThrSer----- 182
|||||

Db 6382 CTTCATGAACATGGCGATGGCTGCCGTCTCCTGCCCCACGTA-ATTCTAGCTGTCTGG 6440
QY 182 ----- 182
Db 6441 GATGGAGGGAAGGGCGGCTGGGACAGACAGAGGGCCTGGGGTGGGCGAGTGTCTGG 6500
QY 182 ----- 182
Db 6501 TTCAGGAATTAGGAAGAGGGGATAGGAGAGGAGGAGCGCTTGCCCTGTGATGGTGGCCC 6560
QY 182 ----- 182
Db 6561 CACTTCAGGCAAACTTAGATGGCAAAAGACAAATCTGATCCGCCCTTAGCCAGATACATA 6620
QY 182 ----- 182
Db 6621 AGGTAATTGCCCTTCACTTTCAGCCAGCATTCCCCCGACGATCCTAGCCAGATATTACA 6680
QY 182 ----- 182
Db 6681 GATGATTTGTCACTTACACAGAGATCACATGTGATATAGCTTTAAAACTTGGGCTGAAG 6740
QY 182 ----- 182
Db 6741 AGGTTAGGCGCTGCAGTGAAGTATGATCGTCCACTGCACCTTCAGCCTGGCAACAGACG 6800
QY 182 ----- 182
Db 6801 AGACCTATTAAATAAATAAATAATTAATCTATTAAATATTAATATTAATCTATT 6860
QY 182 ----- 182
Db 6861 AAATAAATAATACAAAGGGCTGAGAGTCAGGACTGTGCTGCTAGTCTCTAGGGGATCT 6920
QY 182 ----- 182
Db 6921 TGGGCAAGTGCAGAGAATTCCGCTCTGTGATGTGTGTGTCCTTCTCAACATGGGATG 6980
QY 182 ----- 182
Db 6981 TTAGCAGCTAATTACAGAGCGCTTGATCAGAGGTAAGGACTTCTGTAGCTATTCAAGT 7040
QY 182 ----- 182
Db 7041 CTTTTTTTTTTTTTTTTTTTTTTTGTGAGATGAGACTTGCTGTCAACCAGGCTG 7100
QY 182 ----- 182
Db 7101 GAGTGCAGTGGCAGCATCTTGCTCACTACAACCTCTGCTGCTGGCTTCAAGTATCTT 7160
QY 182 ----- 182
Db 7161 CCTGCTCAGCCTCCCAAGTAGCTGGGACTACAGAGGCCACACACCCCGGCTAATT 7220
QY 182 ----- 182
Db 7221 TTTGTATTTTGTAGAGACGGGTTTCACCGGTGTAGCAAGATGGTCTGTGATCACCT 7280
QY 182 ----- 182
Db 7281 GACCTCGTATCCACCCGCTTGCCCTCCCAAGTGTGGGATTACAGGCATGAGCCACC 7340
QY 182 ----- 182
Db 7341 GCGCCCGGCTCCATTCAAGTCTTATTGAATATCTGCTATGTCTTACACACTGTCTAG 7400
QY 182 ----- 182
Db 7401 GTGCTGGGGATGCACAGGGGACAATAAGGCAAAATCCCTGTCTTTTGGGGTTGACAT 7460
QY 182 ----- 182
Db 7461 TCTAGTCACTCTTCATGTAGTCTAGAGAAGAGCTCAGTGAATAGTGTCTGTGTGTACC 7520

QY 182 ----- 182
Db 7521 AGGACACATGACAGAACATCTTGGTAGAGTGAAGCCCTGGGAGGAAGGCTCT 7580
QY 182 ----- 182
Db 7581 CTAGAGTGAAGAGATGCTGGGACAGTCTTAGGAGCCCTCTGGCATGCACCCCTCAT 7640
QY 183 ----- 192
Db 7641 CCTCAGGCCACCCCTGCTTGCAGAGCACCCCTGGGAGCTGTCCAGAGCGCTGTGC 7700
QY 192 aAlaValCysGlyTyrArg----- 198
Db 7701 CGCTGCTCTGTGGCTGAGAGCAGATAGGTGTGTGCTGGGAATGCGAGTGGAGAACTGG 7760
QY 198 ----- 198
Db 7761 GATGGACCGAGGGAGCGGGGTGAGAGGGGGGCAACCAACCAACCAACCACTGCTT 7820
QY 199 -GlnMetPheTyrPvalGlnValLeuLeuAlaGlyLeuValValProLeuLeuGlyAl 218
Db 7821 TCAGTG-TTCTGGGTCCAGGTGCTGCTGGCTGTGGCTGTGGCTGTGGCTGTGGGGC 7879
QY 218 aThrLeuThrTyrThrTyrArgHisCysTrpProHisLysProLeuValThr----- 235
Db 7880 CACCTGACCTACACATACACCCGACCTGTGGCTTCACAAAGCCCTGTACTGTGAAGTA 7939
QY 235 ----- 235
Db 7940 CACACACCCACACACACCAAGAGCTGGGTCAAGATGGGTAGCCCAAGTCTACTC 7999
QY 235 ----- 235
Db 8000 AACCTGATACAGAGGGGAAACTGAGGCAAGGAGTGTGGGTGCAGAGAACTTAGAG 8059
QY 235 ----- 235
Db 8060 GAGCTGTACCAGCAACCAAGTCCAGAGAGCTTGCCTGGTGGCTGACCCCAATCTCTGT 8119
QY 236 ----- 247
Db 8120 GTCTGTACAGATGAAGCTGGGATGAGGCTCTGACCCACACCGGTAAAGAACTCAC 8179
QY 247 ----- 247
Db 8180 TGTGTATCTGGGCTGCTTCTGTGAGCTGAAGATCAAGCCTTATGATCCTTGAG 8239
QY 247 ----- 247
Db 8240 CTTGGCAGCGGCGCACGACCGGTAGCCCTAGTGACAGAGGTGTGGGAGCAGATCAT 8299
QY 247 ----- 247
Db 8300 CAGTGAATGAGACACGACAGTGCCTGCCCTCAAGGGGTGCTCAGTCACTGGAGTTCA 8359
QY 247 ----- 247
Db 8360 ATTCTACACAGAGCTAATCAATGAAGAGAGACCCCATGCTGCTGGGAGACAAG 8419
QY 247 ----- 247
Db 8420 AGGAAGAGCGCGGGGAGGAGCTCAAGGCAAGCAAGATTCTGCTGGCTACAGTG 8479
QY 247 ----- 247
Db 8480 AGAGCAGGCGCAACTGTGGAGGTGTCAATTGCGGGGTGTCTGACTGAACCAAGGAG 8539
QY 247 ----- 247
Db 8540 TGTCCCTCTCTGAGAGGCACTGGCGGGGTAAAGGGCTTACTTGCCAAGCAGGCTGACT 8599

QY 248 ----- 261
Db 8600 GGGGCCCTCTTGGCTTCCAGAGCCACCACTCTGTCAACCTTGGACAGCGCCACACCTT 8659
QY 262 LeuAlaProProAspSerSerGlnLysIleCysThrValGlnLeuValGlyAsnSerTrp 281
Db 8660 CTAGCAGCTCTGACAGAGTGAAGATGTGCACCGCTCCAGTTGGTGGTTAACAGCTGG 8719
QY 282 ThrProGlyTyrProGlnThrGlnGlnAlaLeuCysProGlnValThrTrpSerTrp 301
Db 8720 ACCCTGGCTACCCCGAGACCAAGAGGCGCTTCCCGCAGGTGACATGTCTGGGAG 8779
QY 302 GlnLeuProSerArgAlaLeu----- 308
Db 8780 CAGTTGCCAGCAGACTCTTGTGAAGGACATCATGTGGCTGAGGCTTGAACCCATTC 8839
QY 308 ----- 308
Db 8840 TCCTGTGCGGTGGGAAGTTGTGTTTCAACAGTGTCCCTTCTGCCCCCTAAGTGA 8899
QY 308 ----- 308
Db 8900 CGGAGTCCGCTATGCCCTGACCAACCGGATCCAGCGGCTTACGCCCTGGGGTACCCG 8959
QY 308 ----- 308
Db 8960 CAGCAAGCCCTGACTCTGCTCCGACCGCGGCCACGTAACCCCAATTGGCTCTCTCT 9019
QY 309 ----- 324
Db 9020 GGCCCTGCCCGAGCGCCGCTGTGCTGCGCCACACTCTGCGCAGAGTCCCAAGCGGCTG 9079
QY 325 ProAlaMetLeuGlnProGlyProGlnLeuTyrAspValMetAspAlaValProAla 344
Db 9080 CCAGCCATGATGCTGCAGCGCGCGCCGACGCTTACGACGATGATGACGCGGTCCAGCG 9139
QY 345 ArgArgTyrLysGlnPheValArgThrLeuGlyLeuArgGlnAlaGlnIleGlnAlaVal 364
Db 9140 CGGCGCTGGAAGAGTTCGTGCGCACGCTGGGCTGGCGGAGAGATCGAAGCGGTG 9199
QY 365 GlnValGlnIleGlyArgPheArgAspGlnIleTyrGlnMetLeuLysArgTrpArgGln 384
Db 9200 GAGGTGAGATCGGCGCTTCCGAGCACAGCAGTACGAGATGCTCAAGCGCTGGCGCAG 9259
QY 385 GlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGlnArgMetGlyLeuAspGly 404
Db 9260 CAGCAGCCCGCGGCGCTCGAGCCGTTTACGCGGCTCGAGCGCATGGGCTGACGCGC 9319
QY 405 CysValGlnAspLeuArgSerArgLeuGlnArgGlyPro 417
Db 9320 TGCGTGAAGACTTGCGCAGCGCGCTGCAAGCGCGCGCG 9358
RESULT 10
US-10-081-280-5
Sequence 5, Application US/10081280
Patent No. US2002016517A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/081,280
FILING DATE: 21-Feb-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/829,270
FILING DATE: 31-Mar-1997
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5416
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1438 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-081-280-5

Alignment Scores:
Pred. No.: 2.32e-86 Length: 1438
Score: 1066.00 Matches: 187
Percent Similarity: 94.47% Conservative: 1
Best Local Similarity: 93.97% Mismatches: 3
Query Match: 45.89% Indels: 8
DB: 9 Gaps: 1

US-09-993-234-6 (1-417) x US-10-081-280-5 (1-1438)

QY 1 MetGluGlnArgProArgGlyCysAlaAlaValAlaAlaLeuLeuValLeu 20
Db 377 ATGAGCAGCGCGCGGGCTGCGCGGGCTGCGCGGGCTCCTCGTGTGCTG 436
QY 21 GlyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHis 40
Db 437 GGGGCCCGGGCCAGGGCGGCACCTGAGCCCGCAGGTGTGACTGTGCCGTGACTTCCAC 496
QY 41 LysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaPro 60
Db 497 AAGAAGATTGCTGTGTTGTGACAGAGGCTGCCAGCGGGGCACTACCTGAAGGCCCT 556
QY 61 CysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAla 80
Db 557 TGCACGGAGCCCTGCGGCACTCCACCTGCTGTGTGTCCTCCCAAGACACCTTCTTGGCC 616
QY 81 TrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSer 100
Db 617 TGGGAGAACCAACATTAATTCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCCCTCC 676
QY 101 GlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGly 120
Db 677 CAGGTGGCGCTGGAGAACTGTTCAAGCAGTGGCGCACCCGCTGTGGCTGTAAGCCAGGC 736
QY 121 TrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCysGlnPro 140
Db 737 TGGTTTGTGAGTGCAGGTCAAGCAATGTGTCAAGAGTTCAACCTTCTACTGCCAACCA 796
QY 141 CysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThr 160
Db 797 TGCCTAGACTGCGGGGCTGCACCGGCACACACGCGCTACTCTGTCCCGCAGAGATACT 856
QY 161 AspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysPro 180
Db 857 GACTGTGGAGCCTGCGCTGCTTCTATGAACATGGCGATGGCTGCGTGTCTTCCGCC 916
QY 181 ThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTyrPargGln 199
Db 917 ACGTAATTCCTA-----GCTGTGCTGGATGAGGGA 949

RESULT 11
US-10-112-793-5
Sequence 5, Application US/10112793
Publication No. US20020192729A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/112,793
FILING DATE: 28-Mar-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/828,683A
FILING DATE: 31-Mar-1997
APPLICATION NUMBER: 08/625328
FILING DATE: 1-Apr-1996
APPLICATION NUMBER: 08/710802
FILING DATE: 23-Sep-1996
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1438 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-112-793-5

Alignment Scores:
Pred. No.: 2.32e-86 Length: 1438
Score: 1066.00 Matches: 187
Percent Similarity: 94.47% Conservative: 1
Best Local Similarity: 93.97% Mismatches: 3
Query Match: 45.89% Indels: 8
DB: 9 Gaps: 1

US-09-993-234-6 (1-417) x US-10-112-793-5 (1-1438)

QY 1 MetGluGlnArgProArgGlyCysAlaAlaValAlaAlaLeuLeuValLeu 20
Db 377 ATGAGCAGCGCGCGGGCTGCGCGGGCTGCGCGGGCTCCTCGTGTGCTG 436
QY 21 GlyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHis 40
Db 437 GGGGCCCGGGCCAGGGCGGCACCTGTAAGCCCGCAGGTGTGACTGTGCCGTGACTTCCAC 496
QY 41 LysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaPro 60
Db 497 AAGAAGATTGCTGTGTTGTGACAGAGGCTGCCAGCGGGGCACTACCTGAAGGCCCT 556
QY 61 CysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAla 80
Db 557 TGCACGGAGCCCTGCGGCACTCCACCTGCTGTGTGTGCCCAAGACACCTTCTTGGCC 616

QY 81 TrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSer 100
Db 617 TGGGAGAACCAACCATTAATTCGAATGTGCCCGCTGCCAGGCGCTGTGATGAGCAGCGCTCC 676
QY 101 GlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGly 120
Db 677 CAGGTGGCGCTGGAGAACTGTTCAGAGAGTGGCCGACACACCGCTGTGGCTGTAGCCAGGC 736
QY 121 TrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCysGlnPro 140
Db 737 TGGTTGTGGAGTGGCAGGTCCAGCAATGTGTACAGAGTTCACCCCTTCTACTGCCAACCA 796
QY 141 CysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThr 160
Db 797 TGCCTAGACTGGCGGCGCTGCACCGCACACACGCGCTACTCTGTCCCGCAGAGATACT 856
QY 161 AspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysPro 180
Db 857 GACTGTGGAGCTGCCTGCCTGCCTCTATGACATGGCGATGGCTGCCTGTCTGCCCCC 916
QY 181 ThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTrpArgGln 199
Db 917 ACCTAATTCCTA-----GCTGTCGTGGATGAGGGAA 949

RESULT 12
US-10-112-193-5
; Sequence 5, Application US/10112193
; Publication No. US20030004313A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-3 POLYPEPTIDE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/112,193
; FILING DATE: 28-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/928,069
; FILING DATE: 11-Sep-1997
; APPLICATION NUMBER: 60/026943
; FILING DATE: 23-Sep-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1052R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1438 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-112-193-5

Alignment Scores:
Pred. No.: 2.32e-86 Length: 1438
Score: 1066.00 Matches: 187
Percent Similarity: 94.47% Conservative: 1

Best Local Similarity: 93.97% Mismatches: 3
Query Match: 45.89% Indels: 8
DB: 9 Gaps: 1

US-09-993-234-6 (1-417) x US-10-112-193-5 (1-1438)

QY 1 MetGluGlnArgProArgGlyCysAlaAlaValAlaAlaLeuLeuValLeuLeu 20
Db 377 ATGAGACAGCGCGCGGGGCTGCGCGCGGGTGGCGCGCGCTCTCTGCTGCTG 436
QY 21 GlnAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHis 40
Db 437 GGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 496
QY 41 LysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaPro 60
Db 497 AAGAAGATTGGTCTTTTGTGTGACAGAGGCTGCCAGCGGGGCGCGCGCGCGCG 556
QY 61 CysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAla 80
Db 557 TGCACGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 616
QY 81 TrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSer 100
Db 617 TGGGAGAACCAACCATTAATTCGAATGTGCCCGCTGCCAGGCGCTGTGATGAGCAGCGCTCC 676
QY 101 GlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGly 120
Db 677 CAGGTGGCGCTGGAGAACTGTTCAGAGAGTGGCCGACACACCGCTGTGGCTGTAGCCAGGC 736
QY 121 TrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCysGlnPro 140
Db 737 TGGTTGTGGAGTGGCAGGTCCAGCAATGTGTACAGAGTTCACCCCTTCTACTGCCAACCA 796
QY 141 CysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThr 160
Db 797 TGCCTAGACTGGCGGCGCTGCACCGCACACACGCGCTACTCTGTCCCGCAGAGATACT 856
QY 161 AspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysPro 180
Db 857 GACTGTGGAGCTGCCTGCCTGCCTCTATGACATGGCGATGGCTGCCTGTCTGCCCCC 916
QY 181 ThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTrpArgGln 199
Db 917 ACCTAATTCCTA-----GCTGTCGTGGATGAGGGAA 949

RESULT 13
US-09-884-733-5
; Sequence 5, Application US/09884733
; Patent No. US20020123116A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-2 Ligand Inhibitor
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/884,733
; FILING DATE: 19-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/304,003
; FILING DATE: 14-JUNE-2000

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5416
; TELEFAX: 415/952-9881
; TELEEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1438 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-884-733-5

Alignment Scores:
Pred. No.: 2.32e-86 Length: 1438
Score: 1066.00 Matches: 187
Percent Similarity: 94.47% Conservative: 1
Best Local Similarity: 93.97% Mismatches: 3
Query Match: 45.89% Indels: 8
DB: 10 Gaps: 1

US-09-993-234-6 (1-417) x US-09-884-733-5 (1-1438)
QY 1 MetGlunlArpProArgGlyCysAlaAlaValAlaAlaLeuLeuValLeuLeu
Db 377 ATGGAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTCCTGCTGCTG
QY 21 GlYAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHis
Db 437 GGGGCCCCGGCCAGGGGGGCACTGTAAGCCCAAGGTTGACTGTGCCGGTACTTCCAC
QY 41 LysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaPro
Db 497 AAGAAGATTGGTCTGTTTGTTCAGAGAGGCTGCCAGCGGGGCACCTACCTGAAGGCCCT
QY 61 CysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAla
Db 557 TGCACGAGCCCTGCGGCACTCCACCTGCTGTGTGCCCAAGACACCTTCTTGCCC
QY 81 TrpGluAsnHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSer
Db 617 TGGGAGAACCACCATATTCTGAATGTGCCCGCTGCCAGGCCCTGTGATGAGCAGGCCCTCC
QY 101 GlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGly
Db 677 CAGGTGGCGCTGAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGGCTGAAGCCAGGC
QY 121 TrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCysGlnPro
Db 737 TGGTTTGTGAGTGGCAGCTCAGCCAAATGTGTCAAGTTCACCTTCTACTGCCAACCA
QY 141 CysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThr
Db 797 TGCCTAGACTGCGGGCCCTGCACCGCCACACACGCGTACTCTGTCCCGCAGAGACTACT
QY 161 AspCysGlyThrCysLeuProGlyPheTyrGlnHisGlyAspGlyCysValSerCysPro
Db 857 GACTGTGGGACCTGCTGCTGCTTATGAAACATGGGATGGCTGCTGCTGCTGCTGCTG
QY 181 ThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTyrPargGln
Db 917 ACCTAATTCCTA-----GCTGTGCTGGGATGGAGGGA 949

RESULT 14
US-09-993-234-5
; Sequence 5, Application US/09993234
; Patent No. US20020146768A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
```

```

; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinpatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/993,234
; FILING DATE: 19-No. US20020146768A1-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/828,683
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1007P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5416
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1438 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-993-234-5

Alignment Scores:
Pred. No.: 2.32e-86 Length: 1438
Score: 1066.00 Matches: 187
Percent Similarity: 94.47% Conservative: 1
Best Local Similarity: 93.97% Mismatches: 3
Query Match: 45.89% Indels: 8
DB: 10 Gaps: 1

US-09-993-234-6 (1-417) x US-09-993-234-5 (1-1438)
QY 1 MetGlunlArpProArgGlyCysAlaAlaValAlaAlaLeuLeuValLeuLeu
Db 377 ATGGAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTCCTGCTGCTG
QY 21 GlYAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHis
Db 437 GGGGCCCCGGCCAGGGGGGCACTGTAAGCCCAAGGTTGACTGTGCCGGTACTTCCAC
QY 41 LysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaPro
Db 497 AAGAAGATTGGTCTGTTTGTTCAGAGAGGCTGCCAGCGGGGCACCTACCTGAAGGCCCT
QY 61 CysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAla
Db 557 TGCACGAGCCCTGCGGCACTCCACCTGCTGTGTGCCCAAGACACCTTCTTGCCC
QY 81 TrpGluAsnHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSer
Db 617 TGGGAGAACCACCATATTCTGAATGTGCCCGCTGCCAGGCCCTGTGATGAGCAGGCCCTCC
QY 101 GlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGly
Db 677 CAGGTGGCGCTGAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGGCTGAAGCCAGGC
QY 121 TrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCysGlnPro
```

Db 737 TGGTTTGTGAGTGCAGCGTCCAGCCAAATGTGTGACAGTTCACCCCTTCTACTGCCAACCA 796
QY 141 CysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThr 160
Db 797 TGCCTAGACTGCGGGCCCTGCACCGCCACACACAGCGCTACTCTGTCCCGCAGAGTACT 856
QY 161 AspCysGlyThrCysLeuProGlyPheTyrGlnHisGlyAspGlyCysValSerCysPro 180
Db 857 GACTGTGGACCTGCTGCTGCTGCTTCTATGACATGGCGATGGCTGCGTCTGCTGCC 916
QY 181 ThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTyrPargln 199
Db 917 ACGTAATTCCTA-----GCTGTCTGGGATGAGGGA 949

RESULT 15

US-09-964-824A-292
; Sequence 292, Application US/09964824A
; Patent/No. US20020102531A1
; GENERAL INFORMATION:
; APPLICANT: Horrigan, Stephen
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-73
; CURRENT APPLICATION NUMBER: US/09/964,824A
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/60/236,033
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,032
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,028
; NUMBER OF SEQ ID NOS: 583
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 292
; LENGTH: 816
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-824A-292

Alignment Scores:

Pred. No.: 2.76e-84 Length: 816
Score: 1039.50 Matches: 205
Percent Similarity: 74.39% Conservative: 7
Best Local Similarity: 71.93% Mismatches: 48
Query Match: 44.75% Indels: 26
DB: 10 Gaps: 4

US-09-993-234-6 (1-417) x US-09-964-824A-292 (1-816)

QY 7 GlyCysAlaAlaValAlaAlaAlaLeuLeuValLeuLeuGlyAlaArgAlaGlnGly 26
Db 3 GGCTGGCGGGGGTGGCGGGCGGCTCTCTGTGTGCTGCTGGGGGCCCGGCCAGGGC 62
QY 27 GlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGlyLeuPhe 46
Db 63 GGCACCTCGTAGCCCAAGGTGTGACTGTGCCGGTGACTTCCACAGAAGATTGGTCTGTTT 122
QY 47 CysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluProCysGly 66
Db 123 TGTTCAGAGGCTGCCAGCGGGGACTACTGAAAGGCCCTTGCACGAGCCCTGCGGC 182
QY 67 AsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHisAsn 86
Db 183 AACTCCACCTGCTGTGTGTGTCCCAAGACACCTTCTGTGCTGGGAGAGAACCATATAT 242
QY 87 SerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeuGluAsn 106
Db 243 TCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCTCTCCAGGTGGCGCTGAGAAC 302
QY 107 CysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTyrPheValGluCysGln 126
Db 303 TGTTCAGCAGTGGCGGACACCCGCTGTGGCTGTAAGCCAGGCTGTTTGTGAGTCCAG 362

QY 127 ValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCysGlyAla 146
Db 363 GTCAGCCAAATGTGTACAGCATGTCACCCCTTCTACTGCCAACCATGCTAGACTGCGGGCC 422
QY 147 LeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThrCysLeu 166
Db 423 CTGCACCGCCACACAGCGCTACTCTGTTCCTCCGAGAGATACTGACTGTGGAGACTGCTG 482
QY 167 ProGlyPheTyrGlnHisGlyAspGlyCysValSerCysProThrSerThrLeuGlySer 186
Db 483 CCTGGCTTCTATGACATGGCGATGGCTGCTGCTGCTGCCACGTAATTCTA----- 536
QY 187 CysProGluArgCysAlaAlaValCysGlyTyrPargln-MetPheTyrValGlnValle 206
Db 537 -----GCTGTCTGGGATGAGGGAAGGCGGCTGGGAGCAGAGCAG 578
QY 206 uLeuAlaGlyLeuValValProLeuLeu-----LeuGlyAlaThr 219
Db 579 GGGACCTGGGGTGGCGCAGGTGCTGCTGTTCAGGAATAGGAAGAGGGGATAGGAGC-- 636
QY 219 rLeuThrTyrThrTyrArgHisCysTyrPro-----HisLysProLeuValThrAl 236
Db 637 -----AGGAGCCTTGCCCTGTGATGGGTGGGCCCACTTCAGGCAAA 680
QY 236 aAspGluAlaGlyMetGluAlaLeuThrProProProAlaThrHisLeuSerProLeuAs 256
Db 681 CTAGATGGCAA-AAGAGCAATCTGATCCGCTTAGCCAGATACATAAGGTATTGCTC 739
QY 256 pSerAlaHisThrLeuLeuAlaProProAspSerSerGluLysIleCysThrValGlnLe 276
Db 740 TTCACCTTCAGCCAGCATTCCTCCCGCAGCATCTAGCCAGATATATACAGATGTAAACCT 799
QY 276 uValGlyAsnSer 280
Db 800 CGTGCCGAATTCT 812

Search completed: April 7, 2003, 03:57:53
Job time : 212.782 secs

GenCore version 5.1.4-p5-4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 6, 2003, 16:19:54 ; Search time 2608.38 Seconds

(without alignments)
2589.161 Million cell updates/sec

Title: US-09-993-234-6

Perfect score: 2323

Sequence: 1 MEQRPRGCAVAVALLLVLL.....ERMGLDGCVEDLRSLQRRGP 417

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh
-O=/cgn2_1/USPTO_spool/US09993234/runat_27032003_115456_15362/app_query.fasta_1.2346
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPECL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=biosum62 -TRANS-human40.cdl -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09993234_CGN_1_1_4749_@runat_27032003_115456_15362 -NCPU=6 -ICPU=3
-NO_XLPHY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estinu:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1423	61.3	1010	14	BQ068309	BQ068309 AGENCOURT
2	1258	54.2	698	9	A1807913	A1807913 wf52c03.x
3	1201.5	51.7	767	13	B1909448	B1909448 603065172
4	1179	50.8	681	10	BE563566	BE563566 601334867
5	1125	48.4	632	10	AM268610	AM268610 xv41b12.x
6	1121	48.3	688	9	A1424936	A1424936 tq19b08.x
7	1082	46.6	651	13	BM009354	BM009354 603629813
8	1078	46.4	562	9	A1140043	A1140043 qa87a04.x
9	1066.5	45.9	647	14	BM794760	BM794760 K-EST0076
10	1051	45.2	585	10	AM517358	AM517358 xp93q02.x
11	999	43.0	552	14	BM783972	BM783972 K-EST0062
12	990	42.6	565	14	BM744307	BM744307 K-EST0017
13	984	42.4	514	14	BM756372	BM756372 K-EST0034
14	984	42.4	514	14	BM783979	BM783979 K-EST0062
15	979	42.1	508	9	A1203624	A1203624 qe75f02.x
16	968	41.7	539	12	BF726557	BF726557 by08d05.Y
17	940	40.5	488	14	BM770798	BM770798 K-EST0054
18	935	40.2	492	14	BM741016	BM741016 K-EST0013
19	869.5	37.4	494	10	BE220347	BE220347 hv71b04.x
20	861.5	37.1	478	10	AM002222	AM002222 wt85c09.x
21	839	36.1	673	13	BM251737	BM251737 BOTL01000
22	795	34.2	427	12	BE696572	BE696572 PM4-CT040
23	780.5	33.6	434	14	BM826048	BM826048 K-EST0098
24	779	33.5	422	9	A1700459	A1700459 wd14b11.x
25	698	30.0	439	14	BM824360	BM824360 K-EST0095
26	692	29.8	433	14	H41522	H41522 yn90f12.s1
27	666	28.7	572	10	BE668836	BE668836 159213.MA
28	654	28.2	687	10	BE670189	BE670189 7e31c12.x
29	653	28.1	432	14	N71143	N71143 za80b09.s1
30	597.5	25.7	500	9	AA476747	AA476747 zw94b11.r
31	560.5	24.1	345	14	BM853061	BM853061 K-EST0134
32	537	23.1	623	9	A1811528	A1811528 tw43h06.x
33	535	23.0	345	9	AA934992	AA934992 op33h05.s
34	518.5	22.3	443	14	H46211	H46211 yo14h09.r1
35	487	21.0	755	13	B1655045	B1655045 603282719
36	486.5	20.9	372	14	w76376	w76376 zd66a06.r1
37	480.5	20.7	322	9	AA971249	AA971249 op73c01.s
38	479.5	20.6	435	10	AV664983	AV664983 AV664983
39	472	20.3	587	9	A1380959	A1380959 tq18c01.x
40	467	20.1	775	12	BG867742	BG867742 602786852
41	463	19.9	468	14	H46374	H46374 yo12d07.r1
42	455	19.6	633	10	BB212432	BB212432 BB212432
43	446	19.2	618	10	AM074008	AM074008 xb06c09.x
44	445.5	19.2	582	10	AW182875	AW182875 xp99a04.x
45	443	19.1	330	14	N71141	N71141 za80g11.s1

ALIGNMENTS

RESULT 1
BQ068309
LOCUS BQ068309 1010 bp mRNA linear EST 02-APR-2002
DEFINITION AGENCOURT_6794093 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5770562
5', mRNA sequence.
ACCESSION BQ068309
VERSION BQ068309.1 GI:19897355
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1010)
NIH-MGC http://mgc.ncl.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE

JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-r@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 plate: LLAM12833 row: n column: 03
 High quality sequence stop: 689.

FEATURES
 source
 1. 1010
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5770562"
 /clone_lib="NIH_MGC_121"
 /lab_host="DH10B"
 /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH_MGC Library."
 BASE COUNT 179 a 353 c 287 g 191 t
 ORIGIN

Alignment Scores:
 Pred. No.: 5.52e-109 Length: 1010
 Score: 1423.00 Matches: 257
 Percent Similarity: 91.58% Conservative: 4
 Best Local Similarity: 90.18% Mismatches: 13
 Query Match: 61.26% Indels: 11
 DB: 14 Gaps: 3

US-09-993-234-6 (1-417) x BQ068309 (1-1010)

QY 54 GYHISTYRLEULYSALAPROCYSTHRLUPROCYSGLYASNSETHRCYSLEUVALCYS 73
 DB 50 GGGCACTACCTGAGAGGCCCTTGACAGGAGCCCTGCGCAACTCCACTGCTGTGTGT 109
 QY 74 PROGLNASPTHRPHEUVALATPRGLUASNHISHISASNSETHRCYSALAAARGCYSGLN 93
 DB 110 CCCCAGACACTTCTTGCGCTGGAGAACCAACCATATCTGAATGTGCCCCGCTGCCAG 169
 QY 94 ALACYSASPLUGLINALASERGLNVALALALEUGLUASNCYSSERLALVALAASPTHR 113
 DB 170 GCCTGTGATGAGCAGGCCCTCCAGGTGGCGCTGGAGAACTGTTACAGAGTGCCGACACC 229
 QY 114 ARGCYSGLYCYSLYSPROGLYTRPHEVALGLUCYSGLNVALSERGLNVALSERSER 133
 DB 230 CGCTGTGCTGTAAGCCAGCGCTGTTGTGAGAGTCCAGGTACGCCAATGTGTACAGCAGT 289
 QY 134 SERPROPHETRYCYSGLNPROCYSLLEUASPCYSGLYALALEUHHISARGHISTHRAGLEU 153
 DB 290 TCACCCCTTACTGCCAACCATGCTAGACTGCGGGGCCCTGCACCGCCACACAGCGCTA 349
 QY 154 LEUCYSSERARGARGASPTHRASPSCYSGLYTHRCYSLEUPROGLYPHETRYGLUHSIGLY 173
 DB 350 CTCTGTTCCTCCGACAGATAGTACTGTGGACCTGCTGCTGCTCTATGAACATGGC 409
 QY 174 ASPGLYCYSVALSERCYSPTHRSETHRLEUGLYSERCYSPTHRGLUARGCYSALALA 193
 DB 410 GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 469
 QY 194 VALCYSGLYTRPARGLINMETPHETRPVALGLN-VALLEUVALAGLYLEUVALVALPR 213
 DB 470 GTCTGTGCTGAGG-----CAGAGTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 514

QY 213 OLEULEUENGLYALATHRLEUTHRTYRTHRTYRARGHISCYSTPRPROHISLYSPROLE 233
 DB 515 CTCTCTGCTTGGGGCCACCTGACCTACACATACCGCCACTGCTGCTGCTGCTGCTGCTGCTGCT 574
 QY 233 UVALTHRALAASPLUALAGLYMETGLUALALEUTHRPROPROALATHRHISLEUSE 253
 DB 575 GGTACTGACATGAAGCTGGATGAGGCTGTGACCCACACACCGGCCACCATCTGTC 634
 QY 253 PROLEUASPSERLALHISTHRLLEUVALPROPROAASPSERSERGLULYSILECYSTH 273
 DB 635 ACCCTTGACAGCGGCCACACACCTTCTAGACACTCTGACAGCAGTAGAGATCTGCAC 694
 QY 273 RVALGLNLEUVALGLYASNSETHRTPHTRPGLYTYRPROGLUTHRGLNGLUALALEUCY 293
 DB 695 CGTCCAGTGTGGTGAACAGCTGAGACCCCTGCTACCCCAAGACCCAGAGGCGCTCTG 754
 QY 293 SPROGLNVALTHRTSPSERTRPASPGLNLEUPROSERARG---ALALEUGLYPROALAAL 312
 DB 755 CCGCAAGTAGACATGTCTCTGAGACCAATTGCCCCAGCAAGCTCTGCGCCCGCTGGC 814
 QY 312 AALAPROTHRLSEUSERPROGLUSERPROALAGLY-----SERPROALAMETME 328
 DB 815 TCGCCCCCAATTCTTGCCAGAAAGTCCCGACGCGGCTCCGCGCCACCATGTATGCC 874
 QY 328 TLEUGLNPROGLY 332
 DB 875 TTGCCAACCCGGG 887

RESULT 2
 A1807913
 LOCUS 698 bp mRNA linear EST 19-DEC-1999
 DEFINITION wf52c03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359204 3' similar to SW:WSL1_HUMAN Q93038 WSL-1 PROTEIN PRECURSOR ;, mRNA sequence.
 ACCESSION A1807913
 VERSION A1807913 GI:5394479
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 698)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-r@mail.nih.gov
 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert length: 1568 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 459.

FEATURES
 source

1. 698
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2359204"
 /clone_lib="Soares_NFL_T_GBC_S1"
 /lab_host="DH10B"
 /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NBHL19w, testis NHR, and B-cell NCI-CGAP-GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT	111 a	218 c	214 g	155 t
ORIGIN				

Alignment Scores:	
Pred. No.:	2.12e-95
Score:	1258.00
Percent Similarity:	95.26%
Best Local Similarity:	95.26%
Query Match:	54.15%
DB:	9
	Gaps:
	0
	Length:
	698
	Matches:
	221
	Conservative:
	0
	Mismatches:
	11
	Indels:
	0
	Gaps:
	0

US-09-993-234-6 (1-417) x AI807913 (1-698)

QY	14	AlAlaLeuLeuLeuValLeuLeuGlyAlaArgAlaGlnGlyGlyThrArgSerProArgCys	33
Db	3	GGGCTCTCTGTGTGCTGCTGGGGGGGGGGGGCCAGGGGGGGGCTGTATCCCCAGGTGT	62
QY	34	AspCysAlaGlyAspPheHisLysLysIleGlyLeuPheCysCysArgGlyCysProAla	53
Db	63	GACTGTGCGCGTGAAGCTTCCACAAGAAGATGTCTGTTTGTGTGACAGAGCGTCGCCACGC	122
QY	54	GlyHisTyrLeuLysAlaProCysThrGluProCysGlyAsnSerThrCysLeuValCys	73
Db	123	GGGCACTACTGAAGGCCCCCTTGCACGGAGCCCCCTGGCGCACTCCACTGCTGTGTGT	182
QY	74	ProGlnAspThrPheLeuAlaTrpGluAsnHisHisAsnSerGluCysAlaArgCysGln	93
Db	183	CCCCAAGACACTTCTTGGCCCTGGGAGAACCAACCATATTTGATGTGCCCGCTGCCAG	242
QY	94	AlaCysAspGluGlnAlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThr	113
Db	243	GCCTGTGATGAGCAGGCGCTCCAGGTGGCGCTGGAGAACTGTTCAAGCAGTGGCCGACACC	302
QY	114	ArgCysGlyCysLysProGlyTrpPheValGluCysGlnValSerGlnCysValSerSer	133
Db	303	CGCTGTGGCTGTAAAGCCAGGCTGTGTGTGAGTGCACAGTCAAGTCAATGTGTCAAGCAGT	362
QY	134	SerProPheTyrCysGlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeu	153
Db	363	TCACCCCTTCACTGCCAACCATGCGCTAAGCTGGGGGCCCTGCACCGCCACACAGCGCTA	422
QY	154	LeucysSerArgArgAspThrAspCysGlyThrCysLeuProGlyPheTyrGluHisGly	173
Db	423	CTCTGTTCGCCGACAGATACTGACTGTGGGAACTGCCTGCCCTGTGCTTATGAACATGGC	482
QY	174	AspGlyCysValSerCysProThrSerThrLeuGlySerCysProGluArgCysAlaAla	193
Db	483	GATGGCTGGCTGTCCCTGCCTCACAGAACCTGTGGAGCTGTCCAGAGCGCTGTGCCGCT	542
QY	194	ValCysGlyTrpArgGlnMetPheTrpValGlnValLeuLeuAlaGlyLeuValPro	213
Db	543	GTCTGTGGCTGGAGGACAGATGTTCTGGGTGCAGGTGCTCCTGGCTGTGTGTGTCGCC	602
QY	214	LeuLeuLeuGlyAlaThrLeuThrTyrThrTyrArgHisCysTrpProHisLysProLeu	233
Db	603	CTCCTGCTGAAGCCACCCCTGACCTACACATACTGCACACTGCTGGCTCACATGCACGCT	662
QY	234	ValThrAlaAspGluAlaGlyMetGluAlaLeuThr	245
Db	663	GGTACTGCAATGAAGCTTGGATGGAGGCTCTGACT 698	

RESULT 3				
BI909448				
LOCUS	767 bp	mRNA	linear	EST 16-OCT-2001
DEFINITION	603065172F1 NIH_MGC_118	Homo sapiens	CDNA clone IMAGE:5214568	5' ,
	mRNA sequence.			
ACCESSION	BI909448			
VERSION	BI909448.1	GI:16172666		
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			

REFERENCE	1 (bases 1 to 767)
AUTHORS	NIH-MGC http://mgc.ncl.nih.gov/ .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, ph.D.

Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM1538 row: 0 column: 17
High quality sequence stop: 754.

FEATURES

Source

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5214568"
/clone_1kb="NIH_MGC_118"
/tissue_type="leukocyte"
/lab_host="DH10B"
/notes="vector: pCMV-Sport6; site_1: NotI; site_2: EcoRV
(destroyed); RNA source leukocytes from anonymous pool of
non-activated adult donors. Library is oligo-dT primed
and directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
1.2-3.3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(invitrogen). Research Genetics tracking code 027. Note:
this is a NIH_MGC Library."

```

BASE COUNT	122 a	243 c	241 g	161 t
ORIGIN				

Alignment Scores:

Pred. No.:	1.31e-90	Length:	76
Score:	1201.50	Matches:	22
Percent Similarity:	92.31%	Conservative:	1
Best Local Similarity:	91.90%	Mismatches:	5
Query Match:	51.72%	Indels:	17
DB:	13	Gaps:	2

US-09-993-234-6 (1-417) x BI909448 (1-767)

QY	8	CysAlaAlaValAlaAla-----	AlaLeuLeu	16
		:::		
Db	24	TGCCCCACGTTGGCAGCTGGCGTGAAGATCAGCAGCACCGTGTGCCCCAGTGCCTCCTC		83
QY	17	LeuValLeuLeuGlyAlaArg-AlaGlnGlyGlyThrArgSerProArgCysAspCysAl		36
Db	84	CTGTGCTGCTGGGGGCCCGGTGCCCCAGGGCGGCACTCGTAGCCCAAGGTGTGACTGTGC		143
QY	36	agIAspPheHisLysLysIleGlyLeuPheCysCysArgGlyCysProAla-GlyHis		56
Db	144	CGGTGACTTCCACAAGAAGATGTGTGTTTGTGTGCAGAGGCTGCCACAGCTGGGGCACT		203
QY	56	yrLeuLysAlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGln		76
Db	204	ACCTGAAGGCCCTTGCACGAGGCCCTGCCCAACTCCACCCTGCTGTGTCTCCCAAG		263
QY	76	sPThrPheLeuAlaTrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCys		96
Db	264	ACACCTTCTTGGCGCTGGGAGAACCAACCATTAATCTGAAATGTGCCCGCTGCCAGGCTGTG		323
QY	96	spGluGlnAlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysG		116
Db	324	ATGAGCAGGCGCTCCAGGTGGCGCTGGACAACCTGTTACAGCAGTGGCGGACACCCGCTGTG		383
QY	116	lyCysLysProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerProp		136
Db	384	GCTGTAAAGCCAGCGCTGTTGTGTGAGTGCAGGTCCAGGCAGTGTGTACAGCAGTTCAACCT		443

QY 136 heYrCysGlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysS 156
|||||
Db 444 TCTACTGCCAACCATGCTAGACTGCGGGGCCCTGCACCGCCACACAGGCTACTCTGTT 503
QY 156 eTArGArGAsPThrAspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyC 176
|||||
Db 504 CCGCAGAGATACTGACTGTGGGACCTGCTGCTGCTTCTATGAACATGGCGATGGCT 563
QY 176 ySVaISerCysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysG 196
|||||
Db 564 GCGTGTCTGCCCCCAGAGCAGCCTGGGAGCTGTCCAGAGCGCTGTGCCGTGTCTGTG 623
QY 196 lYTrPARgGlnMetPheTrpValGlnValLeuAlaGlyLeuValAlaProLeuLeu 216
|||||
Db 624 GCTGAGGCGAGATGTTCTGGTCCAGAGTGTCTGCTGCTGCTGTGTGTCCTGCTGCT 683
QY 216 euGlyAlaThrLeuThrTyrThrTyrArgHisCysTrpProHisLysProLeuValThra 236
|||||
Db 684 TTGGGGCCACCTG-ACCTACACATACGC-CACTGTGTGGCT-CACAAAGCCCTGTACT- 739
QY 236 lAAsPGlUAglAglMet 241
|||||
Db 740 --GATGAAGCTGGAGTG 754

RESULT 4
BE563566
LOCUS 681 bp mRNA linear EST 15-AUG-2000
DEFINITION 60134867F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3688721 5',
mRNA sequence.
ACCESSION BE563566
VERSION BE563566.1 GI:9807286
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 681)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L1CM382 row: f column: 18
High quality sequence stop: 681.

FEATURES
source
1. 681
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3688721"
/clone_1ib="NIH_MGC_39"
/tissue_type="adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGACGAG(G). Library constructed
by Ling Hong in the laboratory of Gerald M. Rubin
(University of California, Berkeley) using ZAP-cDNA
synthesis kit (Stratagene) and Superscript II RT (Life
Technologies)."
BASE COUNT 110 a 236 c 220 g 115 t
ORIGIN

Alignment Scores:
Pred. No.: 8.43e-89
Score: 1179.00

Length: 681
Matches: 225

Percent Similarity: 99.12%
Best Local Similarity: 99.12%
Query Match: 50.75%
DB: 10
US-09-993-234-6 (1-417) x BE563566 (1-681)
Conservative: 0
Mismatches: 2
Indels: 2
Gaps: 0

QY 175 GlyCysValSerCysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaVal 194
|||||
Db 3 GCGTGCCTGCTGCTGCCCCAGAGCAGCAGCCTGGGAGCTGTCCAGAGCGCTGTGCGCTGTC 62
QY 195 CysGlyTrPARgGlnMetPheTrpValGlnValLeuAlaGlyLeuValAlaProLeu 214
|||||
Db 63 TGTGGCTGAGGAGAGATGTTCTGGGTCCAGGTGCTCTGCTGCTGCTGTGTGTCCTGCTC 122
QY 215 LeuLeuGlyAlaThrLeuThrTyrThrTyrArgHisCysTrpProHisLysProLeuVal 234
|||||
Db 123 CTGCTTGGGGCCACCTGACCTACACATACCGCACTGCTGGCTCAGAGCCCTGCTGTT 182
QY 235 ThrAlaAspGluAlaGlyMetGluAlaLeuThrProProAlaThrHisLeuSerPro 254
|||||
Db 183 ACTGCAGATGAAGCTGGAGTGAAGGCTGTGACCCACACACCGGCGCCACCATCTGTACACC 242
QY 255 LeuAspSerAlaHisThrLeuLeuAlaProAspSerSerGluLysIleCysThrVal 274
|||||
Db 243 TTGGACAGCGCCACACACCTTCTAGCACCTCTGACAGCAGTGAAGATCTGCACCGTC 302
QY 275 GlnLeuValGlyAsnSerTrpThrProGlyTyrProGluThrGlnAlaLeuCysPro 294
|||||
Db 303 CAGTTGGTGGGTACAGCTGAGACCCCTGGCTACCCCGAGACCCAGAGGCGCTGTGCCG 362
QY 295 GlnValThrTrpSerTrpAspGlnLeuProSerArgAlaLeuGlyProAlaAlaPro 314
|||||
Db 363 CAGGTGACATGTCCTTGGGACAGCAGTGTGCCACAGAGCTTGTGCCCTGCTGCCGCC 422
QY 315 ThrLeuSerProGluSerProAlaGlySerProAlaMetMetLeuGlnProGlyProGln 334
|||||
Db 423 ACACCTCTGCCAGAGATGCCAGCGGCTGCCAGCAGCATGATGCTGCAGCGCGCAG 482
QY 335 LeuTyrAspValMetAspAlaValProAlaAlaArgArgTrpLysGluPheValArgThrLeu 354
|||||
Db 483 CTCTACGACGTGATGGAGCGCGGTCCACCGCGGCTGGAAGAGATTCTGCGCAGCGCTG 542
QY 355 GlyLeuArgGluAlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGln 374
|||||
Db 543 GGGCTGCCGAGGAGAGATGGAAGCGGCTGGAGGTGAGATGGCGCTTCCGAGACAG 602
QY 375 GlnTyrGlnMetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyr 394
|||||
Db 603 CAGTACGAGATGCTCAAGCGCTGGCCAGCAGCAGCCCGG-GGCCCTGGAGCGCTTAC 661
QY 395 AlaAlaLeuGluArgMetGly 401
|||||
Db 662 GCGGC-CTGGAGCGCATGGGG 681

RESULT 5
AW268610
LOCUS 632 bp mRNA linear EST 03-JAN-2000
DEFINITION xva1b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:2815679 3' similar to SW:WSL1_HUMAN Q93038 WSL-1 PROTEIN
PRECURSOR ;, mRNA sequence.
ACCESSION AW268610
VERSION AW268610.1 GI:6655640
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 632)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)

Db 2 CGGCGCGGGCGTGGCGGCGGCTGCGGCGGCGCTCCTGGTGTGCTGCGGGGCGGG 61
 QY 24 AlaGInGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIle 43
 Db 62 GGGCGGGCGGCGACTCGTAGCCCCAGGTGTGACTGTGCCGGTGACTTCCACAGAAGATT 121
 QY 44 GlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGlu 63
 Db 122 GGTCTGTTTGTGTGAGAGAGGCTGCCACGCGGGCAGCTAAGGCCCCCTTGACCGAG 181
 QY 64 ProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsn 83
 Db 182 CCCTGGCGCACTCCACCTGCGCTGTGTGTCCCAAGACACCTTCTTGCCCTGGGAGAAC 241
 QY 84 HisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAla 103
 Db 242 CACCATATTTCTGAATGTGCCCGCTGCCAGCGCTGTATGAGCAGAGCCCTCCACAGGTGGCG 301
 QY 104 LeuGlnAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheVal 123
 Db 302 CTGGAGAAGCTGTTCCAGCAGTGGCCGACACCCGCTGTGGCTGAAGCCAGGCTGTTGTG 361
 QY 124 GluCysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAsp 143
 Db 362 GAGTGCCAGGTCCAGCCAAATGTGTACAGAGTTCAACCTTCTACTGCCAACCATGCTAGAC 421
 QY 144 CysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGly 163
 Db 422 TGGCGGGCGCTGCACCGCCACACACGCGTACTGTGTCCCGCAGAGGTAAGTACTGTGGG 481
 QY 164 ThrCysLeuProGlyPheTyrGlnHisGlyAspGlyCysValSerCysProThrSerThr 183
 Db 482 ACCTGCTGCTGCTGCTTATGAACATGGCGATGGCTGCGTGTCTGCCCCACGAGCACC 541
 QY 184 LeuGlySerCysProGluArgCysAlaValCysGlyTrpArgGlnMetPheTrp 202
 Db 542 CTGGGAGCTGTCCAGAGCGCTGTGCCCTGTGTGGCTTGAGGCGACAGTAAGTGG 598
 RESULT 7 651 bp mRNA linear EST 30-OCT-2001
 LOCUS BM009354
 DEFINITION 603629813P1 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5443659 5',
 mRNA sequence.
 ACCESSION BM009354
 VERSION BM009354.1 GI:16523708
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 651)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: DCTD/DTF
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: L1CM1921 row: 1 column: 04
 High quality sequence stop: 649.
 Location/Qualifiers
 1..651

/lab_host="DH10B (phage-resistant)"
 /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCACGAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC Library."

BASE COUNT	107 a	224 c	204 g	116 t
ORIGIN				

Alignment Scores:

Pred. No.:	1.05e-80	Length:	651
Score:	1082.00	Matches:	210
Percent Similarity:	98.14%	Conservative:	1
Best Local Similarity:	97.67%	Mismatches:	2
Query Match:	46.58%	Indels:	4
DB:	13	Gaps:	0

US-09-993-234-6 (1-417) x BM009354 (1-651)

QY	166	LeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeuGly	185
Db	4	CTGCCTGGCTTCTATGAACATGGCGATGGCTGCTGTC-TGCCCCACGAGCACCTGGGG	62
QY	186	SerCysProGluThrGlySerAlaAlaValCysGlyTyrPargGlnMetPheTyrValGlnVal	205
Db	63	AGCTGTCAGAGCGCTGTGCCGCTGTCTGTGGCTGAGGCGAGATGTTCTGGTCCAGGTG	122
QY	206	LeuLeuAlaGlyLeuValValProLeuLeuLeuGlyAlaThrLeuThrTyrThrTyrArg	225
Db	123	CTCCTGGCTGGCTTGTGTGGTCCCTCTGCTGTGGGGCCACCCTGACCTTACATACCGC	182
QY	226	HisCysTrpProHisLysProLeuValThrAlaAspGluAlaGlyMetGluAlaLeuThr	245
Db	183	CACGTGCTGGCTTCAACAAGCCCTGTGTTACTACGATGAAGCTGGATGGAGGCTCTGACC	242
QY	246	ProProProAlaThrHisLeuSerProLeuAspSerAlaHisThrLeuLeuAlaProPro	265
Db	243	CCACACACGGC-ACCCATCTGTACACCTTGGACAGCGCCACACACCTTACACACTCTCT	301
QY	266	AspSerSerGlyLysIleCysThrValGlnLeuValGlyAsnSerTyrThrProGlyTyr	285
Db	302	GACAGCAGTGAGAAGATCTGCACACCGTCCAGTTGGTGGTAACAGCTGACGCCCTGGCTAC	361
QY	286	ProGluThrGlnGluAlaLeuCysProGlnValThrTrpSerTyrAspGlnLeuProSer	305
Db	362	CCCGAGACCCAGGAGGCGCTGTGCCCGGAGGTGACATGTTCTTGGGACAGTTGCCACAGC	421
QY	306	ArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSerProAlaGlySerPro	325
Db	422	AGAGCTCTTGGCCCCGCTGTGTCGCCACACTCTGCCAGAGTCCCAAGCCGGCTCGCCA	481
QY	326	AlaMetMetLeuGln-ProGlyProGlnLeuTyrAspValMetAspAlaValProAlaAr	345
Db	482	GCCATGATGCTGCAGACCCCGGGCCGACACTCTACGACGTGATGGACGGGTCCACAGCGG	541
QY	345	GArgTrpLysGluPheValArgThrLeuGlyLeuArgGluAlaGluIleGluAlaValG1	365
Db	542	GCGCTGGAAGGAGTTCTGTGCGCACGCTGGGGCTGCGCGAGGCGAGAGATCGAAGCCGTGA	601
QY	365	uValGluIleGly-ArgPheArgAspGlnGlnTyrGluMet 378	
Db	602	GGTGGAGATCGGCCCGCTTCCGAGACCGACGATGAGATT 642	
RESULT 8			
LOCUS	A1140043	562 bp	mrna
DEFINITION	q87a04.x1 Soares_fetal_heart_NbHH19w Homo sapiens cDNA clone	linear	EST 13-APR-1999
	IMAGE:1693710 3' similar to SW:WSL1_HUMAN Q93038 WSL-1 PROTEIN		
	PRECUSOR ;, mRNA sequence.		
ACCESSION	A1140043		

Best Local Similarity: 99.01% Mismatches: 0
Query Match: 45.91% Indels: 1
DB: 14 Gaps: 1

US-09-993-234-6 (1-417) x BM794760 (1-647)

QY 200 MetPheTrpValGlnValLeuLeuAlaGlyLeuValValProLeuLeuGlyAlaThr 219
Db 40 GTGTCTGGGGTCCAGGTGCTCTGCTGGCTGGCTTGTGTGCTCCCTCTCTGCTGGGCCAC 99
QY 220 LeuThrTrpThrTrpArgHisCysTrpProHisLysProLeuValThrAlaAspGluAla 239
Db 100 CTGACCTACACATACCGCCACTGCTGCTGGCTCACAAGCCCTGTGTTACT--GATGAAGCT 156
QY 240 GlyMetGluAlaLeuThrProProAlaThrHisLysSerProLeuAspSerAlaHis 259
Db 157 GGGATGGAGGCTCTGACCCCAACCCGACCATCTGTACACCTTGACAGCGCCAC 216
QY 260 ThrLeuLeuAlaProProAspSerSerGlyLysIleCysThrValGlnLeuValGlyAsn 279
Db 217 ACCCTTCTAGCACCTCTCTGACAGCAGTGAGAAGATCTGCACCGTCCAGTTGGTGGTAAC 276
QY 280 SerTrpThrProGlyTrpProGluThrGlnGluAlaLeuCysProGlnValThrTrpSer 299
Db 277 AGCTGGACCCCTGGCTACCCCGAGAACCCAGAGCGCTCTGCCCGCAGGTGACATGGTCC 336
QY 300 TrpAspGlnLeuProSerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGlu 319
Db 337 TGGGACCAAGTGGCCACAGAGCTCTTGGCCCCCTGCTGCGCCACACACTCTGCGCAGAG 396
QY 320 SerProAlaGlySerProAlaMetMetLeuGlnProGlyProGlnLeuTrpAspValMet 339
Db 397 TCCCCAGCCGGCTCGCCAGCATGATGCTGCAGCGGGCCCGCAGCTCTACGACGTGATG 456
QY 340 AspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGluAla 359
Db 457 GACGGCGTCCACAGCGCGCGCTGGAAGAGTTCTGCGCACGCTGGGGCTGCGCGAGGCA 516
QY 360 GluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTrpGluMetLeu 379
Db 517 GAGATCGAAGCCGTGGAGGTGAGATCGCGCTCCGAGACAGCAGATGATGCTC 576
QY 380 LysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArg 399
Db 577 AAGCGCTGGCGCCAGCAGCAGCCCGCGGCTCGAGACCGTTTACGCGGCTTGAGAGCGC 636
QY 400 MetGlyLeu 402
Db 637 ATGGGGCTG 645

RESULT 10 585 bp mRNA linear EST 03-MAR-2000
AWS17358
LOCUS
DEFINITION xp93902.x1 Soares_NHCE_cervix Homo sapiens CDNA clone IMAGE:2747954
3' similar to TR:000276 000276 LYMPHOCYTE ASSOCIATED RECEPTOR OF
DEATH 2. ; mRNA sequence.

ACCESSION AWS17358
VERSION AWS17358.1 GI:7155440
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 585)

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov

This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand

FEATURES
source
Possible reversed clone: polyT not found
Seq primer: -40UP from Gibco
High quality sequence stop: 489.
Location/Qualifiers
1..585

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2747954"
/clone_lib="Soares_NHCE_cervix"
/lab_host="DH10B (phage-resistant)"
/note="Organ: cervix; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer (5'
TGTACCAATCTGAAGTGGAGCGCGCGGCGGCTTTTCTTTTCTTTTCTTTT
T 3'); double-stranded cDNA was ligated with Not I and Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT7T3 vector.
Library is normalized; constructed by Bento Soares and
M.Fatima Bonaldo."

BASE COUNT 94 a 181 c 193 g 117 t
ORIGIN

Alignment Scores:
Pred. No.: 3.53e-78 Length: 585
Score: 1051.00 Matches: 184
Percent Similarity: 94.39% Conservative: 1
Best Local Similarity: 93.88% Mismatches: 3
Query Match: 45.24% Indels: 8
DB: 10 Gaps: 1

US-09-993-234-6 (1-417) x AWS17358 (1-585)

QY 4 ArgProArgGlyCysAlaAlaValAlaAlaLeuLeuValLeuGlyAlaArg 23
Db 2 CGGCGCGGGGCTGCGCGCGGCGGTGGCGGGCGCTCTCTGCTGGCTGGGGCCCG 61
QY 24 AlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIle 43
Db 62 GCCCAGGGCGGCACTGTAAGCCCAAGGTGACTGTGCGCGGTGACTTCCACAAGAAAT 121
QY 44 GlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGlu 63
Db 122 GGTCTGTTTGTTCAGAGGCTGCGCCAGCGGGGCACTACCTGAAGGCCCTTGACAGAG 181
QY 64 ProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsn 83
Db 182 CCCTGGGCACTCCACCTGCTGTGTGTCCCAAGACACACTTCTTGGCTGGAGAAC 241
QY 84 HisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAla 103
Db 242 CACCATTAATTCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCCCTCCAGGTGGC 301
QY 104 LeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheVal 123
Db 302 CTGAGAGACTGTTACAGCAGTGGCGGCACACCCGCTGTGCTGTAAAGCCAGGCTGTTGTG 361
QY 124 GluCysGlnValSerGlnCysValSerSerSerProPheTyrCysGlnProCysLeuAsp 143
Db 362 GAGTGCAGGTCAGCCATGTGTACAGCATTCACCCCTTCTACTGCCAACCATGCTTAGAC 421
QY 144 CysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGly 163
Db 422 TGGCGGGCCCTGCACCGCCACACAGGCTACTCTGTGTCCGAGAGATAGTACTGTGGG 481
QY 164 ThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThr 183
Db 482 ACCTGGCTGCTGCTTCTATGAACATGGCGATGGCTGGCTGCTGCCACAGTAATTC 541
QY 184 LeuGlySerCysProGluArgCysAlaAlaValCysGlyTrpArgGln 199
Db 542 CTA-----GCTGCTGGGATGAGGAA 565
RESULT 11

BM783972 552 bp mRNA linear EST 05-MAR-2002
LOCUS BM783972
DEFINITION K-EST0062019 S6SNU620 Homo sapiens cDNA clone S6SNU620-31-H06 5',
mRNA sequence.
ACCESSION BM783972
VERSION BM783972.1 GI:19132204
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 552)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE 21C Frontler Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel.: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 31 row: H column: 06
High quality sequence stop: 552.
FEATURES
source
1. .552
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="S6SNU620-31-H06"
/clone_1lb="S6SNU620"
/sex="F"
/tissue_type="Ascites"
/cell_type="Scattering floating"
/cell_line="SNU-620"
/lab_host="Top10F,"
/note="Organ: Stomach; Vector: pcNS; Site_1: EcoRI;
Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tabacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including Ecor
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F' by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."

BASE COUNT 92 a 172 c 173 g 115 t
ORIGIN

Alignment Scores:
Pred. No.: 7.35e-74 length: 552
Score: 999.00 Matches: 174
Percent Similarity: 94.09% Conservative: 1
Best Local Similarity: 93.55% Mismatches: 3
Query Match: 43.00% Indels: 8
DB: 14 Gaps: 1

US-09-993-234-6 (1-417) x BM783972 (1-552)

OY 14 AlaLeuLeuLeuValLeuLeuGlyAlaArgAlaGlnGlyThrArgSerProArgCys 33
Db 5 GCGCTCCTCCTGCTGCTGGGGCCCGGGCCAGGCGGCACCTGAGCCCAAGTGT 64
OY 34 AspCysAlaGlyAspPheHisLysLysIleGlyLeuPheCysCysArgGlyCysProAla 53
Db 65 GACTGTGCCGGTGACTTCACAGAAGATTGCTCTGTTGTTCAGAGAGGCTGCCACGC 124

OY 54 GlyHisTyrLeuLysAlaProCysThrGlnProCysGlyAsnSerThrCysLeuValCys 73
Db 125 GGGCACTACCTGAAGGCCCTTGCAGGAGCCCTGGCGCAACTCCACCTGTGTGT 184
OY 74 ProGlnAspThrPheLeuAlaTyrGluAsnHisHisAsnSerGluCysAlaArgCysGln 93
Db 185 CCCAAGACACCTTCTTGCGCTGGGAGAACCAACATATTCGATGTGCCCGTCCAG 244
OY 94 AlaCysAspGluGlnAlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThr 113
Db 245 GCCTGTGATGAGCAGGCGCTCCAGGTGGCGCTGGAGAACTGTCAGCAGTGCCGACACC 304
OY 114 ArgCysGlyCysLysProGlyTyrPheValGluCysGlnValSerGlnCysValSerSer 133
Db 305 CGCTGGCTGCTGAAGCCAGGCTGTTGTGAGTGCAGGTCCAGGTCAATGTGTACAGCAGT 364
OY 134 SerProPheTyrCysGlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeu 153
Db 365 TCACCTTCTACTGCAACCATGCTTAGACTGCGGGGCCCTGCACCGCACACAGGCTA 424
OY 154 LeuCysSerArgArgAspThrAspCysGlyThrCysLeuProGlyPheTyrGluHisGly 173
Db 425 CTCTGTCCCGCAGAGATACTGACTGTGGGAGACCTGCCTGCCTGTATGACATGGC 484
OY 174 AspGlyCysValSerCysProThrSerThrLeuGlySerCysProGluArgCysAlaAla 193
Db 485 GATGGCTGGCTGTCTCTGCCCCACAGTAATTCCTA-----GCT 520
OY 194 ValCysGlyTrrPargGln 199
Db 521 GTCGTGGATGAGGAA 538

RESULT 12
BM744307

LOCUS BM744307 565 bp mRNA linear EST 01-MAR-2002
DEFINITION K-EST0017828 S6SNU620 Homo sapiens cDNA clone S6SNU620-17-C06 5',
mRNA sequence.

ACCESSION BM744307
VERSION BM744307
KEYWORDS BM744307.1 GI:19065636
SOURCE EST.

ORGANISM human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 565)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.

TITLE 21C Frontler Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel.: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 17 row: C column: 06
High quality sequence stop: 565.

FEATURES
source
1. .565
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="S6SNU620-17-C06"
/clone_1lb="S6SNU620"
/sex="F"
/tissue_type="Ascites"
/cell_type="Scattering floating"
/cell_line="SNU-620"
/lab_host="Top10F,"
/note="Organ: Stomach; Vector: pcNS; Site_1: EcoRI;
Site_2: NotI; The poly (A)+ RNA was dephosphorylated with

bacterial alkaline phosphatase (BAP) and then dephosphorylated with tobacco acid pyrophosphatase (TAP). The dephosphorylated intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

BASE COUNT 95 a 175 c 178 g 117 t
ORIGIN

Alignment Scores:

Pred. No.:	4.31e-73	length:	565
Score:	990.00	Matches:	173
Percent Similarity:	93.55%	Conservative:	1
Best Local Similarity:	93.01%	Mismatches:	4
Query Match:	42.62%	Indels:	8
DB:	14	Gaps:	1

US-09-993-234-6 (1-417) x BM744307 (1-565)

```
OY 14 AlaleuLeuValLeuLeuGlyAlaArgAlaGlnGlyThrArgSerProArgCys 33
Db 5 GCGCTCCTCCTGCTGCTGGGGGGCCCGGCCAGCTCGTAGCCCGAGGTGT 64
OY 34 AspcysAlaGlyAspPheHisLysLysIleGlyLeuPheCysCysArgGlyCysProAla 53
Db 65 GACTGTGCCGGTGAAGTCCACAAGAAGATGCTGTTTGTGTGACAGAGGCTGCCACAGCG 124
OY 54 GlyHisTrpLeuLysAlaProCysThrGluProCysGlyAsnSerThrCysLeuValCys 73
Db 125 GGGCACTACCTGAAGGCCCTTGACAGAGCCCTGGGCACTCCACCTGCTGTGTGT 184
OY 74 ProGlnAspThrPheLeuAlaTrpGluAsnHisAsnSerGluCysAlaArgCysGln 93
Db 185 CCCCAAGACACCTTCTTGCCCTGGAGACACCATTAATTCTGAATGTGCCCTGCCAG 244
OY 94 AlaCysAspGlnAlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThr 113
Db 245 GCCTGTGATGAGCAGCCCTCCAGGTGGCGCTGAGAACTGTTCAAGCAGTGGCCGACACC 304
OY 114 ArgCysGlyCysLysProGlyTrpPheValGluCysGlnValSerGlnCysValSerSer 133
Db 305 CGCTGTGGCTGTAGACCCAGGCTGTTGTGTGAGTGCACAGTCAATGTGTGCAGCAGT 364
OY 134 SerProPheTrpCysGlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeu 153
Db 365 TCACCCCTTCTACTGCCAACCATGCTAGACTGCGGGGCCCTGCACCGCCACACAGGCTA 424
OY 154 LeuCysSerArgArgAspThrAspCysGlyThrCysLeuProGlyPheTrpGluHisGly 173
Db 425 CTCTGTTCGCGAGAGATACTGACTGTGGACCTGCTGCTGCTCTATGAACATGGC 484
OY 174 AspGlyCysValSerCysProThrSerThrLeuGlySerCysProGluArgCysAlaAla 193
Db 485 GATGGCTGCTGCTGCTGCCACGTAATTCCTA-----GCT 520
OY 194 ValCysGlyTrpArgGln 199
Db 521 GTCGTGGATGAGAGGAA 538
```

RESULT 13
LOCUS BM756372 514 bp mRNA linear EST 04-MAR-2002
DEFINITION R-EST0034666 S6SNU620 Homo sapiens cDNA clone S6SNU620-27-G03 5',
mRNA sequence.
ACCESSION BM756372

VERSION BM756372.1 GI:19085987
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 514)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.

TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center

Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 27 row: G column: 03
High quality sequence stop: 514.

FEATURES
source Location/Qualifiers
1..514

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="S6SNU620-27-G03"
/clone_lib="S6SNU620"
/sex="F"
/tissue_type="Ascites"
/cell_type="Scattering floating"
/lab_host="Top10F"

/note="Organ: Stomach; Vector: pcNS; Site_1: EcoRI; Site_2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then dephosphorylated with tobacco acid pyrophosphatase (TAP). The dephosphorylated intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

BASE COUNT 86 a 166 c 153 g 109 t
ORIGIN

Alignment Scores:			
Pred. No.:	1.19e-72	length:	514
Score:	984.00	Matches:	168
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	42.36%	Indels:	0
DB:	14	Gaps:	0

US-09-993-234-6 (1-417) x BM756372 (1-514)

```
OY 14 AlaleuLeuValLeuLeuGlyAlaArgAlaGlnGlyThrArgSerProArgCys 33
Db 5 GCGCTCCTCCTGCTGCTGGGGGGCCCGGCCAGCTCGTAGCCCGAGGTGT 64
OY 34 AspcysAlaGlyAspPheHisLysLysIleGlyLeuPheCysCysArgGlyCysProAla 53
Db 65 GACTGTGCCGGTGAAGTCCACAAGAAGATGCTGTTTGTGTGACAGAGGCTGCCACAGCG 124
OY 54 GlyHisTrpLeuLysAlaProCysThrGluProCysGlyAsnSerThrCysLeuValCys 73
Db 125 GGGCACTACCTGAAGGCCCTTGACAGAGCCCTGGGCACTCCACCTGCTGTGTGT 184
```

OY	74	ProGlnAspThrPheLeuAlaTArgLValasNHISHisasnSergLucysAlaArgCysGln	93
Db	185	CCCCAAGACACCCTTCCTGGCCCTGGAGAACCACCATTATTTCTGAATGTGCCCGCTGCCAG	244
OY	94	AlAcysAspGluGlnAlaSerGlnValAlaLeuGluasnCysSeraLaValAlaAspThr	113
Db	245	GCCGTGTGATGAGCAGGECCTCCAGGTGGCGCTGGAGAACTGTTCAGCAGTGCCGACACC	304
OY	114	ArgCysGlyCysIysProGlyTrpPheValGluCysGlnValSergInCysValSerSer	133
Db	305	CGCTGTGGCTGTAAAGCCAGGCTGTGTTGTGTGAGATGCCAGGTCAAGCCAATGTGTACAGACT	364
OY	134	SerProPheTyrCysGlnProCysIleuaspcCysGlyAlaIalaLeuHISArgHISThrArgLeu	153
Db	365	TCAACCTTCTACTGCACCAACCATGCTTAGACTGCGGGCCCTGCACCGCACACACGGCTA	424
OY	154	LeucysSerArgArgAspThrAspcCysGlyThrCysIleuProGlyPheTyrGluHISgly	173
Db	425	CTCTGTTCGCCGACAGATACTGACTGTGGAGACCTGCCTGCCTTCTATGAACATGGC	484
OY	174	AspGlyCysValSerCysProThr	181
Db	485	GATGGCTGCCTGTCTGCCCCACG	508

LOCUS	514 bp	mRNA	linear	EST 05-MAR-2002
DEFINITION	BM783979	K-EST0062030 S6SNU620	Homo sapiens cDNA clone S6SNU620-32-A05 5',	
ACCESSION	BM783979	mRNA sequence.		
VERSION	BM783979.1	GI:19132211		
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
REFERENCE	1 (bases 1 to 514)	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.			
TITLE	21C Frontier Korean EST Project 2001			
JOURNAL	Unpublished (2002)			
COMMENT	Contact: Kim YS Genome Research Center Korea Research Institute of Bioscience & Biotechnology 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea Tel: +82-42-860-4470 Fax: +82-42-860-4409 Email: yongsung@email.kr b.re.kr Plate: 32 row: A column: 05 High quality sequence stop: 514.			
FEATURES	Location/Qualifiers			
source	1..514			
	/organism="Homo sapiens"			
	/db_xref="taxon:9606"			
	/clone="S6SNU620-32-A05"			
	/clone_lib="S6SNU620"			
	/sex="F"			
	/tissue_type="Ascites"			
	/cell_type="Scattering floating"			
	/cell_line="SNU-620"			
	/lab_host="Top10F"			
	/note="Organ: Stomach; Vector: pcNS; Site_1: EcoRI; Site_2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand			

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 6, 2003, 16:28:24 ; Search time 70.3944 Seconds

(without alignments)
1816.682 Million cell updates/sec

Title: US-09-993-234-6
Perfect score: 2323
Sequence: 1 MEQRPRGCAVAALLLVLL.....ERMGLDGCVEDLRSLRQGP 417

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh
-O=/cgn2_1/USPTO_spool/US0993234/runat_27032003_115457_15378/app_query.fasta_1.2346
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=tni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US0993234 @CGN_1_116 @runat_27032003_115457_15378 -NCPU=6 -ICPU=3
-NO_XLPHY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued_Patents_NA: *
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq: *
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq: *
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PCTUS.COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2323	100.0	1254	3	US-08-815-469-3
2	2323	100.0	1634	4	US-08-928-069-11
3	2323	100.0	1634	4	US-08-828-683A-9
4	2267	97.6	1783	3	US-08-815-469-1
5	1066	45.9	1438	4	US-08-928-069-5
6	1066	45.9	1438	4	US-08-828-683A-5
7	692	29.8	433	4	US-08-928-069-2
8	692	29.8	433	4	US-08-828-683A-2
9	404.5	17.4	1956	2	US-08-762-308-10
10	387.5	16.7	2440	4	US-09-513-007-1
11	376	16.2	2062	1	US-08-050-319B-24
12	376	16.2	2062	2	US-08-465-982-24

13	374	16.1	2161	3	US-09-106-038A-1	Sequence 1, Appl
14	374	16.1	2161	4	US-09-505-250-3	Sequence 3, Appl
15	374	16.1	2175	1	US-08-321-668-1	Sequence 1, Appl
16	374	16.1	2175	1	US-08-837-941-1	Sequence 1, Appl
17	374	16.1	2175	1	US-08-126-016-1	Sequence 1, Appl
18	374	16.1	2175	4	US-08-054-970-1	Sequence 1, Appl
19	231.5	10.0	1724	5	PCT-US96-12374-1	Sequence 1, Appl
20	230.5	9.9	1724	4	US-08-509-024-1	Sequence 1, Appl
21	230.5	9.9	1724	4	US-09-333-279-1	Sequence 1, Appl
22	218.5	9.4	6889	1	US-08-286-740-2	Sequence 2, Appl
23	218.5	9.4	6889	5	PCT-US95-09576-2	Sequence 2, Appl
24	217	9.3	1049	4	US-08-804-166-1	Sequence 1, Appl
25	217	9.3	1049	4	US-08-910-991-1	Sequence 1, Appl
26	216.5	9.3	1929	4	US-09-146-950-1	Sequence 1, Appl
27	216	9.3	1202	4	US-08-804-166-3	Sequence 3, Appl
28	216	9.3	1202	4	US-08-910-991-3	Sequence 3, Appl
29	216	9.3	1301	4	US-08-804-166-7	Sequence 7, Appl
30	216	9.3	1301	4	US-08-910-991-7	Sequence 7, Appl
31	210	9.0	600	1	US-08-050-319B-47	Sequence 47, Appl
32	210	9.0	600	2	US-08-465-982-47	Sequence 47, Appl
33	210	9.0	6896	2	US-08-627-151A-6	Sequence 6, Appl
34	203.5	8.8	1323	3	US-08-883-036A-1	Sequence 1, Appl
35	203	8.7	1147	4	US-08-804-166-5	Sequence 5, Appl
36	203	8.7	1147	4	US-08-910-991-5	Sequence 5, Appl
37	200.5	8.6	483	4	US-09-326-394-1	Sequence 1, Appl
38	200.5	8.6	1478	4	US-09-149-922-6	Sequence 6, Appl
39	199.5	8.6	1167	5	PCT-US95-17083-1	Sequence 1, Appl
40	199.5	8.6	2534	2	US-08-219-237B-1	Sequence 1, Appl
41	199.5	8.6	2534	4	US-08-468-560C-1	Sequence 1, Appl
42	199.5	8.6	2534	4	US-09-180-100-16	Sequence 16, Appl
43	199.5	8.6	2551	4	US-09-290-640-1	Sequence 1, Appl
44	197.5	8.5	1596	4	US-09-146-950-17	Sequence 17, Appl
45	196	8.4	1480	4	US-09-290-640-65	Sequence 65, Appl

ALIGNMENTS

RESULT 1
US-08-815-469-3
Sequence 3, Application US/08815469
Patent No. 6153402
GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang
APPLICANT: Ni, Jian
APPLICANT: Dixit, Vishva
APPLICANT: Gentz, Reiner L.
APPLICANT: Dillon, Patrick J.
TITLE OF INVENTION: Death Domain Containing Receptors
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/815,469
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: No. 6153402 Yet Assigned
FILING DATE: 06-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,711
FILING DATE: 17-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,285

FILING DATE: 12-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1254 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1251
US-08-815-469-3

Alignment Scores:
Pred. No.: 1.79e-181 Length: 1254
Score: 2323.00 Matches: 417
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-993-234-6 (1-417) x US-08-815-469-3 (1-1254)

QY 1 MetGlnGlnArgProArgGlyCysAlaAlaAlaAlaLeuLeuValLeuLeu 20
DB 1 ATGAGACAGCGCGCGGGGGCTGCGCGGGGGGGCGGCGCTCTCTGCTGCTG 60
QY 21 GAlaAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHis 40
DB 61 GGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
QY 41 LysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaPro 60
DB 121 AAGAAGATGGTCTGTTTGTGTCAGAGGCTGCCAGCGGGGCACTTGAAGGCCCT 180
QY 61 CysThrGlnProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAla 80
DB 181 TGCACGGAGCCCTGCGCACTCACTGCTGTGTGCCAAGACACCTTCTTGCC 240
QY 81 TrpGlnAsnHisHisAsnSerGlyCysAlaArgCysGlnAlaCysAspGlnAlaSer 100
DB 241 TGGGAGAACCAACATATTTGAATGTGCCCGCTGCCAGGCGCTGTATGAGCAGCGCTCC 300
QY 101 GlnValAlaLeuGlnAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGly 120
DB 301 CAGGTGGCGCTGGAGAACTGTTCAGCAGTGGCGACACCGCGCTGTGCTGAAGCCAGGC 360
QY 121 TrpPheValGlnCysGlnValSerGlnCysValSerSerProPheTyrCysGlnPro 140
DB 361 TGGTTTGTGAGTGCAGGTCAACCAATGTGTCAAGCAAGTTCACCTTCTACTGCCAACCA 420
QY 141 CysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgAlaGlyAspThr 160
DB 421 TGCCTAGACTGCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
QY 161 AspCysGlyThrCysLeuProGlyPheTyrGlnHisGlyAspGlyCysValSerCysPro 180
DB 481 GACTGTGGAGCTGCGCTGCTCTATGAACATGGCGATGGCTGCTGCTGCC 540
QY 181 ThrSerThrLeuGlySerCysProGlnArgCysAlaAlaValCysGlyTyrPargGlnMet 200
DB 541 ACGAGCACCCCTGGGAGCTGTCAGAGCGCTGCGCGCTGTGTGCTGAGGAGCATG 600
QY 201 PheTrpValGlnValLeuLeuAlaGlyLeuValAlaProLeuLeuGlyAlaThrLeu 220
DB 601 TTCTGGGTCCAGGTGCTCTGCTGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 660

QY 221 ThrTyrThrTyrArgHisCysTrpProHisLysProLeuValThrAlaAspGlnAlaGly 240
DB 661 ACCACACATACCGCCACTGCTGCGCTCAGACGCCCTGCTTACTGAGATGAAGCTGG 720
QY 241 MetGlnAlaLeuThrProProProAlaThrHisLeuSerProLeuAspSerAlaHisThr 260
DB 721 ATGAGGCTCTGACCCCAACACCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780
QY 261 LeuLeuAlaProProAspSerSerGlyLysIleCysThrValGlnLeuValGlyAsnSer 280
DB 781 CTCTAGCACCTCTCTGACAGCAGTGAAGATCTGCACCGCTTGTGCTGAGTAAACAGC 840
QY 281 TrpThrProGlyTyrProGlnThrGlnGlnAlaLeuCysProGlnValThrTrpSerTrp 300
DB 841 TGGACCCCTGGCTACCCCGAGACCCAGAGGCGCTCTGCGCGCGAGGTGACATGCTCTGG 900
QY 301 AspGlnLeuProSerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGlnSer 320
DB 901 GACCAGTTGCCAGCAGAGCTCTTGGCCCCCGCTGCTGCGCGCACACTCTCGCAGAGTCC 960
QY 321 ProAlaGlySerProAlaMetMetLeuGlnProGlyProGlnLeuTyrAspValMetAsp 340
DB 961 CCAGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1020
QY 341 AlaValProAlaArgArgTyrPlyGlnPheValArgThrLeuGlyLeuArgGlnAlaGlu 360
DB 1021 GCGGTCCAGCGCGCGCGCTGGAAGAGTTCGTGCGCACGCTGGGGCTGCGGAGGAGAG 1080
QY 361 IleGlnAlaValGlnValGlnIleGlyArgPheArgAspGlnGlnTyrGlnMetLeuLys 380
DB 1081 ATGGAAGCCGTGAGGTGAGATCGCGCGCTTCCGAGACAGCAGTACGAGATGCTCAAG 1140
QY 381 ArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGlnArgMet 400
DB 1141 CGCTGGCGCGCAGCAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1200
QY 401 GlyLeuAspGlyCysValGlnAspLeuArgSerArgLeuGlnArgGlyPro 417
DB 1201 GGGGTGAGCGGCTGCTGGAAGACTTGGCAGCGCGCGCTGCGCGCGCGCG 1251

RESULT 2
US-08-928-069-11
Sequence 11, Application US/08928069
Patent No. 6462176
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-3 POLYPEPTIDE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,069
FILING DATE: 11-Sep-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/026943
FILING DATE: 09/23/1996
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1052R1
TELECOMMUNICATION INFORMATION:

```

; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1634 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
;
US-08-928-069-11

```

Alignment Scores:

Pred. No.:	2 64e-181	Length:	1634
Score:	2323.00	Matches:	417
Best Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-09-993-234-6 (1-417) x US-08-928-069-11 (1-1634)

QY	1	MetGluGlnArgProArgGlyCysAlaAlaValAlaAlaAlaLeuLeuValLeuLeu	20
Db	89	ATGGAGCAGCGCGCGGGCTGCGGGCGGTGGCGGGCGGCTCTCTGCTGCTG	148
QY	21	GlyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHis	40
Db	149	GGGGCCCCGGCCAGGGGGCAGCTGTAAGCCCAAGGTGTGACTGTGCCGGTGAATTCCAC	208
QY	41	LysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaPro	60
Db	209	AAGAAGATTGGTCTGTTTGTGCAAGAGCTGCCACGGGGCCTACTGTAAGCCCCCT	268
QY	61	CysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAla	80
Db	269	TGCACGGAGCCCTCGCGCACTCCACTGCTGTGTCTCCCAAGACACCTTCTTGCCC	328
QY	81	TrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSer	100
Db	329	TGGGAGAACCCATTAATCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCTCC	388
QY	101	GlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGly	120
Db	389	CAGGTGGCGCTGGAGAACTGTTCAAGCAGTGGCCGACACCCGCTGTGGCTGTAGCCAGGC	448
QY	121	TrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCysGlnPro	140
Db	449	TGGTTTGTGGAGTGCCAGGTCAAGCCAAATGTGTCAAGCAGTTCAACCTTCTACTGCCAACCA	508
QY	141	CysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThr	160
Db	509	TGCCTAGACTGCGGGCCCTGCACGCCACACACAGGCTACTCTGTCCCGCAGAGATACT	568
QY	161	AspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysPro	180
Db	569	GACTGTGGGACCTGCCTGCCTGTATGAACATGGCGATGGCTGCGGTCTGCCCC	628
QY	181	ThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTPrpArgGlnMet	200
Db	629	ACGAGCACCCCTGGGGAGCTGTCCAGACGGCTGTGCCGCTGTCTGTGGCTGCAGCAGATG	688
QY	201	PheTrpValGlnValLeuLeuAlaGlyLeuValValProLeuLeuLeuGlyAlaThrLeu	220
Db	689	TTCGTGGCTCCAGGTGCTCTGTGCTGCTGTGTGCTGCCCTCTGCTGGGGCCACCCTG	748
QY	221	ThrTyrThrTyrArgHisCysTrpProHisLysProLeuValThrAlaAspGluAlaGly	240
Db	749	ACCTACACATACCGCCACTGCTGCTTCAACAAGCCCTGTTACTGCAGATGAAGCTGGG	808
QY	241	MetGluAlaLeuThrProProProAlaThrHisLeuSerProLeuAspSerAlaHisThr	260
Db	809	ATGGAGGCTCTGACCCCAACCGGCCACCCATCTGTCAACCTTGGACAGGCCCAACACC	868
QY	261	LeuLeuAlaProProAspSerSerGluLysIleCysThrValGlnLeuValGlyAsnSer	280

SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-08-828-683A-9

Alignment Scores:
Pred. No.: 2.64e-181 Length: 1634
Score: 2323.00 Matches: 417
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-993-234-6 (1-417) x US-08-828-683A-9 (1-1634)

QY 1 MetGluGlnArgProArgGlyCysAlaAlaValAlaAlaLeuLeuValLeuLeu 20
DB 89 ATGAGACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 148
QY 21 GlyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHis 40
DB 149 GGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 208
QY 41 LysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaPro 60
DB 209 AAGAAGATTGGTCTGTTTGTGTCAGAGGCTGCCAGCGGGGCACTACCTGAAGGCCCT 268
QY 61 CysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAla 80
DB 269 TGCACGAGCCCTGCGGCAACTCCACTGCTTGTGTGCCAAGACACACCTTCTGGCC 328
QY 81 TrpGluAsnHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSer 100
DB 329 TGGAGAACCAACCATATTCTGAATGTGCCCGCTGCCAGGCGCTGATGAGCAGCGCTCC 388
QY 101 GlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGly 120
DB 389 CAGGTGGGCTGGAGAACTGTTCAGAGTGGCCGACACCCCGCTGTGCTGAAGCCAGGC 448
QY 121 TrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCysGlnPro 140
DB 449 TGGTTGTGAGTGCACAGGTACGCAATGTGTACAGCATTCACCTTCTACTGCCAACCA 508
QY 141 CysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThr 160
DB 509 TGCCTAGACTGCGGGGCCCTGCACCGCCACACACAGCGCTACTCTGTCCCGCAGATACT 568
QY 161 AspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysPro 180
DB 569 GACTGTGGGACCTGCGCTGCTGCTTATGAACATGGCGATGGCTGCTGCTGCC 628
QY 181 ThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTyrParGlnMet 200
DB 629 ACGAGCACCCCTGGGAGCTGTCCAGAGCGCTGTGCCGTCTGTGGCTGAGGACAGATG 688
QY 201 PheTrpValGlnValLeuLeuAlaGlyLeuValProLeuLeuGlyAlaThrLeu 220
DB 689 TTCTGGGTCAGGTGCTCTGCTGGCTGTGTGTCCTCCCTGCTGGGGCCACCTG 748
QY 221 ThrTyrThrTyrArgHisCysTrpProHisLysProLeuValThrAlaAspGluAlaGly 240
DB 749 ACCATACACATACCGCCACTGTGCGCTCACAAAGCCCTGCTTACTGCAGATGAAGTGG 808
QY 241 MetGluAlaLeuThrProProProAlaThrHisLeuSerProLeuAspSerAlaHisThr 260
DB 809 ATGAGAGGCTGTGACCCACACCGGCGCACCCCATCTGTCAACCTTGACAGCGCCACACC 868
QY 261 LeuLeuAlaProProAspSerSerGlyLysIleCysThrValGlnLeuValGlyAsnSer 280
DB 869 CTCTAGCACCTCTGACAGCAGTGAAGAATCTGCACCGCTCCAGTGTGGGTACACAGC 928
QY 281 TrpThrProGlyTyrProGluThrGlnGluAlaLeuCysProGlnValThrTyrSerTrp 300
DB 929 TGGACCCCTGGCTACCCGAGACCCAGAGGCGCTGTGCCCGCAGGTGACATGTCTCTGG 988

QY 301 AspGlnLeuProSerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSer 320
DB 989 GACCAAGTTCAGCAGAGAGCTCTTGCGCCGCTGCTGCGCCACACTCTCCGACAGTCC 1048
QY 321 ProAlaGlySerProAlaMetMetLeuGlnProGlyProGlnLeuTyrAspValMetAsp 340
DB 1049 CCAGCGCGGCTGCGCAGCCATGATGCTGAGCGCGCGCGCGCGCGCGCGCGCG 1108
QY 341 AlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGluAlaGlu 360
DB 1109 GCGGTCCAGCGCGCGCGCGCTGGAAGAGATTCTGCGCACCGCTGGGCGCTGCCGAGCAGAG 1168
QY 361 IleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGluMetLeuLys 380
DB 1169 ATCGAAGCCGTGAGAGTGTGAGATCGGCCCTTCGAGACCAAGTACGAGATGCTCAAG 1228
QY 381 ArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMet 400
DB 1229 CGCTGGCGCCAGACAGACCGCGCGCGCTCGAGCGGTTTACGCGCGCGCTGAGCGCATG 1288
QY 401 GlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 417
DB 1289 GGGCTGACGGCTGCGTGAAGACTTGCAGACCGCGCTGACGCGCGCGCG 1339

RESULT 4

US-08-815-469-1
: Sequence 1, Application US/08815469
: Patent No. 6153402

GENERAL INFORMATION:

APPLICANT: Yu, Guo-Liang
APPLICANT: Ni, Jian
APPLICANT: Dixit, Vishva
APPLICANT: Gentz, Reiner L.
APPLICANT: Dillon, Patrick J.
TITLE OF INVENTION: Death Domain Containing Receptors
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/815,469
FILING DATE: HEREWITH
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: No. 6153402 Yet Assigned
FILING DATE: 06-FEB-1997
APPLICATION DATA:
APPLICATION NUMBER: US 60/028,711
FILING DATE: 17-OCT-1996
APPLICATION DATA:
APPLICATION NUMBER: US 60/013,285
FILING DATE: 12-MAR-1996

ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688

REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1783 base pairs
TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 198..1481
US-08-815-469-1

Alignment Scores:
Pred. No.: 1.16e-176 Length: 1783
Score: 2267.00 Matches: 409
Percent Similarity: 97.39% Conservative: 1
Best Local Similarity: 97.15% Mismatches: 5
Query Match: 97.59% Indels: 6
DB: 3 Gaps: 1

US-09-993-234-6 (1-417) x US-08-815-469-1 (1-1783)

QY 3 GlnArgProArgGly-----CysAlaAlaValAlaAlaLeuLeu 16
DB 219 GAGGCCCCACGTCGGAGCTGCGGAGAGTCAGACACCTGTCCCCAGCGCTCTC 278
QY 17 LeuValLeuLeuGlyAlaArgAlaGlnGlyThrArgSerProArgCysAspCysAla 36
DB 279 CTGCTGCTGTCGGGGCGGGCCAGGCGGCACTCGTAGCCCCAGGTGTGACTGTGCC 338
QY 37 G1AspPheHisIstLysIleGlyLeuPheCysArgGlyCysProAlaGlyHisTyr 56
DB 339 GGTGACTTCCACAGAAGATGTGCTGTGTGTGTCAGAGGCTGCCACGGGGCACTAC 398
QY 57 LeuLysAlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAsp 76
DB 399 CTGAAGGCCCTTGCACGAGAGCCCTGCGGCACTCCACCTGTGTGTCTCCCAAGAC 458
QY 77 ThrPheLeuAlaTrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAsp 96
DB 459 ACCTTCTTGGCTGGGAGAACCCATATTTGATGTGCCCGCTGCCAGGCTGTGAT 518
QY 97 GluGlnAlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGly 116
DB 519 GAGCAGGCCCTCCAGGTGGCGCTGGAGAACTGTTCAGCAGTGGCGACACCCGCTGTGCC 578
QY 117 CysLysProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerProPhe 136
DB 579 TGTAAAGCCAGGCTGTTTGTGAGTGCACAGGTCAATGTGTACAGCAGTTCACTTC 638
QY 137 TyrCysGlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuSer 156
DB 639 TACTGCCAACCAATGCTAGACTGCGGGGCCCTGCACCCACACAGGCTACTCTGTTC 698
QY 157 ArgArgAspThrAspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCys 176
DB 699 CGCAGAGATACTGACTGTGGGACCTGCTGCTGCTTCTATGACATGGCGATGGCTGC 758
QY 177 ValSerCysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaCysGly 196
DB 759 GTGTCTGCCCCACAGCACCCCTGGGAGCTGTCCAGAGCGCTGTGCCGCTGTGTC 818
QY 197 TrpArgGlnMetPheTrpValGlnValLeuAlaGlyLeuValProLeuLeu 216
DB 819 TCGAGGACAGATGTTCTGGGTCCAGGTGCTCTGCTGCTGTGTGCTCCCTCTGCTT 878
QY 217 GlyAlaThrLeuThrTyrThrTyrArgHisCysTrpProHisLysProLeuValThrAla 236
DB 879 GGGGCCACCTGACTACACATACCGCCACTGTGCTGACAAAGCCCTGTACTGCA 938
QY 237 AspGluAlaGlyMetGluAlaLeuThrProProAlaThrHisLeuSerProLeuAsp 256
DB 939 GATGAAGCTGGGATGAGGCTTGACCCACACCGGCCACCATCTGTCTACCTTGGAC 998
QY 257 SerAlaHisThrLeuLeuAlaProProAspSerSerGluLysIleCysThrValGlnLeu 276
DB 999 AGCGCCACACCTTCTAGACCTCTGACAGAGTGAGAAGATCTGCACCGTCCAGTTG 1058

QY 277 ValGlyAsnSerTrpThrProGlyTyrProGluThrGlnGluAlaLeuCysProGlnVal 296
DB 1059 GTGGTAACAGCTGGACCCCTGGCTACCCCGAGAGACCGAGGGCGCTGTGCCGAGGTG 1118
QY 297 ThrTrpSerTrpAspGlnLeuProSerArgAlaLeuGlyProAlaAlaProThrLeu 316
DB 1119 ACATGCTCTGGGACACAGTTGCCACAGAGAGCTCTTGCCCCGCTGCGCCACACTC 1178
QY 317 SerProGluSerProAlaGlySerProAlaMetLeuGlnProGlyProGlnLeuTyr 336
DB 1179 TCGCCAGAGTCCCCACCGGCTGCCAGCCATGATGTGCAGCCGGCGCCAGCTCTAC 1238
QY 337 AspValMetAspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeu 356
DB 1239 GACGTGATGACGCGGCTCCAGCGCGGCTGGAAGAGTTCGTGCGCACGCTGGGCTG 1298
QY 357 ArgGluAlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnIntYr 376
DB 1299 CGCGAGCCAGAGATCGAAGCCGTGAGGTGAGATCGGCCCTTCGAGACCAAGACTAC 1358
QY 377 GluMetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAla 396
DB 1359 GAGATGCTCAAGCGCTGGGCCACAGCAGACGCCCGGCGCTCGGAGCGTTTACGGGCC 1418
QY 397 LeuGluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGly 416
DB 1419 CTGAGCGCATGGGCTGTGACGGCTGCGTGGAAAGACTTGGCGACCGCCTGCAGCGGCC 1478
QY 417 Pro 417
DB 1479 CCG 1481

RESULT 5

US-08-928-069-5
Sequence 5, Application US/08928069
Patent No. 6462176

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: APO-3 POLYPEPTIDE
NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/928,069
FILING DATE: 11-Sep-1997
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/026943
FILING DATE: 09/23/1996
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1052R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1438 base pairs
TYPE: Nucleic Acid

STRANDEDNESS: Single
TOPOLOGY: Linear

US-08-928-069-5

Alignment Scores:

Pred. No.: 2.27e-78 Length: 1438
Score: 1066.00 Matches: 187
Percent Similarity: 94.47% Conservative: 1
Best Local Similarity: 93.97% Mismatches: 3
Query Match: 45.89% Indels: 8
DB: 4 Gaps: 1

US-09-993-234-6 (1-417) x US-08-928-069-5 (1-1438)

QY 1 MetGlunArgProArgGlyCysAlaAlaAlaAlaAlaLeuLeuValLeu 20
Db 377 ATGAGACAGCGCGCGGGCTGCGCGCGGTGGCGCGCTCTCTGCTGCTG 436
QY 21 GLYAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHis 40
Db 437 GGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 496
QY 41 LysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaPro 60
Db 497 AAGAAGATGCTGTCTTTTGTTCAGAGAGCTGCCAGCGGGGCGACTACTGAAGGCCCT 556
QY 61 CysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAla 80
Db 557 TGCACGAGCGCTGCGGCAACTCCACCTGCTGTGTGCCAAGACACTTCTTGCC 616
QY 81 TrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGlnAlaSer 100
Db 617 TGGAGAACCAACATAATTCTGAATGTGCCGCTGCCAGGCGCTGTGATGAGCAGGCTCC 676
QY 101 GlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGly 120
Db 677 CAGGTGCGCGTGGAGAACTGTTCAGACAGTGGCGGACACCGCGCTGTGTAAGCCAGGC 736
QY 121 TrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCysGlnPro 140
Db 737 TGGTTGTGGAGTGCAGGTCAAGCAATGTGTACAGAGTTCAACCTTCTACTGCCAACCA 796
QY 141 CysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThr 160
Db 797 TGCCTAGACTGGCGGGCGCGCTGCACCGCACACAGGCTACTCTGTCTCCGACAGATACT 856
QY 161 AspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysPro 180
Db 857 GACTGTGGACCTGCGCTGCGCTCTATGAACATGGCGATGCGTGTCTGCTGCC 916
QY 181 ThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTyrPargln 199
Db 917 ACGTAATTCCTA-----GCTGTGCTGGATGAGGGAA 949

RESULT 6

US-08-828-683A-5
Sequence 5, Application US/08828683A
Patent No. 6469144

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,683A

FILING DATE: 31-Mar-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/625328

FILING DATE: 1-Apr-1996

APPLICATION NUMBER: 08/710802

FILING DATE: 23-Sep-1996

ATTORNEY/AGENT INFORMATION:

NAME: Marschang, Diane L.

REGISTRATION NUMBER: 35,600

REFERENCE/DOCKET NUMBER: P1007P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-5416

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 1438 base pairs

TYPE: Nucleic Acid

STRANDEDNESS: Single

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-08-828-683A-5

Alignment Scores:

Pred. No.: 2.27e-78 Length: 1438
Score: 1066.00 Matches: 187
Percent Similarity: 94.47% Conservative: 1
Best Local Similarity: 93.97% Mismatches: 3
Query Match: 45.89% Indels: 8
DB: 4 Gaps: 1

US-09-993-234-6 (1-417) x US-08-828-683A-5 (1-1438)

QY 1 MetGlunArgProArgGlyCysAlaAlaAlaAlaAlaLeuLeuValLeu 20
Db 377 ATGAGACAGCGCGCGGGCTGCGCGCGGTGGCGCGCTCTCTGCTGCTG 436
QY 21 GLYAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHis 40
Db 437 GGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 496
QY 41 LysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaPro 60
Db 497 AAGAAGATGCTGTCTTTTGTTCAGAGAGCTGCCAGCGGGGCGACTACTGAAGGCCCT 556
QY 61 CysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAla 80
Db 557 TGCACGAGCGCTGCGGCAACTCCACCTGCTGTGTGCCAAGACACTTCTTGCC 616
QY 81 TrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGlnAlaSer 100
Db 617 TGGAGAACCAACATAATTCTGAATGTGCCGCTGCCAGGCGCTGTGATGAGCAGGCTCC 676
QY 101 GlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGly 120
Db 677 CAGGTGCGCGTGGAGAACTGTTCAGACAGTGGCGGACACCGCGTGTGCTGTAAGCCAGGC 736
QY 121 TrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCysGlnPro 140
Db 737 TGGTTGTGGAGTGCAGGTCAAGCAATGTGTACAGAGTTCAACCTTCTACTGCCAACCA 796
QY 141 CysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThr 160
Db 797 TGCCTAGACTGGCGGGCGCGCTGCACCGCACACAGGCTACTCTGTCTCCGACAGATACT 856
QY 161 AspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysPro 180
Db 857 GACTGTGGACCTGCGCTGCGCTCTATGAACATGGCGATGCGTGTCTGCTGCC 916
QY 181 ThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTyrPargln 199
Db 917 ACGTAATTCCTA-----GCTGTGCTGGATGAGGGAA 949

RESULT 7

US-08-928-069-2
; Sequence 2, Application US/08928069
; Patent No. 6462176
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-3 POLYPEPTIDE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,069
; FILING DATE: 11-Sep-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/026943
; FILING DATE: 09/23/1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1052R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 433 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; US-08-928-069-2

Alignment Scores:
Pred. No.: 1.74e-48 Length: 433
Score: 692.00 Matches: 133
Percent Similarity: 93.10% Conservative: 2
Best Local Similarity: 91.72% Mismatches: 6
Query Match: 29.79% Indels: 5
DB: 4 Gaps: 0

US-09-993-234-6 (1-417) x US-08-928-069-2 (1-433)

OY 19 LeuLeuGlyAlaArgAlaGlnGlyThrArgSerProArgCysAspCysAlaGlyAsp 38
DB 1 CTGCTGGGGGGCCCGCCAGNGCGGCACCTCGTAGCCCCCAGGTGTGACTGTCCGGGTGAC 60
OY 39 PheHisLysLysIleGlyLeuPheCysCysArgGlyCysProAla-GlyHisTyrLeuLys 58
DB 61 TTCACACAAGAAGATTGCTGTTTGTGTGACAGGCTGCCAGCGGGGCACTACCTGAA 120
OY 58 sAlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPh 78
DB 121 GGCCCTTGACAGGAGCCCTGCGC-AACTCCACCTGCTTGTGTGCCCAAGACACCTT 179
OY 78 eleuAlaTPrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluG 98
DB 180 CTTGGCCTGGGAGAACCATATATCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCA 239
OY 98 nAlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 118
DB 240 GGCTCCCAAGGTGGCGCTGGAGAACTGTTCAGCAGCTGGCCGACACCCCGCTGTGCTTAA 299
OY 118 sProGlyTPrpPheValGluCysGln-ValSerGlnCysValSerSer-SerProPheTyr 137

DB 300 GCAGGGCTGTTGTGAGAGTGCCAGGGCTACGCCAATGTGTACAGCAGTTCACCTTCTAA 359
OY 138 CysGlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCys-SerAr 157
DB 360 TGCCAACCATGCTAGACTGCGGGGCCCTGCACACGCAACACACAGGCTAATNTGTTCCCG 419
OY 157 gArgAsp 159
DB 420 CAGAGAT 426

RESULT 8

US-08-828-683A-2
; Sequence 2, Application US/08828683A
; Patent No. 6469144
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,683A
; FILING DATE: 31-Mar-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/625328
; FILING DATE: 1-Apr-1996
; APPLICATION NUMBER: 08/710802
; FILING DATE: 23-Sep-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1007P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 433 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-08-828-683A-2

Alignment Scores:
Pred. No.: 1.74e-48 Length: 433
Score: 692.00 Matches: 133
Percent Similarity: 93.10% Conservative: 2
Best Local Similarity: 91.72% Mismatches: 6
Query Match: 29.79% Indels: 5
DB: 4 Gaps: 0

US-09-993-234-6 (1-417) x US-08-828-683A-2 (1-433)

OY 19 LeuLeuGlyAlaArgAlaGlnGlyThrArgSerProArgCysAspCysAlaGlyAsp 38
DB 1 CTGCTGGGGGGCCCGCCAGNGCGGCACCTCGTAGCCCCCAGGTGTGACTGTCCGGGTGAC 60
OY 39 PheHisLysLysIleGlyLeuPheCysCysArgGlyCysProAla-GlyHisTyrLeuLys 58
DB 61 TTCACACAAGAAGATTGCTGTTTGTGTGACAGGCTGCCAGCGGGGCACTACCTGAA 120

QY 295 GlnValThrTrpSerTrpAspGlnLeuProSerArgAlaLeuGlyProAlaAlaPro 314
 DB 1104 ACCTCTGTTGAGAAATGGGAAGAC-----1127
 QY 315 ThrLeuSerProGlnSerProAlaGlySerProAlaMetMetLeuGlnProGlyProGln 334
 DB 1128 TCCGCCACCCGCAACGTCCTGACAAATGCAGACCTTGCGATT-----1169
 QY 335 LeuTyrAspValMetAspAlaValProAlaArgTrpLysGluPheValArgThrLeu 354
 DB 1170 CTGTATGCTGTGTGGATGGCGTGCCTCCAGCGCGCTGGAAGAGATTCAATGCTTCATG 1229
 QY 355 GlyLeuArgGluAlaGluIleGluAlaValGluIleGlyArg---PheArgAsp 373
 DB 1230 GGGCTGAGCGAGACGACGATCGAGAGGCTGGAGATGCAGAACGGCGCTGCTGCGCGAG 1289
 QY 374 GlnGlnTyrGlnMetLeuLysArgTrpArgGlnGlnProAla-----GlyLeu 390
 DB 1290 GCTCAGTACAGCATGCTGGAAGCCTGGCGGCGCGCACCGCGCCACGAGACACGCTG 1349
 QY 391 GlyAlaValTyrAlaAlaLeuGluArgMetGlyLeuAspGlyCysValGluAspLeuArg 410
 DB 1350 GAAGTAGTGGCGCTGCTGCTTTCACAGATGAACCTGGCTGGTGGCTGAGATATCTC 1409
 QY 411 SerArgLeuGlnArgGlyPro 417
 DB 1410 GAGGCTCTG--AGAAATCCC 1427

RESULT 10

US-09-513-007-1
 ; Sequence 1, Application US/09513007
 ; Patent No. 6406907
 ; GENERAL INFORMATION:
 ; APPLICANT: Taylor, J. Michael
 ; APPLICANT: Kehrl, Jr., Marcus
 ; APPLICANT: Lee, Eun-Kyung
 ; APPLICANT: Mwangi, Simon
 ; TITLE OF INVENTION: BOVINE TUMOR NECROSIS FACTOR RECEPTOR-1
 ; FILE REFERENCE: 08411-018001
 ; CURRENT APPLICATION NUMBER: US/09/513,007
 ; CURRENT FILING DATE: 2000-02-25
 ; PRIOR APPLICATION NUMBER: 60/122,156
 ; PRIOR FILING DATE: 1999-02-26
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 2440
 ; TYPE: DNA
 ; ORGANISM: Bos taurus
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (294)..(1706)
 ; US-09-513-007-1

Alignment Scores:

Pred. No.: 1.98e-22 Length: 2440
 Score: 387.50 Matches: 130
 Percent Similarity: 36.57% Conservative: 47
 Best Local Similarity: 26.86% Mismatches: 186
 Query Match: 16.68% Indels: 121
 DB: 4 Gaps: 18

US-09-993-234-6 (1-417) x US-09-513-007-1 (1-2440)

QY 11 ValAlaAlaLeuLeuValLeuGluAlaArgAlaGlnGlyThrArgSer 30
 DB 333 GTGCTTCCAGCTGTGTGGCAGATGTGTACCCCGCAGGGGTTCAAGGGCTGCTCCAC 392
 QY 31 ProArgCysAspCysAlaGlyAspPhe-----39
 DB 393 CCC-----GGGACCTGAGAGAGAGAGAGTCCCTGTCCCAAGAAAA 437

QY 40 -----HisLysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeu 57
 DB 438 TATAACCAACCCGCAAAATAGCACCATTTGCTGCACCAAGTGCACAAAGGTACTATCTG 497
 QY 58 LysAlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThr 77
 DB 498 TACATGACTGTCCGGGTCCAGGGCGAGACACGACTGCAGGGGTGTGTCCTCCCTGGCAC 557
 QY 78 PheLeuAlaTrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGlu 97
 DB 558 TACACTGCCCTTGAGAACCATCTCAGA--CGATGCCCTGAGCTGCTCCAGGTGCGGGAC 614
 QY 98 GlnAlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCys 117
 DB 615 GAAATGTTCCAGGTGAGATTTCCGCTTGTGTAGTGAACCGGACACTGTGTGCGGCTGC 674
 QY 118 LysProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyr 137
 DB 675 AGCAAGAAC-----CAGTACCGGGAATACTGGGGTGAACCTGGCTTCCGG 719
 QY 138 CysGlnProCysLysAspCys-----GlyAlaLeuHisArgHisThrArgLeuCys 155
 DB 720 TGTCTGAAGTGCAGCCCTGTCTCCCATGACACAGTAAT-----ATCCCCCTGC 767
 QY 156 ---SerArgArgAspThrAspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAsp 174
 DB 768 CAGGAGAGACAGACACCATCTGC--CACTGCCATATGGGCTTCTTCTTAAGCGGCC 824
 QY 175 GlyCysValSerCysProThrSerThrLeuGlySerCysProGluArg---CysAlaAla 193
 DB 825 AAGTGCATCTCTGT-----CATGATTGAAGAACAGAGAGTGGAGAAG 869
 QY 194 ValCysGlyTrpArg-----GlnMetPhe 201
 DB 870 TTATGTCCAACCCGACCTTCAACTGTGAAGACTCTCAGAGACCAGCACATACACTA 929
 QY 202 TrpValGlnValLeuAlaGlyLeuValProLeuLeuGluAlaThrLeuThr 221
 DB 930 TTACCCCTGTGATGTCTTCGGGCTTGGCTGCACTCCCTCTGTCTGCTTAGCA 989
 QY 222 TyrThrTyrArgHisCysTrpProHisLys-----231
 DB 990 TGTGCTTACCAAGCG--TGAAGCCCAAGCTTACTTCATCATTTGCGGGAGTGCAGT 1046
 QY 231 -----231
 DB 1047 CTGCTAAAGAGGGGAGCCAGAACTCTGTGTCGGGCCAGGCTTCAACCCACACC 1106
 QY 232 -----ProLeuValThr 235
 DB 1107 ACCATCTGCTTCAAGTCCACCCCAAGTTCACATCTCTCCATTCSSCTTACATCTCC 1166
 QY 236 AlaAspGluAlaGlyMetGluAlaLeuThrProProProAlaThrHisLeuSerProLeu 255
 DB 1167 TGTGACCGGTCCAACTTCGAGCGCGTGCATCTCCCTCCAGCGAGACGGCCCGCCCAT 1226
 QY 256 AspSerAlaHisThrLeuLeuAlaProProAspSerSerGluLysIleCysThrValGln 275
 DB 1227 CTAAGAGCTGGCCCACTCTCCCGGGGCTCCGGGCTCCACCCACTGTGTACCCCGGG 1286
 QY 276 LeuValGlyAsnSer-----TrpThrProGlyTyrProGluThrGlnGluAlaLeuCys 293
 DB 1287 CCTCCGGCTCCACCCACTCTGTACCCCGGGGCTCCGGGCTCCACCCACTCTGCACC 1346
 QY 294 ProGlnValThrTrpSerTrpAspGlnLeuProSerArgAlaLeuGlyProAlaAlaAla 313
 DB 1347 CCAGTTCCAGAGTGG-----GAAGCCAGCGCCCGCCCGCCCGCC 1385
 QY 314 ProThrLeuSerProGlnSerProAlaGlySerProAlaMetMetLeuGlnProGlyPro 333
 DB 1386 GATCAGCTCGCGGAGTCCGACCCCGC-----1412

OY	334	GlnLeuTyrAspValMetAspAlaValProAlaArgArgTrpLysGluPheValArgThr	353
Db	1413	ACCCTGTACGGCGGTGTGTGCAGCGCGGTGCCCCCGTCGCGCTGGAAAGAGTTGGTGCGGCGG	1472
OY	354	LeuGlyLeuArgGluAlaGluIleGluAlaValGluValGluIleGlyArg--PheArg	372
		:: ::	
Db	1473	CTGGGACTGAGCGAGCAGCACGATCGAGCGGCGCTGGAGCTGGAACAACGGCGCACCTGCGC	1532
OY	373	AspGlnGlnTyrGluMetLeuLysArgTrpArgGlnGlnPro-----AlaGly	389
		::: ::::	
Db	1533	GAGGCGCAGTACAGCATGCTGCGCGGCTGGCGGCGGCGCAACCGCGCGAGGCCAAG	1592
OY	390	LeuGlyAlaValTyrAlaAlaLeuGluArgMetGlyLeuAspGlyCysValGluAspLeu	409
		::: :: :::	
Db	1593	CTGGAGCTGCTGGGCGCGCTGCTCAGGGACATGGAACCTGCTGGGTTCCTGGAAAACATA	1652
OY	410	ArgSerArgLeu 413	
Db	1653	GAGGAGCGCGCTG 1664	

```

RESULT 11
US-08-050-319B-24
; Sequence 24, Application US/08050319B
; Patent No. 5633145
; GENERAL INFORMATION:
; APPLICANT: M.Feldmann, P.W. Gray,
; APPLICANT: M.J.C. Turner, F.M Brennan
; TITLE OF INVENTION: Modified human TNFalpha (Tumor
; TITLE OF INVENTION: Necrosis Factor alpha) Receptor
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reed & Robbins
; STREET: 635 Bryant Street
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/050,319B
; FILING DATE: 10-May-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Robbins, Roberta L.
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 5150-0030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 617-8999
; TELEFAX: (415) 327-3231
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2062 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 155..1519
US-08-050-319B-24

```

Alignment Scores:	
Pred. No.:	1.36e-21
Score:	376.00
Percent Similarity:	39.09%
Best Local Similarity:	28.29%
Query Match:	16.19%
DB:	1
Length:	2062
Matches:	131
Conservative:	50
Mismatches:	182
Indels:	100
Gaps:	22

US-09-993-234-6 (1-417) x US-08-050-319B-24 (1-2062)
<p> 15 LeuLeuLeuValLeuLeuGlyAlaArgAlaGlnGly----- 197 CTTCTGGAGCTGTGGTGGGAATATACCCCTCAGGGGTATTGGACTGTGCCCTACCTA 27 GlyThrArgSerProArg-----CysAspCysAlaGlyAspPheHisLysIle 43 257 GGGGACAGGGAGAGAGAGATAGTGTGTGTCCCAAGAAATATATATCCACCCTCAAAAT 44 GlyLeuPheCysCysArgGlyCysProAlaGlyHisIleLysAlaProCysThrGlu 63 317 AATTGATTTGCTGTACCAAGTGCACAAAGGAACCTACTGTACATGACTGTCCAGGC 64 ProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsn 83 377 CCGGGGACAGATACGAGCTGACGGAGTGTGAGAGCGGCTCTTCACCGCTCAGAAAC 84 HisHisAsnSerGlyCysAlaArgCysGlnAlaCysAspGlnGlnAlaSerGlnValAla 103 437 CACTCTCAGA---CACTGCTCAGCTGCTCCAAATGCCGAAGGAATGGGTACGTGGAG 493 104 LeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheVal 123 494 ATCTCTTCTTGCACAGTGGACCGGACACCGTGTGTGGCTGCAGAGAACCAGTACCGG 553 124 GluCys-----GlnValSerGlnCysValSerSerProPheThrCysGlnPro 140 554 CATTTATTGGAGTGAATAACCTTTTCCAGTGC-----TTCAATTGCAGCTC 598 141 CysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThr 160 599 TGCCTCAAT---GGGACCGTGCAC-----CTCTCTGCCAGGAGAAACAGAAC 643 161 AspCysGlyThrCysLeuProGlyPheTyrgluHisGlyAspGlyCysValSerCysPro 180 644 ACCGTGTGCACCTGCCATGACGAGTTCTTCTTAAGAGAAACGAGTGTGTCTCTCTGT--- 700 181 ThrSerThrLeuGlySerCysProGlu-----ArgCysAlaAlaValCys----- 195 701 -----AGTAACTGTAAAGAAAGCCGTGAGTGCACGAAAGTTGTGCCCTACCCAG 748 196 -----GlyTrpArgGlnMetPheTrpValGlnValLeu 206 749 ATTGAGAAATGTTAAGGGCAGTGAAGACTCAGGACACCAAGTGTGCCCTGGTCAATT 808 207 LeuAlaGlyLeuValProLeuLeuGlyAlaThrLeuThrTrpThrArgHis 226 809 TTTCTTGTCTTGGCTTTTATCCCTCTCTTCAATTGGTTAATGATATCGTTACCAACGG 868 227 CysTrpProHisLys-----ProLeuValThrAlaAspGluAla 239 869 ---TGGAAGTCCAAAGCTCTACTCCATTGTTGTGGGAATCGACACCTGAAAAAGAGGGG 925 240 GlyMetGluAlaLeuThrProProProAlaThrHisLeuSerProLeuAspSer----- 257 926 GAGCTTGAAGAACTACTAAGACCC-----CTGGCCCCAAACCAAGCTTCAGT 976 258 -----AlaHisThrLeuLeuAlaProProAspSerSerGlyLysIleCys 272 977 CCCACTCCAGGCTTACCCCCACCCCTGGGCTTCAGTCCCGTCCAGTTCCACCTTCACC 1036 273 ThrValGlnLeuValGlyAsnSerTrpThrProGlyTyTrProGluThrGlnGlnAlaLeu 292 1037 TCC-----AGCTCCACCTATACCCCGGTAC----- 1063 293 CysProGlnValThrTrpSerTrpAspGlnLeuProSerArgAlaLeuGlyPro----- 310 1064 TGTCCCAACTTGGC-----GCTCCCGCAGAGAGGTGGCACCACCTAT 1108 311 -----AlaAlaAlaProThrLeuSerPro--- 318 1109 CAGGGGGCTGACCCCACTTGGCAGACAGCCCTGCGCTCCGACCCCATCCCAACCCCTTT 1168 </p>

QY 319 -----GluSerProAlaGlySerProAlaMetLeuGlnProGlyProGln--- 334
Db 1169 CAGAAGTGGAGAGACGTCCCAACAGCCACAGAGACCTAGACATGATGACCCCGGAGC 1228
QY 335 LeuTyrAspValMetAspAlaValProAlaArgTrrpLysGluPheValArgThrLeu 354
Db 1229 CTGTACGCCGTGTGTGAGAACGTGCCCGCGTGTGCGCTGGAAGGAATTCGTGGCGGCCCTA 1288
QY 355 GlyLeuArgGluAlaGluIleGluAlaValGluValGluIleGlyArg---PheArgAsp 373
Db 1289 GGGCTGAGCGACACGAGATCGATCGGCTGGAGCTGCAGAACGGCGCTGCCCTGCCGAG 1348
QY 374 GlnGlnTyrGluMetLeuLysArgTrrpArgGlnGlnPro-----AlaGlyLeu 390
Db 1349 GCGCAATACAGCATGCTGGCGACCTGGAGCGCGCGCACGCGCGCGCGAGGCCACGCTG 1408
QY 391 GlyAlaValTyrAlaAlaLeuGluArgMetGlyLeuAspGlyCysValGluAspLeuArg 410
Db 1409 GAGCTGCTGGAGCGCTGCTCCGCGACATGACCTGTGCGCTGCGCTGGAGGACATCGAG 1468
QY 411 SerArgLeu 413
Db 1469 GAGCGCGCTT 1477
RESULT 12
US-08-465-982-24
; Sequence 24, Application US/08465982
; Patent No. 5863786
; GENERAL INFORMATION:
; APPLICANT: M.Feldmann, P.W. Gray,
; APPLICANT: M.J.C. Turner, F.M Brennan
; TITLE OF INVENTION: Modified human TNFalpha (Tumor
; TITLE OF INVENTION: Necrosis Factor alpha) Receptor
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reed & Robblins
; STREET: 635 Bryant Street
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,982
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/050,319
; FILING DATE: 10-May-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Robblins, Roberta L.
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 5150-0030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 617-8999
; TELEFAX: (415) 327-3231
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2062 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 155..1519
US-08-465-982-24

Alignment Scores:
Pred. No.: 1.36e-21 Length: 2062
Score: 376.00 Matches: 131
Percent Similarity: 39.09% Conservative: 50
Best Local Similarity: 28.29% Mismatches: 182
Query Match: 16.19% Indels: 100
DB: 2 Gaps: 22
US-09-993-234-6 (1-417) x US-08-465-982-24 (1-2062)
QY 15 LeuLeuLeuValLeuLeuGlyAlaArgAlaGlnGly----- 26
Db 197 CTCTGGAGCTGTGTGGGAATATACCCCTCAGGGGTATGTGACTGTGCTCCACCTA 256
QY 27 GlyThrArgSerProArg-----CysAspCysAlaGlyAspPheHisLysLysIle 43
Db 257 GGGGACAGGGAAGAAGAGATAGTGTGTCCCAAGGAATAATATCCACCCTCAAAAT 316
QY 44 GlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGlu 63
Db 317 AATTGCATTGTCTGTATACCAAGTGCACAAAGAACCTACTTGTACATGACTGTCCAGGC 376
QY 64 ProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrrpGluAsn 83
Db 377 CCGGGCAGGATACGAGCTGACGGAGGTGTGAGAGCGGCTCTTCACCGCTTCAGAAAC 436
QY 84 HisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAla 103
Db 437 CACCTTCAGA---CACTGCTCAGCTGCTCCAAATGCCGAAGAAATGGGTACAGTGGAG 493
QY 104 LeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrrpPheVal 123
Db 494 ATCTTCTCTTGCACAGTGGACCGGACACCGTGTGTGGCTGCAGAAACACAGTACCGG 553
QY 124 GluCys-----GlnValSerGlnCysValSerSerProPheTyrCysGlnPro 140
Db 554 CATTAATTGGAGTGAATAACCTTTTCCAGTGC-----TTCAATTGCAGCCTC 598
QY 141 CysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThr 160
Db 599 TGGCTCAAT---GGAGCCGTGCAC-----CTCTCTGCCAGGAGAAACAGAAC 643
QY 161 AspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysPro 180
Db 644 ACCGTGTCACCTGCCATGCAGGTTCTTCTTAAGAGAAACAGAGTGTCTCTCTGT--- 700
QY 181 ThrSerThrLeuGlySerCysProGlu-----ArgCysAlaAlaValCys----- 195
Db 701 -----AGTAACTGTAAAGAAAGCCTGAGTGCACGAAAGTGTGTGCTACCCAG 748
QY 196 -----GlyTrrpArgGlnMetPheTrrpValGlnValLeu 206
Db 749 ATTGAGAATGTTAAGGCGACTGAGACTCAGGCACACACAGTGTGCTGCCCCGTGCATT 808
QY 207 LeuAlaGlyLeuValValProLeuLeuGluGlyAlaThrLeuThrTyrThrArgHis 226
Db 809 TTTCTTGTGCTTTGCTTTTATCCCTCTCTTCATTTGTTTAATGTATCGCTACCAACGG 868
QY 227 CysTrrpProHisLys-----ProLeuValThrAlaAspGluAla 239
Db 869 ---TGGAAGTCCAAAGCTCTACTCATTGTTGTGGAAATGCACACCTGAATAAGAGGGG 925
QY 240 GlyMetGluAlaLeuThrProProProAlaThrHisLeuSerProLeuAspSer----- 257
Db 926 GAGCTGAAGAACTACTACTAAGCCC-----CTGGCCCAAAACCAAGCTTCAGT 976
QY 258 -----AlaHisThrLeuLeuAlaProProAspSerSerGluLysIleCys 272
Db 977 CCCACTCCAGGCTTCACCCCGCTGGGCTTCAGTCCCGTCCCAAGTTCACCTTCACC 1036
QY 273 ThrValGlnLeuValGlyAsnSerTrrpThrProGlyTyrProGluThrGlnGluAlaLeu 292
Db 1037 TCC-----AGCTCACCTATACCCCGGTGAC----- 1063

OY 293 CysProGlnValThrTrpSerTrpAspGlnLeuProSerArgAlaLeuGlyPro----- 310
|||
Db 1064 TGTCCTCAACTTGGC-----GCTCCCCGAGAGAGGTGGCACCACCTAT 1108
OY 311 -----AlaAlaAlaProThrLeuSerPro--- 318
|||
Db 1109 CAGGGGGCTGACCCCATCTTGGCAGACAGCCCTCGCTCCGACCCCATCCCAACCCCTT 1168
OY 319 -----GluSerProAlaGlySerProAlaMetLeuGlnProGlyProGln--- 334
|||
Db 1169 CAGAAGTGGAGAGACAGTCCCAACAAGCCACAGACCTAGACACTGATGACCCCGGACG 1228
OY 335 LeuTyrAspValMetAspAlaValProAlaArgTrpLysGluPheValArgThrLeu 354
|||||
Db 1229 CTGTACGCCGTGTGTGAGAACCTGCCCCCTTGGCTGGAAAGAAATTCTGCGCGCCTA 1288
OY 355 GlyLeuArgGluAlaGluIleGluAlaValGluValGluIleGlyArg--PheArgAsp 373
|||||
Db 1289 GGGCTGAGCGACACGACATCGATCGCTGAGCTGCAGAACGGCGCTGCTGCGCGAG 1348
OY 374 GlnGlnTyrGlnMetLeuLysArgTrpArgGlnGlnPro-----AlaGlyLeu 390
|||||
Db 1349 GCCCAATACAGCATGCTGGCGACCTGGAGCGCGCACGCCGCGCGAGGCCACGCTG 1408
OY 391 GlyAlaValTyrAlaAlaLeuGluArgMetGlyLeuAspGlyCysValGluAspLeuArg 410
|||
Db 1409 GAGCTGCTGGAGCGCTGCTCGCGACATGACCTGCTGGCTGCTGAGAGACATCGAG 1468
OY 411 SerArgLeu 413
|||
Db 1469 GAGCGCTT 1477
RESULT 13
US-09-106-038A-1
; Sequence 1, Application us/09106038A
; Patent No. 6007995
; GENERAL INFORMATION:
; APPLICANT: Brenda F. Baker and Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF TNFR1
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Isis Pharmaceuticals, Inc.
; STREET: 2292 Faraday Avenue
; CITY: Carlsbad
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92008
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows NT
; SOFTWARE: Microsoft Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/106,038A
; FILING DATE: June 26, 1998
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Laurel Spear Bernstein
; REGISTRATION NUMBER: 37,280
; REFERENCE/DOCKET NUMBER: RTS-0004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (760) 931-9200
; TELEFAX: (760) 603-3820
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2161
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-106-038A-1

Alignment Scores:
Pred. No.: 2,12e-21 Length: 2161
Score: 374.00 Matches: 131
Percent Similarity: 38.88% Conservative: 49
Best Local Similarity: 28.29% Mismatches: 183
Query Match: 16.10% Indels: 100
DB: 3 Gaps: 22
US-09-993-234-6 (1-417) x US-09-106-038A-1 (1-2161)
OY 15 LeuLeuLeuValLeuLeuGlyAlaArgAlaGlnGly----- 26
|||||
Db 298 CTCTGAGCTGTGTGGGAATATACCCCTCAGGGGTTATGGACTGTCCTCACCCTA 357
OY 27 GlyThrArgSerProArg-----CysAspCysAlaGlyAspPheHisLysLysIle 43
|||
Db 358 GGGACAGAGGAGAAAGAGATAGTGTGTCTCCCAAGAAATATATCCACCCTCAAAAT 417
OY 44 GlyLeuPheCysCysArgGlyCysProAlaGlnHisIleTyrLeuLysAlaProCysThrGlu 63
|||||
Db 418 AATTGATTTGCTGTACCAAGTGCACAAAGAACCTACTTGTTACAATGACTGTCCAGGC 477
OY 64 ProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsn 83
|||
Db 478 CCGGGCAGAGATACGAGCTGCAGGAGGTGAGAGCGGCTCTTCACCGCTTCAGAAAC 537
OY 84 HisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGlnAlaSerGlnValAla 103
|||
Db 538 CACCTCAGA---CACTGCCTCAGCTGCTCCAAATGCCGAAGAAATGGTCAAGGTGAG 594
OY 104 LeuGlnAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheVal 123
|||
Db 595 ATCTCTCTTGACACAGTGGACCGGAGACCCGTGTGTGTGCTGCAGGAAGAACAGTACCGG 654
OY 124 GluLys-----GlnValSerGlnCysValSerSerProPheTyrCysGlnPro 140
|||
Db 655 CATATTGGAGTGAAGAAACCTTTTCCAGTGC-----TTCAATTGCAGCCTC 699
OY 141 CysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThr 160
|||||
Db 700 TGCTCAAT---GGACCGTGCAC-----CTCTCTGCGCAGAGAAACAGAAC 744
OY 161 AspCysGlyThrCysLeuProGlyPheTyrGlnHisGlyAspGlyCysValSerCysPro 180
|||||
Db 745 ACCGTGTACCTGCCATGCGAGGTTCTTCTAAGAAAGAGAGTGTCTCTCTG--- 801
OY 181 ThrSerThrLeuGlySerCysProGlu-----ArgCysAlaAlaValCys----- 195
|||
Db 802 -----AGTAACGTGAAGAAAGCCTGAGTGCACAGAGTGTGCTTACCCACG 849
OY 196 -----GlyTrpArgGlnMetPheTrpValGlnValLeu 206
|||
Db 850 ATTGAGATGTTAAGGCACTGAGACTCAGGCAACACAGTGTGTCCTGCTCATY 909
OY 207 LeuAlaGlyLeuValValProLeuLeuLeuGlyAlaThrLeuThrTyrThrArgHis 226
|||||
Db 910 TTCTTTGCTTGTGCTTTTATCCCTCCTCTTCATTTGTTAATGATATGCTTACCAACGG 969
OY 227 CysTrpProHisLys-----ProLeuValThrAlaAspGluAla 239
|||
Db 970 ---TGAGAGTCCAGCTCTACTCATTTGTTGTGGGAAATCGACACCTGAAAGAGGGG 1026
OY 240 GlyMetGluAlaLeuThrProProProAlaThrHisLeuSerProLeuAspSer----- 257
|||
Db 1027 GAGCTTGAAGGAATACTAAGCCC-----CTGGCCCAACCAAGCTTCAGT 1077
OY 258 -----AlaHisThrLeuLeuAlaProProAspSerSerGluLysIleCys 272
|||
Db 1078 CCCACTCAGGCTTCAACCCACCTGGGCTTCACTCCGTCAGGTCACCTTACAC 1137
OY 273 ThrValGlnLeuValGlyAsnSerTrpThrProGlyTyrProGluThrGlnGluAlaLeu 292
|||
Db 1138 TCC-----AGCTCAGCTATACCCCGGTGAC----- 1164

QY 293 CysProGlnValThrTrpSerTrpAspGlnLeuProSerArgAlaLeuGlyPro----- 310
|||
Db 1165 TGTCCCACTTTCG-----GCTCCCGCAGAGAGTGGCACCACCTAT 1209
QY 311 -----AlaAlaAlaProThrLeuSerPro--- 318
|||
Db 1210 CAGGGGCTGACCCCATCTTGGCAGAGCCCTCGCTCCGACCCCATCCCAACCCCTT 1269
QY 319 -----GluSerProAlaGlySerProAlaMetLeuGlnProGlyPro---Gln 334
|||
Db 1270 CAGAAGTGGAGACAGCGCCCAACAAGCCACAGACCTAGACACTGATGACCCCGCAGC 1329
QY 335 LeuTyrAspValMetAspAlaValProAlaArgTrpLysGluPheValArgThrLeu 354
|||||
Db 1330 CTGTACGCCGTGTGGAGAACGTGCCCCCTTGCGCTGGAAGGAATTCTGCGCGCCTA 1389
QY 355 GlyLeuArgGluAlaGluIleGluAlaValGluValGluIleGlyArg--PheArgAsp 373
|||||
Db 1390 GGGCTGAGCGACACGACGATCGATCGGCTGAGCTGCAGAACGGCGCTGCTGCGCGAG 1449
QY 374 GlnGlnTyrGluMetLeuLysArgTrpArgGlnGlnPro-----AlaGlyLeu 390
|||||
Db 1450 GCGCAATACAGCATGCTGCGCAGCTGAGCGCGCGCAGCGCGCGCAGCGCAGCTG 1509
QY 391 GlyAlaValTyrAlaAlaLeuGluArgMetGlyLeuAspGlyCysValGluAspLeuArg 410
|||
Db 1510 GAGCTGCTGGGACGCGTCTCCGCGACATGACCTGTGGCTGCTGAGAGACATCGAG 1569
QY 411 SerArgLeu 413
|||
Db 1570 GAGCGCGCTT 1578

RESULT 14

US-09-505-250-3
; Sequence 3, Application US/09505250A
; Patent No. 6329148
; GENERAL INFORMATION:
; APPLICANT: Rosen, Glenn
; APPLICANT: Kao, Peter
; TITLE OF INVENTION: Synergistic Anti-Cancer Therapy with
; TITLE OF INVENTION: Triptolides and Death Domain Ligands
; FILE REFERENCE: SUN-109PRV2
; CURRENT APPLICATION NUMBER: US/09/505,250A
; CURRENT FILING DATE: 2000-02-15
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 2161
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (256)...(1623)
US-09-505-250-3

Alignment Scores:

Pred. No.:	2,12e-21	Length:	2161
Score:	374.00	Matches:	131
Percent Similarity:	38.88%	Conservative:	49
Best Local Similarity:	28.29%	Mismatches:	183
Query Match:	16.10%	Indels:	100
DB:	4	Gaps:	22

US-09-993-234-6 (1-417) x US-09-505-250-3 (1-2161)

QY 15 LeuLeuLeuValLeuLeuGlyAlaArgAlaGlnGly----- 26
|||||
Db 298 CTCCTGAGCTGTGTGGGAATATACCCCTCAGGGGTATTGACTGTCCCTCACCTA 357
QY 27 GlyThrArgSerProArg-----CysAspCysAlaGlyAspPheHisLysLysIle 43
|||||
Db 358 GGGGACAGGAGAGAGATAGTGTGTGTCCCAAGAAATATATATCCACCCCTCAAAAT 417

QY 44 GlyLeuPheCysCysArgGlyCysProAlaGlnHisTyrLeuLysAlaProCysThrGlu 63
|||||
Db 418 AATTGCATTGTCTGTACCAGAGTGCACAAAGAACCTACTGTACATGACTGTCCAGGC 477
QY 64 ProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsn 83
|||
Db 478 CCGGGCAGGATACGAGCTGACGAGAGTGTGAGAGCGCGCTCTTCACCGCTCAGAAAC 537
QY 84 HisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAla 103
|||
Db 538 CACCTCAGA--CACTGCTCAGCTGCTCCAAATGCCGAAAGAAATGCTCAGGTGAG 594
QY 104 LeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheVal 123
|||
Db 595 ATCTCTTCTTGACAGTGGACCGGGACACCGTGTGTGCTGCAGGAAGAACAGTACCGG 654
QY 124 GluCys-----GlnValSerGlnCysValSerSerSerProPheTyrCysGlnPro 140
|||
Db 655 CATTATTGAGTGAACCACTTTCAGTGC-----TTCAATTGCAGCCTC 699
QY 141 CysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThr 160
|||||
Db 700 TGCCTCAAT--GGGACCGTGAC-----CTCTCTTCCACAGGAGAAACAGAAC 744
QY 161 AspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysPro 180
|||
Db 745 ACCGTGTGCACCTGCATGACAGTTCTTCTTAAGAGAAACGAGTGTCTCTCTGT 801
QY 181 ThrSerThrLeuGlySerCysProGlu-----ArgCysAlaAlaValCys----- 195
|||
Db 802 -----AGTAACGTGAGAAAGCCCTGAGTGCAGGAAGTGTGCTTACCCAG 849
QY 196 -----GlyTrpArgGlnMetPheTrpValGlnValLeu 206
|||
Db 850 ATTGAGAATGTTAAGGCGACTGAGGACTCAGGCACACAGAGCTGTGCCCTGCTCAT 909
QY 207 LeuAlaGlyLeuValAlaProLeuLeuLeuGlyAlaThrLeuThrTyrThrTyrArgHis 226
|||||
Db 910 TTCTTTGGTCTTGTGCTTTATCCCTCTCTCATTTGTTAATGATATCGCTACCAACGG 969
QY 227 CysTrpProHisLys-----ProLeuValThrAlaAspGluAla 239
|||
Db 970 ---TGGAAGTCCAAGCTTACTTCATTTGTTGGAATGACACCTGAAAAAGAGGGG 1026
QY 240 GlyMetGluAlaLeuThrProProProAlaThrHisLeuSerProLeuAspSer----- 257
|||
Db 1027 GAGCTTGAAGAACTACTACTAAGCCC-----CTGGCCCCAAACCAAGCTTCAGT 1077
QY 258 -----AlaHisThrLeuLeuAlaProProAspSerSerGluLysIleCys 272
|||
Db 1078 CCCACTCCAGGCTTCACCCCGCCTGGGCTTCAGTCCCGTCCACCTTCACCTTCACC 1137
QY 273 ThrValGlnLeuValGlyAsnSerTrpThrProGlyTyrProGluThrGlnGluAlaLeu 292
|||
Db 1138 TCC-----AGCTCCACCTATACCCCGGTGAC----- 1164
QY 293 CysProGlnValThrTrpSerTrpAspGlnLeuProSerArgAlaLeuGlyPro----- 310
|||||
Db 1165 TGTCCCACTTTCG-----GCTCCCGCAGAGAGTGGCACCACCTAT 1209
QY 311 -----AlaAlaAlaProThrLeuSerPro--- 318
|||
Db 1210 CAGGGGCTGACCCCATCTTGGCAGAGCCCTCGCTCCGACCCCATCCCAACCCCTT 1269
QY 319 -----GluSerProAlaGlySerProAlaMetLeuGlnProGlyPro---Gln 334
|||
Db 1270 CAGAAGTGGAGACAGCGCCCAACAAGCCACAGACCTAGACACTGATGACCCCGCAGC 1329
QY 335 LeuTyrAspValMetAspAlaValProAlaArgTrpLysGluPheValArgThrLeu 354
|||||
Db 1330 CTGTACGCCGTGTGAGAACGTGCCCCCTTGCGCTGGAAGGAATTCTGCGCGCCTA 1389

QY 355 G1yleuArgGluAlaGluIleGluAlaValGluValGluIleGlyArg---PheArgAsp 373
Db 1390 GGGCTGAGCGACACAGATCGATCGCTGGAGCTGCAGAACGGCGCTGCTGCGGAG 1449
QY 374 G1ngIntyrglUmetleuLysArgTyrpargG1ng1ng1ngPro-----AlaGlyleu 390
Db 1450 GCGCAATACAGCATGCTGGCGACCTGGAGGGCGGCGCGCGCGGCGGCGGCGGCGCTG 1509
QY 391 G1yAlaValTyrAlaAlaLeuGluArgMetGlyLeuAspGlyCysValGluAspLeuArg 410
Db 1510 GAGCTGCTGGAGCGCGTCTCGCGACATGACCTGCTGGCTGCTGAGAGACATCGAG 1569
QY 411 SerArgLeu 413
Db 1570 GAGCGCTT 1578

RESULT 15
US-08-321-668-1
Sequence 1, Application US/08321668
Patent No. 5665859
GENERAL INFORMATION:
APPLICANT: WALLACH, David
APPLICANT: BRAKEBUSCH, Cord
APPLICANT: VAROLOMEEV, Eugene
APPLICANT: BARKIN, Michael
TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF
TITLE OF INVENTION: THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/321,668
FILING DATE: 12-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107268
FILING DATE: 12-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH-13
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2175 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 256..1620
US-08-321-668-1

Alignment Scores:
Pred. No.: 2.14e-21
Score: 374.00
Percent Similarity: 38.888
Best Local Similarity: 28.298
Query Match: 16.108

DB: 1 Gaps: 22
US-09-993-234-6 (1-417) x US-08-321-668-1 (1-2175)
QY 15 LeuLeuValLeuLeuGlyAlaArgAlaG1ngly----- 26
Db 298 CTCCTGAGCTGTGTGGAAATATACCCCTCAGGGGTATTTGACTGTCCCTCACCCTA 357
QY 27 GlyThrArgSerProArg-----CysAspCysAlaGlyAspPheHisLysLysIle 43
Db 358 GGGACAGAGGAGAAGAGATAGTGTGTCCCAAGAAATATATCCACCCTCAAAAT 417
QY 44 GlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGlu 63
Db 418 AATTCGATTGCTGTACCAAGTGCACAAAGAACCTACTTGTACAAATGACTGTCCAGGC 477
QY 64 ProcysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsn 83
Db 478 CCGGGGCGAGATACGGACTGCAGGAGTGTGAGAGCGGCTCTTCACCGCTTCAGAAAC 537
QY 84 HisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAla 103
Db 538 CACCTCAGA---CACTGCTCAGCTGCTCCAAATGCCGAAGAAATGGTCCAGTGCAG 594
QY 104 LeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTyrPheVal 123
Db 595 ATCTCTTCTTGACAGTGCAGCGGACACCGGTGTGTGGCTGCAGGAAGAACAGTACCGG 654
QY 124 GluCys-----GlnValSerGlnCysValSerSerProPheTyrCysGlnPro 140
Db 655 CATATTTGAGAGTGAACACCTTTTCCAGTGC-----TTCAATTGCAGGCTC 699
QY 141 CysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThr 160
Db 700 TGCCCTCAAT---GGGACCGTGCAC-----CTCTCCCTGCCAGAGAAACAGAAC 744
QY 161 AspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysPro 180
Db 745 ACCGTGTGCACCTGCCATGCAGTTTCTTTCTAAGAGAAACGAGTGTCTCTCTGT--- 801
QY 181 ThrSerThrLeuGlySerCysProGlu-----ArgCysAlaAlaValCys----- 195
Db 802 -----AGTAACGTAAAGAAAGCCTGAGTGCAGAAAGTGTGCTTACCCAG 849
QY 196 -----GlyTyrparGlnMetPheTyrValGlnValLeu 206
Db 850 ATTGAGATGTTAAGGGCAGTGAAGACTCAGGACACACAGTCTGTGGCCCTGCATAT 909
QY 207 LeuAlaGlyLeuValProLeuLeuGlyAlaThrLeuThrTyrThrTyrArgHis 226
Db 910 TTCTTTGGTCTTGGCTTTATCCCTCCTCTTCATTTGTTTAAATGATCGGTACCAACGG 969
QY 227 CysTrpProHisLys-----ProLeuValThrAlaAspGluAla 239
Db 970 ---TGGAAGTCCAAGCTCTACTCCATTTGTTGTGGAAATCGACACCTGAAAAGAGGGG 1026
QY 240 GlyMetGluAlaLeuThrProProAlaThrHisLeuSerProLeuAspSer----- 257
Db 1027 GAGCTTGAAGAACTACTAAGCCC-----CTGGCCCCAAACCCCAAGCTTCACT 1077
QY 258 -----AlaHisThrLeuLeuAlaProAspSerSerGluLysIleCys 272
Db 1078 CCCACTCCAGGCTTACCCCCACCTGGGCTTCAGTCCGTCACAGTTCACCTTCACC 1137
QY 273 ThrValGlnLeuValGlyAsnSerTyrThrProGlyTyrProGluThrGlnGluAlaLeu 292
Db 1138 TCC-----AGCTCCACCTATACCCCGGTGAC----- 1164
QY 293 CysProGlnValThrTrpSerTyrAspGlnLeuProSerArgAlaLeuGlyPro----- 310
Db 1165 TGTCCCAACCTTGGC-----GCTCCCGCGCAGAGAGGTGGCACCACCCCTAT 1209
QY 311 -----AlaAlaAlaProThrLeuSerPro--- 318

```
Db 1210 CAGGGGGCTGACCCCATCTTGGCAGACGCCCTCGCTCCGACCCCATCCCAACCCCTT 1269
QY 319 -----GluSerProAlaGlySerProAlaMetLeuGlnProGlyPro---Gln 334
Db 1270 CAGAGTGGGAGAGAGCGCCACACAGCCACAGACCTAGACACTGATGATGACCCCGGACG 1329
QY 335 LeuTyrAspValMetAspAlaValProAlaArgTrpLysGluPheValArgThrLeu 354
Db 1330 CTGTACGCCCGTGTGGAGAACGTGCCCGCTGTGGCTGGAAGAATTCGTGGCGGCCCTA 1389
QY 355 GlyLeuArgGluAlaGluIleGluAlaValGluValGluIleGlyArg---PheArgAsp 373
Db 1390 GGGCTGAGCGACACGACGATCGATCGGCTGGAGCTGCAGAACGGCGCTGCCCTGCCGAG 1449
QY 374 GlnGlnTyrGlnMetLeuLysArgTrpArgGlnGlnGlnPro-----AlaGlyLeu 390
Db 1450 GCGCAATACAGCATGCTGGCGACCTGGAGGCGCGCACGCCGCGGCGGAGGCCACGCTG 1509
QY 391 GlyAlaValTyrAlaAlaLeuGluArgMetGlyLeuAspGlyCysValGluAspLeuArg 410
Db 1510 GAGCTGCTGGAGCGCGTGTCTCCGACATGACCTGTGGCTGCCCTGAGAGACATCGAG 1569
QY 411 SerArgLeu 413
Db 1570 GAGGCGCTT 1578
```

Search completed: April 6, 2003, 23:29:19
Job time : 96.3944 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: Apr11 6, 2003, 15:35:34 ; Search time 2022.14 Seconds
(without alignments)
2504.221 Million cell updates/sec

Title: US-09-993-234-6_COPY_25_198
Perfect score: 1038
Sequence: 1 QGGTRSPRCDCAGDPHKKIG.....CPSTLGSCEPCCAVCGWR 174

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_{p2n}.model -DEV=x1h
-Q=/cgn2_1/USPTO_spool/US09993234/runat_27032003_115455_15349/app_query.fasta_1.2346
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09993234@cgn_1_1_8534_@runat_27032003_115455_15349 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*

29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1038	100.0	1143	9 HSU94510	U94510 Human lymph
2	1038	100.0	1254	6 ARI19657	ARI19657 Sequence
3	1038	100.0	1254	9 HSU72763	U72763 Human death
4	1038	100.0	1254	9 HSU78029	U78029 Human death
5	1038	100.0	1254	9 HSU94501	U94501 Human lymph
6	1038	100.0	1257	9 HSU94502	U94502 Human lymph
7	1038	100.0	1355	9 HSU94503	U94503 Human lymph
8	1038	100.0	1634	9 HSU74611	U74611 Human Apo-3
9	1038	100.0	1662	6 AX055442	AX055442 Sequence
10	1038	100.0	1662	6 AX201344	AX201344 Sequence
11	1038	100.0	1743	6 AX331947	AX331947 Sequence
12	1038	100.0	1743	6 ARI19656	ARI19656 Sequence
13	1038	100.0	1783	9 HSU75380	U75380 Human death
14	1028	99.0	1528	9 HSU75380	U75380 Human death
15	1028	99.0	1557	9 HSU75380	U75380 Human death
16	1002	96.5	1669	9 AF026071	AF026071 Homo sapi
17	1002	96.5	1763	9 AF026071	AF026071 Homo sapi
18	978	94.2	1250	6 AX150176	AX150176 Sequence
19	950	91.5	808	9 HSU75381	U75381 Human death
20	950	91.5	809	9 HSU94512	U94512 Human lymph
21	950	91.5	816	6 AX335086	AX335086 Sequence
22	950	91.5	816	6 HSU83598	U83598 Human death
23	938.5	90.4	1198	9 HSU94504	U94504 Human lymph
24	937	90.3	1087	9 HSU94505	U94505 Human lymph
25	738	71.1	4825	9 AB051850	AB051850 Homo sapi
26	738	70.5	53982	9 AL158217	AL158217 Human DNA
27	731.5	70.4	4811	9 HSU94509	U94509 Human lymph
28	731	70.4	4811	9 AB051851	AB051851 Homo sapi
29	630.5	60.7	952	9 HSU94506	U94506 Human lymph
30	609	58.7	651	9 HSU83599	U83599 Human death
31	562	54.1	1665	10 AF329969	AF329969 Mus muscu
32	474	45.7	838	9 HSU94507	U94507 Human lymph
33	457	44.0	1619	10 BC017526	BC017526 Mus muscu
34	418	40.3	196368	2 AL772240	AL772240 Mus muscu
35	374.5	36.1	665	9 HSU83600	U83600 Human death
36	330.5	31.8	97483	2 AC118359	AC118359 Rattus no
37	230.5	22.2	2600	4 SSJ001202	AJ001202 Sus scrofa
38	214	20.6	2115	10 AF329976	AF329976 Rattus no
39	214	20.6	2115	10 AF329977	AF329977 Rattus no
40	214	20.6	2115	10 AF329978	AF329978 Rattus no
41	214	20.6	2115	10 AF329979	AF329979 Rattus no
42	214	20.6	2115	10 AF329980	AF329980 Rattus no
43	214	20.6	2115	10 AF329981	AF329981 Rattus no
44	214	20.6	2130	6 AX401925	AX401925 Sequence
45	214	20.6	2130	10 RAT122	RAT122 Rat tumor n

RESULT 1

ALIGNMENTS

HSU94510 1143 bp mRNA linear PRI 15-MAY-1997
LOCUS HSN94510
DEFINITION Human lymphocyte associated receptor of death 9 mRNA, alternatively
spliced, complete cds.
ACCESSION U94510
VERSION U94510.1 GI:2071966
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1143)
AUTHORS Sreaton,G.R., Xu,X.N., Olsen,A.L., Cowper,A.E., Tan,R.,
McMichael,A.J. and Bell,J.I.
TITLE LARD: a new lymphoid-specific death domain containing receptor
regulated by alternative pre-mRNA splicing
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)
MEDLINE 97272273
PUBMED 9114039
REFERENCE 2 (bases 1 to 1143)
AUTHORS Sreaton,G.R.
TITLE Direct Submission
JOURNAL Submitted (19-MAR-1997) Molecular Immunology Group, Institute of
Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3
9DU, UK
FEATURES
source Location/Qualifiers
1.1143
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Hela"
/cell_type="lymphocyte"
1.1143
/function="mediates apoptosis"
/note="LARD-9; NGFR family member; similar to Fas and
TNF-R1"
/codon_start=1
/product="lymphocyte associated receptor of death 9"
/protein_id="AAC51315.1"
/db_xref="GI:2071967"
/translation="MEORPRGCAVAALLLVLLGARAOGTRSPDCDAGDFHKKIG
LFCRCGPAGHYLKAPCTEPCNSTCLVCPQDTFLAWENHNHSCARCQACDEQASQV
ALENCASAVADTRCGCKPGWFEVCQVSSSPFYCOPCLDCALHRRHRLCSRDY
DCGTCLPGEYEHGDGVCSPSTSLGSCPERCAAVCGWRONENGAELTPPATLSP
LSAHTLAPDPSSEKICTVQLVGNSTWTPGYPETOALCPQVTWMDQLPSRALGPAA
PTLSPESPAGSPAMLOPGPOLYDMDAVPARRWKEFVRLTGREAETEAWEVEIGRF
RDQYEMLRKRWKQOPAGIGAVYALERMGLDGVEDLRSLQGRP"
598..599
misc_feature
/note="deletion compared to LARD 1a, deposited in GenBank
Accession Number U94501, probable skipping of putative
exon 7 encoding the transmembrane domain"
BASE COUNT 188 a 378 c 378 g 199 t
ORIGIN
Alignment Scores:
Pred. No.: 5.04e-66 Length: 1143
Score: 1038.00 Matches: 174
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-09-993-234-6_COPY_25_198 (1-174) x HSN94510 (1-1143)
QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
Db 73 CAGGGCGGCACTCGTAGCCCGCAGGCTGACTGTGCCGTGACTTCACAGAAGATTGGT 132
QY 21 LeupheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
Db 133 CTGTTTGTGTCAGAGGCTGCCAGGGGCGACACTACCTGAAGGCCCTTGACGAGGCC 192
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
|||||

Db 193 TCGGCAACTCCACCTGCCTTGTGTGTCCCAAGACACCTTCTTGCCCTGGGAGAACCAC 252
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db 253 CATAACTCTGAATGTGCCCCGCTGCCAGGCTGTGATGAGCAGGCGCTCCAGGCTGCCGCTG 312
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
Db 313 GAGAACTGTTCAGCAGAGTGGCCGACACCCCGCTGTGGCTGTAAAGCAGGCTGTTGTGAG 372
QY 101 CysGlnValSerGlnCysValSerSerSerProPheTyrCysGlnProCysLeuAspCys 120
Db 373 TGCCAGGTTCAGCCAAATGTGTACAGACTTCACCTTCTACTGCCAACCATGCTAGACTGC 432
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 433 GGGGCCCTGCACCGCCACACAGGCTACTCTGTCCCGCAGAGATACTGACTGTGGAGC 492
QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db 493 TGCCTGCTGCTGCTTCTATGACATGGCGATGGCTGCTGCTGCTGCCACGAGACCCCTG 552
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArg 174
Db 553 GGGAGCTGTCCAGAGCGCTGTGCCGCTGTCTGTGCTGGAGG 594
RESULT 2
AR119657 1254 bp DNA linear PAT 16-MAY-2001
LOCUS AR119657
DEFINITION Sequence 3 from patent US 6153402.
ACCESSION AR119657
VERSION AR119657.1 GI:14102356
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1254)
AUTHORS Yu,G.-L., Ni,J., Gentz,R.L. and Dillon,P.J.
TITLE Death domain containing receptors
JOURNAL Patent: US 6153402-A 3 28-NOV-2000;
FEATURES Location/Qualifiers
source 1.1254
/organism="unknown"
BASE COUNT 201 a 420 c 407 g 226 t
ORIGIN
Alignment Scores:
Pred. No.: 5.53e-66 Length: 1254
Score: 1038.00 Matches: 174
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-993-234-6_COPY_25_198 (1-174) x AR119657 (1-1254)
QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
Db 73 CAGGGCGGCACTCGTAGCCCGCAGGCTGTGACTGTGCCGGTACTTCACAGAAGATTGGT 132
QY 21 LeupheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
Db 133 CTGTTTGTGTCAGAGGCTGCCAGGGGCGACACTACCTGAAGGCCCTTGACGAGGCC 192
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db 193 TCGGCAACTCCACCTGCCTTGTGTGTCCCAAGACACCTTCTTGCCCTGGGAGAACCAC 252
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db 253 CATAACTCTGAATGTGCCCCGCTGCCAGGCTGTGATGAGCAGGCGCTCCAGGCTGCCGCTG 312
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
|||||

|||||
DB 313 GAGAACTGTTGACAGTGGCCGACACCGCTGTGGCTGTAAGCAGGCTGTTGTGAG 372
QY 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120
Db 373 TGGCAGGTGACCAATGTGTGACAGAGTTCACCCCTTACTGCAACCATGCTAGACTGC 432
QY 121 G1yAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 433 GGGGCCCTGCACCGCCACACACGGCTACTCTGTCCCGCAGAGATGACTGTGGAGCC 492
QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db 493 TGGCTGCTGGCTTCTATGACATGGCGATGGCTGCGTGTCTGCTGCCCGCCAGAGCACCCTG 552
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTyrParg 174
Db 553 GGGAGCTGTCCAGAGCGCTGTGCGCTGTCTGTGGCTGGAGG 594
RESULT 3
HSU72763 1254 bp mRNA linear PRI 15-NOV-1996
LOCUS Human death receptor 3 (DR3) mRNA, complete cds.
DEFINITION U72763
ACCESSION U72763.1 GI:1669511
VERSION
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1254)
AUTHORS Chinnaiyan,A.M., O'Rourke,K., Yu,G.L., Lyons,R.H., Garg,M.,
Duan,D.R., Xing,L., Gentz,R., Ni,J. and Dixit,V.M.
TITLE Signal transduction by DR3, a death domain-containing receptor
related to TNFR-1 and CD95
JOURNAL Science 274 (5289), 990-992 (1996) Nov
MEDLINE 97081063
PUBMED 8875942
REFERENCE 2 (bases 1 to 1254)
AUTHORS Chinnaiyan,A.M., O'Rourke,K., Yu,G.-L., Lyons,R.H., Garg,M.,
Duan,R., Xing,L., Gentz,R., Ni,J. and Dixit,V.M.
TITLE Direct Submission
JOURNAL Submitted (29-SEP-1996) Pathology, University of Michigan Medical
School, 1301 Catherine St., Box 0602, Ann Arbor, MI 48109, USA
FEATURES
source
1..1254
/organism="Homo sapiens"
/db_xref="taxon:9606"
1..1254
/gene="DR3"
1..1254
/gene="DR3"
/codon_start=1
/product="death receptor 3"
/protein_id="AAC50819.1"
/db_xref="GI:1669512"
/translation="MEQRPRGCAVAALLLVLGARAQGGTRSPRCDCAGDFHKKIG
LECCRGCPAGHYLKAPCTEPCGNSTCLVCPDTEFLAMENHNHNSCARCQACDEGASQV
ALENCASAVADTRCGCKPGWFEVCQVSSSPYCPCLDCGALHRTLRILCSRRDT
DCGTCLPGFEYEHGDCVSCPTSLGSCPERCAVCGWRQMFVQVLLAGLVVPLLLGA
TLTYTYRHCPHPRKPLVTADEAGMEALTPPATHSPLDSAHLLAPDSSSEKICTVOL
VGNSTWPGYPTQTEALCPQVWTWSDQLPSRALGPAAPTLSPESPAGSPAMALQPGPO
LYDVMDAVPARRMKFEVRLGLREAIEAVEVEIGFRDQYEMLKRWRRQODPAGLGA
VYALERMGLDGYEDLRSRLQRP"
BASE COUNT 201 a 420 c 407 g 226 t
ORIGIN

Alignment Scores:

Pred. No.: 5.53e-66 Length: 1254
Score: 1038.00 Matches: 174
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

DB: 9 Gaps: 0
US-09-993-234-6_COPY_25_198 (1-174) x HSU72763 (1-1254)
QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
Db 73 CAGGGCGGACTGCTAGCCCGCAGGCTGTGACTGTGCCGCTGCCAAGAAGATTGCT 132
QY 21 LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
Db 133 CTGTTTGTTCAGAGAGCTGCCAGCGGGGCACTACTGAAGGCCCTTGACAGAGCCC 192
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db 193 TGGCGCACTGCCACCTGCCCTGTGTGCCCAAGACACCTTCTGGCCTGGAGAACAC 252
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db 253 CATATTTCTGATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCCCTCCAGGTTGCCGCTG 312
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTyrPheValGlu 100
Db 313 GAGAACTGTTCAGAGTGGCCGACACCCGCTGTGGCTGTAAGCCAGCGCTGTTGTGAG 372
QY 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120
Db 373 TGGCAGGTGACCAATGTGTGACAGAGTTCACCCCTTACTGCCAACCATGCTAGACTGC 432
QY 121 G1yAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 433 GGGGCCCTGCACCGCCACACACGGCTACTCTGTCCCGCAGAGATGACTGTGGAGCC 492
QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db 493 TGGCTGCTGGCTTCTATGACATGGCGATGGCTGCGTGTCTGCTGCCCGCCAGAGCACCCTG 552
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTyrParg 174
Db 553 GGGAGCTGTCCAGAGCGCTGTGCGCTGTCTGTGGCTGGAGG 594
RESULT 4
HSU78029 1254 bp mRNA linear PRI 15-JAN-1997
LOCUS Human apoptosis inducing receptor AIR mRNA, complete cds.
DEFINITION U78029
ACCESSION U78029.1 GI:1778763
VERSION
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1254)
AUTHORS Degli-Esposti,M.A., Din,W.S., Cosman,D., Smith,C.A. and
Goodwin,R.G.
TITLE AIR, A Novel Member of the TNF Receptor Family, Is a Strong Inducer
of Apoptosis
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1254)
AUTHORS Degli-Esposti,M.A. and Goodwin,R.G.
TITLE Direct Submission
JOURNAL Submitted (12-NOV-1996) Biochemistry, Immunex Corporation, 51
University St., Seattle, WA 98101, USA
FEATURES
source
1..1254
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/map="1pter"
/cell_type="peripheral blood T-cells"
1..1254
/codon_start=1
/product="apoptosis inducing receptor AIR"
/protein_id="AAB40918.1"

/db_xref="GI:1778764"
/translation="MEQRPFGCAVAALLLVILGARAOGGTRSPRCDCAGDFHKRTG
LFCRCGPAGHYLKAPCTEPGNSITCLVCPQDTFLAMENHNHNSCARQACDEQASQV
ALENCSAVADTRCGCKPGWFEVCQVSSPCVSPFCQPCDGCALHRTRLCSRDPT
DCGTCLEPGEYHGDGVCSCPTSLGSCPERCAAVCGWRQFWOVLLAGLVPLILGA
TLITYTRHCWPHKPLVTADAGMEALTPPATHLSPIDSAHTLLAPDSSEKICITYOL
VGNSTWPGYRPETQALCPQVWMSDQLPSRALGPAAPTLSPESPAMMLQEPQ
LYDMDAVPARRWKEFVRTGLREAEIAVEVEIGRFRDQYEMLKRWROQRPAGLGA
VYALERMGLDGCVEDLRSRLORGP"

BASE COUNT 201 a 420 c 407 g 226 t
ORIGIN

Alignment Scores:
Pred. No.: 5.53e-66 Length: 1254
Score: 1038.00 Matches: 174
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-993-234-6_COPY_25_198 (1-174) x HSU78029 (1-1254)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
Db 73 CAGGGCGGCACTCGTAGCCCCAGGTGTGACTGTGCCGGTGACTTCCACAAGAAGATTGGT 132
QY 21 LeuphCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
Db 133 CTGTTTGTGTGACAGAGCTGCCCGGGGCACTACCTGAAGCCCCCTTGACAGGAGCCC 192
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db 193 TGCGGCAACTCCACCTGCCTGTGTGTCCCAAGACACCTTCTTGGCCCTGGAGAACCCAC 252
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db 253 CATAATCTGATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCCCTCCAGGTGGCGCTG 312
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
Db 313 GAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGTGTTAAGCCAGGCTGTTTGGAG 372
QY 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120
Db 373 TGCCAGGTTCAGCCAAATGTGTACAGAGTTTACCCCTTCTACTGCCAACCATGCTAGACTGC 432
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 433 GGGGCCCTGCACCGCCACACACAGGCTACTCTGTTCGCCAGAGATACTGACTGGGACC 492
QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db 493 TGCCCTGCTGCTTATGAAATGAGATGGGATGGCTGCTGCTGCCACGAGACACCCTG 552
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArg 174
Db 553 GGGAGCTGTCCAGACGCGCTGTGCCGCTGTCTGTGGCTGGAGG 594

RESULT 5
HSU94501
LOCUS HSU94501 1254 bp mRNA linear PRI 15-MAY-1997
DEFINITION Human lymphocyte associated receptor of death 1a mRNA, complete cds.
ACCESSION U94501
VERSION U94501.1 GI:2071948
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1254)
Screaton,G.R., Xu,X.N., Olsen,A.L., Cowper,A.E., Tan,R.,
McMichael,A.J. and Bell,J.I.

TITLE LARD: a new lymphoid-specific death domain containing receptor regulated by alternative pre-mRNA splicing
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)
MEDLINE 97272273
PUBMED 9114039
REFERENCE 2 (bases 1 to 1254)
AUTHORS Screaton,G.R.
TITLE Direct Submission
JOURNAL Submitted (19-MAR-1997) Molecular Immunology Group, Institute of Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3 9DU, UK

FEATURES
source location/Qualifiers
1..1254
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Hela"
/cell_type="lymphocyte"
1..1254
/function="mediates apoptosis"
/note="LARD-1a; membrane protein; similar to Fas and TNF-R1; contains a death domain"
/codon_start=1
/product="lymphocyte associated receptor of death 1a"
/protein_id="AAC51306.1"
/db_xref="GI:2071949"

CDS

/translation="MEQRPFGCAVAALLLVILGARAOGGTRSPRCDCAGDFHKRTG
LFCRCGPAGHYLKAPCTEPGNSITCLVCPQDTFLAMENHNHNSCARQACDEQASQV
ALENCSAVADTRCGCKPGWFEVCQVSSPCVSPFCQPCDGCALHRTRLCSRDPT
DCGTCLEPGEYHGDGVCSCPTSLGSCPERCAAVCGWRQFWOVLLAGLVPLILGA
TLITYTRHCWPHKPLVTADAGMEALTPPATHLSPIDSAHTLLAPDSSEKICITYOL
VGNSTWPGYRPETQALCPQVWMSDQLPSRALGPAAPTLSPESPAMMLQEPQ
LYDMDAVPARRWKEFVRTGLREAEIAVEVEIGRFRDQYEMLKRWROQRPAGLGA
VYALERMGLDGCVEDLRSRLORGP"

BASE COUNT 201 a 420 c 407 g 226 t
ORIGIN

Alignment Scores:
Pred. No.: 5.53e-66 Length: 1254
Score: 1038.00 Matches: 174
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-993-234-6_COPY_25_198 (1-174) x HSU94501 (1-1254)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
Db 73 CAGGGCGGCACTCGTAGCCCCAGGTGTGACTGTGCCGGTGACTTCCACAAGAAGATTGGT 132
QY 21 LeuphCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
Db 133 CTGTTTGTGTGACAGAGCTGCCCGGGGCACTACCTGAAGGCCCTTGACAGGAGCCC 192
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db 193 TGCGGCAACTCCACCTGCCTGTGTGTCCCAAGACACCTTCTTGGCCCTGGAGAACCCAC 252
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db 253 CATAATCTGATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCCCTCCAGGTGGCGCTG 312
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
Db 313 GAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGTGTTAAGCCAGGCTGTTTGGAG 372
QY 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120
Db 373 TGCCAGGTTCAGCCAAATGTGTACAGAGTTTACCCCTTCTACTGCCAACCATGCTAGACTGC 432
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 433 GGGGCCCTGCACCGCCACACACAGGCTACTCTGTTCGCCAGAGATACTGACTGTGGGACC 492

OY 141 CysLeuProGlyPheTyrgluHisGlyAspGlyCysValSerCysProThrSerThrIleu 160
|||||
Db 493 TGCCGTGCTGGCTTCTATGACATGGCGATGGCTGCGTGTCTGTGCCCCACGACACCCCTG 552
OY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArg 174
|||||
Db 553 GGGAGCTGTCCAGAGCGCTGTGCCCTGTCTGTGGCTGGAGG 594

RESULT 6
HSU94502 1257 bp mRNA linear PRI 15-MAY-1997

LOCUS
DEFINITION Human lymphocyte associated receptor of death 1b mRNA,
alternatively spliced, complete cds.

ACCESSION
U94502
VERSION
U94502.1 GI:2071950

KEYWORDS
SOURCE
ORGANISM Homo sapiens.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 (bases 1 to 1257)
Screation,G.R., Xu,X.N., Olsen,A.L., Cowper,A.E., Tan,R.,
McMichael,A.J. and Bell,J.I.

TITLE
LARD: a new lymphoid-specific death domain containing receptor
regulated by alternative pre-mRNA splicing

JOURNAL
Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)

MEDLINE
97272273

PUBMED
9114039

REFERENCE
2 (bases 1 to 1257)
Screation,G.R.
Direct Submission

TITLE
Submitted (19-MAR-1997) Molecular Immunology Group, Institute of
Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3
9DU, UK

FEATURES
source
Location/Qualifiers

1..1257
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Hela"
/cell_type="lymphocyte"
1..1257
/function="mediates apoptosis"
/note="LARD-1b; membrane protein; similar to Fas and
TNF-R1; contains a death domain"
/codon_start=1
/product="lymphocyte associated receptor of death 1b"
/protein_id="AAC51307.1"
/db_xref="GI:2071951"

misc_feature
708..711
/note="insertion compared to LARD-1a, deposited in GenBank
Accession Number U94501, probably represents alternative
3' splice site"

BASE COUNT 202 a 421 c 408 g 226 t

ALIGNMENT SCORES:

Pred. No.: 5.54e-66 Length: 1257
Score: 1038.00 Matches: 174
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 9

US-09-993-234-6_COPY_25_198 (1-174) x HSU94502 (1-1257)

OY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
|||||
Db 73 CAGGGCGCACTCGTAGCCCCAGAGGTGACTGTGCCGTGACTCCACAGAAGATTGGT 132

OY 21 LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
|||||
Db 133 CTGTTTGTGTGCAGAGGCTGCCACGGGGCACTACTGAAGGCCCTTGCACGGAGCCC 192

OY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
|||||
Db 193 TGCGGCACTCCACCTGCTGTTGTGTCCCAAGACACCTTCTTGCCCTGGAGAACCCAC 252

OY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
|||||
Db 253 CATAAATTCGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGAGGCTCCACAGGTGGCGCTG 312

OY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
|||||
Db 313 GAGAACTGTTCAGACAGTGGCCGACACCCGCTGTGGCTGTAAGCCAGGCTGTTGTGAG 372

OY 101 CysGlnValSerGlnCysValSerSerProPheTyrcysGlnProCysLeuAspCys 120
|||||
Db 373 TGCCAGGTACGCCAATGTGTACAGAGTTCAACCTTCTACTGCCCAACCATGCTAGACTGC 432

OY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
|||||
Db 433 GGGGCCCTGCACCGCCACACACAGGCTACTGTCTCCCGCAGAGATGACTGTGGAGCC 492

OY 141 CysLeuProGlyPheTyrgluHisGlyAspGlyCysValSerCysProThrSerThrIleu 160
|||||
Db 493 TGCCGTGCTGGCTTCTATGACATGGCGATGGCTGCGTGTCTGCCCCACGACACCCCTG 552

OY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArg 174
|||||
Db 553 GGGAGCTGTCCAGAGCGCTGTGCCCTGTCTGTGGCTGGAGG 594

RESULT 7
HSU94503

LOCUS
DEFINITION Human lymphocyte associated receptor of death 2 mRNA, alternatively
spliced, complete cds.

ACCESSION
U94503
VERSION
U94503.1 GI:2071952

KEYWORDS
SOURCE
ORGANISM Homo sapiens.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 (bases 1 to 1355)
Screation,G.R., Xu,X.N., Olsen,A.L., Cowper,A.E., Tan,R.,
McMichael,A.J. and Bell,J.I.

TITLE
LARD: a new lymphoid-specific death domain containing receptor
regulated by alternative pre-mRNA splicing

JOURNAL
Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)

MEDLINE
97272273

PUBMED
9114039

REFERENCE
2 (bases 1 to 1355)
Screation,G.R.
Direct Submission

TITLE
Submitted (19-MAR-1997) Molecular Immunology Group, Institute of
Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3
9DU, UK

FEATURES
source
Location/Qualifiers

1..1355
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Hela"
/cell_type="lymphocyte"
1..762
/function="mediates apoptosis"
/note="LARD-2; similar to Fas and TNF-R1; possibly
soluble; truncated before the transmembrane domain"

CDS

/codon_start=1
/product="lymphocyte associated receptor of death 2"
/protein_id="AAC51308.1"
/db_xref="GI:2071953"
/translation="MEQRRPGCAVAALLVLGARAQGGTRSPRCDCAGDFHKKIG
LFCRCGPAGHYLKAPCTEPGNSCTLCVCPDPTFLAMENHNHNSCARCQACDEQASQV
ALENCSAVADTRCGCKPGWFEVCQVSCVSSSPYCPCLDCGALHRTLRICSRRDT
DCGTCLPGFYEHDGCVSCPTSTLSCPERCAVCGWRQSRWCAGNAGSRIGMDRGEA
GEEGNHPTPTSCFQCSGSRCSWLALWSPSCIGPP"
599..700
/note="insertion compared to IARD 1a, deposited in GenBank
Accession Number U94501, probable retained intron leading
to premature transcriptional termination"

misc_feature
BASE COUNT 223 a 441 c 451 g 240 t
ORIGIN

Alignment Scores:
Pred. No.: 5.97e-66 Length: 1355
Score: 1038.00 Matches: 174
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-993-234-6_COPY_25_198 (1-174) x HSU94503 (1-1355)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
Db 73 CAGGGCGGCACACTCGTAGCCCCAGGTGTGACTGTGCCGGTGACTTCCACAGAAGATTGGT 132
QY 21 LeupheCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
Db 133 CTGTTTGTGTGACAGAGGCTGCCAGCGGGGACTTGAAGGCCCTTGACAGGAGCCC 192
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db 193 TGGCGCACTCCACCTGCTTGTGTCTCCCAAGACACCTTCTTGCGCTGGAGAACCCAC 252
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db 253 CATAATTCTGAATGTGCCCCGCTGCCAGGCTGTGATGAGCAGGCGCTCCAGGTGGCGCTG 312
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
Db 313 GAGAACTGTTCAAGAGTGGCCGACACCGCTGTGCTGTAAGCCAGCGCTGTTGTGGAG 372
QY 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120
Db 373 TGCCAGGTCAGCCAAATGTGTGACAGACTTCACTTACTGCCAACCATGCTAGACTGC 432
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 433 GGGGCCCTGCACCGCACACAGGCTACTCTGTTCGCCGACAGATATGACTGTGGAGCC 492
QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db 493 TGCCTGCGCTGCTCTATGAACATGGCGATGGCTGCGTCTCCTGCCCCACGAGCACCCCTG 552
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArg 174
Db 553 GGGAGCTGTCCAGACGCGCTGTGCCGCTGTCTGTGTGGCTGGAGG 594

RESULT 8
LOCUS HSU74611 1634 bp mRNA linear PRI 02-JAN-1997
DEFINITION Human Apo-3 mRNA, complete cds.
ACCESSION U74611
VERSION U74611.1 GI:1763292
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS 1 (bases 1 to 1634)
Marsters,S.A., Sheridan,J.P., Donahue,C.J., Pitti,R.M., Gray,C.L.,
Goddard,A.D., Bauer,K.D. and Ashkenazi,A.
Apo-3, a new member of the tumor necrosis factor receptor family,
contains a death domain and activates apoptosis and NF-kB
Curr. Biol. (1996) in press
2 (bases 1 to 1634)
Marsters,S.A., Sheridan,J.P., Donahue,C.J., Pitti,R.M., Gray,C.L.,
Goddard,A.D., Bauer,K.D. and Ashkenazi,A.
Direct Submission
Submitted (15-OCT-1996) Molecular Oncology, Genentech, 460 Pt. San
Bruno Blvd., South San Francisco, CA 94080, USA
FEATURES
source
1..1634
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/map="1p36.3"
/tissue_type="heart"
/dev_stage="fetal"
89..1342
/note="contains death domain, activates apoptosis and
NF-kB; TNF receptor family member"
/codon_start=1
/product="Apo-3"
/protein_id="AAB39714.1"
/db_xref="GI:1763293"
/translation="MEQRRPGCAVAALLVLGARAQGGTRSPRCDCAGDFHKKIG
LFCRCGPAGHYLKAPCTEPGNSCTLCVCPDPTFLAMENHNHNSCARCQACDEQASQV
ALENCSAVADTRCGCKPGWFEVCQVSCVSSSPYCPCLDCGALHRTLRICSRRDT
DCGTCLPGFYEHDGCVSCPTSTLSCPERCAVCGWRQSRWCAGNAGSRIGMDRGEA
GEEGNHPTPTSCFQCSGSRCSWLALWSPSCIGPP"
LYDMDAVPARRWKEFVFTGLREAEIEAVEVEIGRRDQYEMLRWRQDPAGLGA
VYALERMGLDGVEDLRSLRQRP"

CDS

BASE COUNT 300 a 528 c 519 g 287 t
ORIGIN

Alignment Scores:
Pred. No.: 7.19e-66 Length: 1634
Score: 1038.00 Matches: 174
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-993-234-6_COPY_25_198 (1-174) x HSU74611 (1-1634)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
Db 161 CAGGGCGGCACACTCGTAGCCCCAGGTGTGACTGTGCCGGTGACTTCCACAGAAGATTGGT 220
QY 21 LeupheCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
Db 221 CTGTTTGTGTGACAGAGGCTGCCAGCGGGGACTTACTTGAAGGCCCTTGACAGGAGCCC 280
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db 281 TGGCGCACTCCACCTGCTGTGTCTCCCAAGACACCTTCTTGCGCTGGAGAGCAC 340
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db 341 CATAATTCTGAATGTGCCCCGCTGCCAGGCTGTGATGAGAGGCCCTCCAGGTGGCGCTG 400
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
Db 401 GAGAACTGTTCAAGAGTGGCCGACACCGCTGTGGCTGTAAAGCCAGGCTGTTGTGGAG 460
QY 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120
Db 461 TGGCAGGTCAGCCAAATGTGTGACAGACTTCACTTACTGCCAACCATGCTAGACTGC 520
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140

|||||
Db 521 GGGGCCCTGCACCGCCACACACGGCTACTCTGTCCCGCAGAGATACTGACTGTGGACC 580
QY 141 CysLeuProGlyPheTyrgluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
|||||
Db 581 TGCCTGCCTGGCTTCTATGAACATGGCGATGGCTGCTCCTGCCCCACGACGACCCCTG 640
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArg 174
|||||
Db 641 GGGAGCTGTCCAGAGCGCTGTGCCGCTGTCTGTGGCTGGAGG 682
RESULT 9
AX055442 1662 bp DNA linear PAT 13-JAN-2001
LOCUS Sequence 72 from Patent WO0073452.
DEFINITION AX055442
ACCESSION AX055442
VERSION AX055442.1 GI:12228713
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1662)
AUTHORS Ashkenazi,A.J., Baker,K.P., Chan,B., Goddard,A., Godowski,P.J.,
Gurney,A.L., Hebert,C., Henzel,W., Kabakoff,R.C., Shelton,D.L.,
Tumas,D., Watanabe,C.K. and Wood,W.I.
TITL Composition and methods for the treatment of immune related
diseases
JOURNAL Patent: WO 0073452-A 72 07-DEC-2000;
Genentech, Inc. (US)
FEATURES
source 1. 1662
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 302 a 540 c 531 g 289 t
ORIGIN
Alignment Scores:
Pred. No.: 7.31e-66 Length: 1662
Score: 1038.00 Matches: 174
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0
US-09-993-234-6_COPY_25_198 (1-174) x AX055442 (1-1662)
QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
|||||
Db 175 CAGGGCGGCACCTCGTAGCCCCAGGTGTGACTGTGCCGGTGACTTCCACAGAGATTGGT 234
QY 21 LeuPheCysCysArgGlyCysProAlaGlyHisTyrlleuLysAlaProCysThrGluPro 40
|||||
Db 235 CTGTTTGTGTGCAGAGGCTGCCACAGCGGGGCACTACCTGAAGGCCCTTGCACGGAGCCC 294
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
|||||
Db 295 TCGGGCAACTCCACCTGCTGTGTGTCGCCAAGACACCTTCTTGGCCGTGGAGAACCCAC 354
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
|||||
Db 355 CATAATTCGATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCTCCAGGTGGCGCTG 414
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
|||||
Db 415 GAGAACTGTTCAGAGTGGCCGACACCCGCTGTGCTGAAGCCAGGCTGGTTTGTGGAG 474
QY 101 CysGlnValSerGlnCysValSerSerProPheTyrcysGlnProCysLeuAspCys 120
|||||
Db 475 TGGCAGGTACAGCCAATGTGTACAGCAGTTACACCTTCTACTGCCAACCATGCTAGACTGC 534
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
|||||

Db 535 GGGGCCCTGCACCGCCACACACGGCTACTCTGTCCCGCAGAGATACTGACTGTGGACC 594
QY 141 CysLeuProGlyPheTyrgluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
|||||
Db 595 TGCCTGCCTGGCTTCTATGAACATGGCGATGGCTGCTCCTGCCCCACGACGACCCCTG 654
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArg 174
|||||
Db 655 GGGAGCTGTCCAGAGCGCTGTGCCGCTGTCTGTGGCTGGAGG 696
RESULT 10
AX201344 1662 bp DNA linear PAT 30-AUG-2001
LOCUS Sequence 23 from Patent WO0153486.
DEFINITION AX201344
ACCESSION AX201344
VERSION AX201344.1 GI:15391165
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1662)
AUTHORS Ashkenazi,A.J., Goddard,A., Godowski,P.J., Gurney,A.L.,
Hillan,K.J., Marsters,S.A., Pan,J., Pitti,R.M., Roy,M.A., Smith,V.,
Stone,D.M., Watanabe,C.K. and Wood,W.I.
TITL Composition and methods for the treatment of tumour
JOURNAL Patent: WO 0153486-A 23 26-JUL-2001;
Genentech, Inc. (US)
FEATURES
source 1. 1662
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 302 a 540 c 531 g 289 t
ORIGIN
Alignment Scores:
Pred. No.: 7.31e-66 Length: 1662
Score: 1038.00 Matches: 174
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0
US-09-993-234-6_COPY_25_198 (1-174) x AX201344 (1-1662)
QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
|||||
Db 175 CAGGGCGGCACCTCGTAGCCCCAGGTGTGACTGTGCCGGTGACTTCCACAGAGATTGGT 234
QY 21 LeuPheCysCysArgGlyCysProAlaGlyHisTyrlleuLysAlaProCysThrGluPro 40
|||||
Db 235 CTGTTTGTGTGCAGAGGCTGCCACAGCGGGGCACTACCTGAAGGCCCTTGCACGGAGCCC 294
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
|||||
Db 295 TCGGGCAACTCCACCTGCTGTGTGTCGCCAAGACACCTTCTTGGCCGTGGAGAACCCAC 354
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
|||||
Db 355 CATAATTCGATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCTCCAGGTGGCGCTG 414
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
|||||
Db 415 GAGAACTGTTCAGAGTGGCCGACACCCGCTGTGCTGAAGCCAGGCTGGTTTGTGGAG 474
QY 101 CysGlnValSerGlnCysValSerSerProPheTyrcysGlnProCysLeuAspCys 120
|||||
Db 475 TGGCAGGTACAGCCAATGTGTACAGCAGTTACACCTTCTACTGCCAACCATGCTAGACTGC 534
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
|||||
Db 535 GGGGCCCTGCACCGCCACACACGGCTACTCTGTCCCGCAGAGATACTGACTGTGGAGCC 594

QY 141 CysLeuProGlyPheTyrgluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db 595 TGCCCTGGCTGGCTTCTATGAACATGGCGATGGCTGCTGCTGCCCCACGAGACACCTG 654
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArg 174
Db 655 GGGAGCTGTCCAGAGCGCTGTGCCCTGTCTGTGTGGCTGAGG 696
RESULT 11
AX331947 1743 bp DNA linear PAT 09-JAN-2002
LOCUS Sequence 2456 from Patent WO0194629.
DEFINITION AX331947
ACCESSION AX331947
VERSION AX331947.1 GI:18122581
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
TITLE Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
Horrigan, S., Soppet, D.R. and Weaver, Z.
Cancer gene determination and therapeutic screening using signature
gene sets
JOURNAL Patent: WO 0194629-A 2456 13-DEC-2001;
Avalon Pharmaceuticals (US)
FEATURES Location/Qualifiers
source 1.1743
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 347 a 543 c 549 g 304 t
ORIGIN
Alignment Scores:
Pred. No.: 7.66e-66 Length: 1743
Score: 1038.00 Matches: 174
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0
US-09-993-234-6_COPY_25_198 (1-174) x AX331947 (1-1743)
QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
Db 141 CAGGGCGGCACTCGTAGCCCGCAGGTGTGACTGTGCCGGTGACTTCCACAGAAGATTTGGT 200
QY 21 LeuPheCysCysArgGlyCysProAlaGlnHisTyrluLysAlaProCysThrGluPro 40
Db 201 CTGTTTGTGTGACAGAGCTGCCAGCGGGCAGCTGAGGCCCTTGACGAGGCC 260
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db 261 TGCGGCACTCCACCTGGCTGTGTGTCCCAAGACACCTTCTTGGCCTGGAGAACAC 320
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db 321 CATTAATTCGTAATGTGCCCGCTGCCAGGCCCTGTGATGAGCAGGCCCTCCAGGTGGCCTG 380
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
Db 381 GAGAACTGTTCAGACAGTGGCCGACACCGCTGTGGCTGTAAAGCCAGGCTGTGTGGAG 440
QY 101 CysGlnValSerGlnCysValSerSerSerProPheTyrcysGlnProCysLeuAspCys 120
Db 441 TGCCAGGTCAGCCCAATGTGTGACAGAGTTCACCCCTTCTACTGCCAACCAATGCCCTAGACTGC 500
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 501 GGGGCCCTGCACGCCACACACAGGCTACTCTGTTCGCCGAGAGATACTGACTGTGGAGCC 560
QY 141 CysLeuProGlyPheTyrgluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
|||||

Db 561 TGCCCTGGCTGGCTTCTATGAACATGGCGATGGCTGCGTGTCTGCCCCACGAGACACCTG 620
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArg 174
Db 621 GGGAGCTGTCCAGAGCGCTGTGCCCTGTCTGTGTGGCTGAGG 662
RESULT 12
HSWSL1 1743 bp mRNA linear PRI 16-DEC-1996
LOCUS H.sapiens mRNA for WSL-LR, WSL-S1 and WSL-S2 proteins.
DEFINITION Y09392
ACCESSION Y09392
VERSION Y09392.1 GI:1669690
KEYWORDS wsl-1 gene; WSL-1R protein; WSL-S1 protein; WSL-S2 protein.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1743)
TITLE Kitson, J., Raven, T., Jiang, Y.P., Goeddel, D.V., Giles, R.M.,
Pun, K.T., Grinham, C.J., Brown, R. and Farrow, S.N.
A death-domain-containing receptor that mediates apoptosis
JOURNAL Nature 384 (6607), 372-375 (1996)
MEDLINE 97088617
PUBMED 8934525
2 (bases 1 to 1743)
REFERENCE Kitson, J.
AUTHORS Direct Submission
TITLE Submitted (12-NOV-1996) J. Kitson, GLAXO-Wellcome, Medicines
JOURNAL Research Centre, Gunneels Wood Road, Stevenage, SG1 2NY, UK
FEATURES Location/Qualifiers
source 1.1743
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_type="T-lymphocyte"
/tissue_type="lymphoid"
1.1742
/gene="wsl-1"
1.610
/gene="wsl-1"
/number=1
join(69..666,768..1423)
/gene="wsl-1"
/codon_start=1
/product="WSL-1R protein"
/protein_id="CAA70561.1"
/db_xref="GI:1669693"
/db_xref="SWISS-PROT:Q93038"
/translation="MEQRPFGCAVAALLLVLLGARAQGGTRSPRCDCAGDFHKKIG
LFCCRGPAGHYLKAPCTEPGNSYCLVCPQDTFLAWENHNHNSCARQACDEQASQV
ALENCSAVADTRCGCKPGWFVEQVSQCVSSSPFYCQPCLDGALHRTLRILCSRDY
DCGTCLPGFEYEHGDGCVSCPSTLGSCEPERCAAVCGWRQMFVQVLLAGLVPLLLGA
TLTYTYRHCPHKLPLVTADAEAGMALTPPATHLSPDLSAHTLAPDSSSEKICTVOL
VGNSTWTPGYETQEALCPQVTFWSMDQLPSRALGPARAPTLSPSPAGSPAMLOPGPO
LYDVMDAVPARRWEFEVRLTGLREAEIAVEVEIGLFRDQYEMLKHWROQDPAGLGA
VVALERMGLDGCVEDLRSRLQRP"
join(69..610,768..882)
/gene="wsl-1"
/codon_start=1
/product="WSL-S1 protein"
/protein_id="CAA70560.1"
/db_xref="GI:1669692"
/db_xref="SWISS-PROT:Q93038"
/translation="MEQRPFGCAVAALLLVLLGARAQGGTRSPRCDCAGDFHKKIG
LFCCRGPAGHYLKAPCTEPGNSYCLVCPQDTFLAWENHNHNSCARQACDEQASQV
ALENCSAVADTRCGCKPGWFVEQVSQCVSSSPFYCQPCLDGALHRTLRILCSRDY
DCGTCLPGFEYEHGDGCVSCPSTLGSCEPERCAAVCGWRQMFVQVLLAGLVPLLLGA
TLTYTYRHCPHKLPLVTADAEAGMALTPPATHLSPDLSAHTLAPDSSSEKICTVOL
VGNSTWTPGYETQEALCPQVTFWSMDQLPSRALGPARAPTLSPSPAGSPAMLOPGPO
LYDVMDAVPARRWEFEVRLTGLREAEIAVEVEIGLFRDQYEMLKHWROQDPAGLGA
VVALERMGLDGCVEDLRSRLQRP"
69..830
/gene="wsl-1"
/codon_start=1
/product="WSL-S2 protein"
/protein_id="CAA70559.1"
/db_xref="GI:1669691"

FEATURES USA
source
1. 1528
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/map="1p36"
1. 1528
/gene="DDR3"
/gene="DDR3"
/function="mediates apoptosis when cross-linked"
/note="A TNFR1-related death-domain containing receptor;
DR3, WSL-LR, Apo-3, TRAMP; transmembrane form; similar to
human EST clone 298913, GenBank Accession Number N71143"
/codon_start=3
/product="death domain receptor 3"
/protein_id="AAB41432.1"
/db_xref="GI:1800293"
/translation="GCAVAAALLLVLGARAOGGTRSPRCDACGDFHKKIGLFCRC
CPAGHYLKAPCTEPCGNSFCLVCPQDTFLAMENHNHNSCARCQACDEGASQVLENC
AVADTRCGCKPGWFEVCQVSCVSSSPFYCOPCLDCGALHRTILCSRRDTCGCL
LGFEYHGDGVCSPSTLGSCEPCAAVCGWRQFWVQVLLAGLVPLLGATLTYY
RHCWPHKPLVTADAGMEALTPPATLSPDLSAHTLLAPDSSERICTVQLVNSWT
PGYPETQALCPQVTVMSWDQLPSRALGPAAFTLSPESPAGSPAMMLQPGPOLYD
AVPARRWKEFVRTLGLREAIEAVEVEIGRFRDQYEMLKRWROQOPAGLGAAYAAE
RMGLDGCVEDLRSRLQRP"
BASE COUNT 280 a 496 c 470 g 282 t
ORIGIN
Alignment Scores:
Pred. No.: 3.51e-65 Length: 1528
Score: 1028.00 Matches: 173
Percent Similarity: 99.43% Conservative: 0
Best Local Similarity: 99.43% Mismatches: 1
Query Match: 99.04% Indels: 0
DB: 9 Gaps: 0
US-09-993-234-6_COPY_25_198 (1-174) x HSU83597 (1-1528)
QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGly 20
Db 57 CAGGGCGGCACTCGTAGCCGCCAGGTGTGACTGTGCGGCTGACTTCCACAGAAGATTGCT 116
QY 21 LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
Db 117 CTGTTTGTGACAGAGCTGCCAGCGGGCAGCTGTAAGGCCCTTGCACGGAGCCCC 176
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTyrGluAsnHis 60
Db 177 TGCAGCACTCCACCTGCTGTGTGTCCCAAGACACCTTCTGGCGCTGGAGAACAC 236
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db 237 CATAATTCTGAATGTGCCCGCTGCCAGGCTGTGATGACGAGGCCCTCCAGGCTGGCGCTG 296
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTyrPheValGlu 100
Db 297 GAGAACTGTTCAAGAGTGGCCGACACCCCGCTGTGGCTGTAAAGCCAGGCTGTGTGGAG 356
QY 101 CysGlnValSerGlnCysValSerSerSerProPheTyrCysGlnProCysLeuAspCys 120
Db 357 TGCAGGTGACCAATGTGTGACAGAGTCAACCTTCTACTGCCAACCATGCTAGACTGC 416
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 417 GGGGCCCTGCACCGCACACACAGGCTACTCTGTGCCGACAGAGATGACTGTGGAGC 476
QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db 477 TGCTGTGCTTGGCTTCTATGAACATGGCATGGCTGCGTGTCTCTGCCCCACGAGCACCCCTG 536
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTyrParg 174

Db 537 GGGAGCTGTCCAGAGCGCTGTGCCCTGTCTGTGCGTGGAG 578
RESULT 15
LOCUS HSU75380 1557 bp mRNA linear PRI 05-APR-1997
DEFINITION Human apoptosis-mediating receptor TRAMP mRNA, partial cds.
ACCESSION U75380
VERSION U75380.1 GI:1695924
KEYWORDS
SOURCE
ORGANISM Homo sapiens.
Homo sapiens.
Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Bodmer, J.L., Burns, K., Schneider, P., Hofmann, K., Steiner, V.,
Thome, M., Bolland, T., Hahne, M., Schroter, M., Becker, K., Wilson, A.,
French, L.E., Browning, J.L., Macdonald, R. and Tschopp, J.
TITLE TRAMP, a novel apoptosis-mediating receptor with sequence homology
to tumor necrosis factor receptor 1 and Fas (Apo-1/CD95)
JOURNAL Immunity 6 (1), 79-88 (1997)
MEDLINE 97205335
PUBMED 9052839
REFERENCE
AUTHORS 2 (bases 1 to 1557)
Bodmer, J.L., Burns, K., Schneider, P., Hofmann, K., Steiner, V.,
Thome, M., Bolland, T., Hahne, M., Schroter, M., Wilson, A.,
French, L.E., Browning, J.L., Macdonald, R. and Tschopp, J.
TITLE Direct Submission
JOURNAL Submitted (18-OCT-1996) Institute of Biochemistry, University of
Lausanne, 155 Chemin des Boveresses, Epalinges, CH 1066,
Switzerland
FEATURES
source
Location/Qualifiers
1. 1557
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/map="1p36.2"
/tissue_type="fetal lung"
<1. 1245
/function="activates NF-kB"
/function="mediates apoptosis"
/note="contains a death domain; similar to TNF receptor"
/codon_start=1
/product="apoptosis-mediating receptor TRAMP"
/protein_id="AAC51192.1"
/db_xref="GI:1695925"
/translation="AAAGCAVAAALLVLGARAOGGTRSPRCDACGDFHKKIGLFC
CRGCPAGHYLKAPCTEPCGNSFCLVCPQDTFLAMENHNHNSCARCQACDEGASQVLE
NCSAVADTRCGCKPGWFEVCQVSCVSSSPFYCOPCLDCGALHRTILCSRRDTCG
TCLLGFEYHGDGVCSPSTLGSCEPCAAVCGWRQFWVQVLLAGLVPLLGATLT
YTYRHWCWPHKPLVTADAGMEALTPPATLSPDLSAHTLLAPDSSERICTVQLVGN
SWTPGYPETQALCPQVTVMSWDQLPSRALGPAAFTLSPESPAGSPAMMLQPGPOLYD
VMDAVPARRWKEFVRTLGLREAIEAVEVEIGRFRDQYEMLKRWROQOPAGLGAAYAA
ALERMGLDGCVEDLRSRLQRP"
BASE COUNT 286 a 508 c 477 g 286 t
ORIGIN
Alignment Scores:
Pred. No.: 3.57e-65 Length: 1557
Score: 1028.00 Matches: 173
Percent Similarity: 99.43% Conservative: 0
Best Local Similarity: 99.43% Mismatches: 1
Query Match: 99.04% Indels: 0
DB: 9 Gaps: 0
US-09-993-234-6_COPY_25_198 (1-174) x HSU75380 (1-1557)
QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGly 20
Db 64 CAGGGCGGCACTCGTAGCCGCCAGGTGTGACTGTGCGGCTGACTTCCACAGAAGATTGCT 123
QY 21 LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40

Db 124 CTGTTTGTTCAGAGGCTGCCAGCGGGCAGCTACCTGAAGCCCCCTTGACAGGAGCCC 183

QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
|||||
Db 184 TGGGGCAACTCCACCTGCCCTGTGTGTGCCCAAGACACCTTCTGGCCGTGGAGAACAC 243

QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
|||||
Db 244 CATTAATCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCTCCCAAGGTGGCGCTG 303

QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
|||||
Db 304 GAGAACTGTTCAAGCAGTGGCCGACACCGCTGTGGCTGTAAAGCCAGGCTGGTTGTGAG 363

QY 101 CysGlnValSerGlnCysValSerSerSerProPheTyrCysGlnProCysLeuAspCys 120
|||||
Db 364 TGGCAGGTCAGCCAATGTGTGACAGTTCAACCTTCTACTGCCAACCATGCTAGACTGC 423

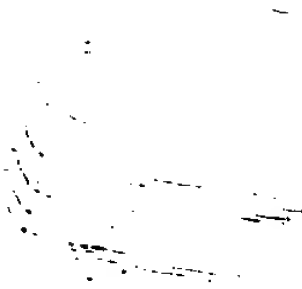
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
|||||
Db 424 GGGGCCCTGCACCGCCACACGGCTACTCTGTGCCGACAGATACTGACTGTGGGACC 483

QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
|||||
Db 484 TGGCTGCTTGGCTTCTATGACATGGCGATGGCTGCGTGTCTGCCCCACAGACACCCCTG 543

QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArg 174
|||||
Db 544 GGGAGCTGTCCAGAGCGCTGTGCCGCTGTGTGGCTGGAGG 585

Search completed: April 6, 2003, 21:07:58
Job time : 2029.14 secs

67



THIS PAGE BLANK (USPTO)

GenCore version 5.1.4-p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 6, 2003, 15:33:09 ; Search time 162.014 Seconds
(without alignments)
2418.610 Million cell updates/sec

Title: US-09-993-234-6_COPY_25_198
Perfect score: 1038
Sequence: 1 QGGTRSPRCDCAGDFHKKIG.....CPTSTLGSCPERCAAVCGWR 174

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPRO.spool/US09993234/runat_27032003_115454_15312/app_query.fasta_1.2346
-DB=N_Geneseq_101002 -QFMT=fastap -SUFFIX=ring -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITs=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdl
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09993234 @cgn_1_1_660 @runat_27032003_115454_15312 -NCPU=6 -ICPU=3
-NO_XLPHY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_101002:*
1: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
8: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
9: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
11: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1038	100.0	1254	18	AAT89427	Death domain conta
2	1038	100.0	1254	20	AAK00925	Death domain conta
3	1038	100.0	1254	21	AAC68777	Human death domain
4	1038	100.0	1634	18	AAT91180	Human apoptosis pr
5	1038	100.0	1634	22	AAH27782	Human genomic DNA
6	1038	100.0	1634	24	AAAL47186	Human rheumatoid a
7	1038	100.0	1662	22	ABK40265	Human PRO779 cDNA.
8	1038	100.0	1662	24	ABK40265	CDNA encoding huma
9	1038	100.0	1743	24	ABL64119	Breast cancer rela
10	1038	100.0	1783	18	AAT89426	Death domain conta
11	1038	100.0	1783	20	AAK00924	Death domain conta
12	1038	100.0	1783	21	AAC68776	Human death domain
13	1038	100.0	1847	19	AAV28700	Human apoptosis in
14	978	94.2	1250	22	AAF83770	Nucleotide sequenc
15	950	91.5	816	24	ABL67258	Thyroid cancer rel
16	950	91.5	1438	18	AAT91179	Human apoptosis pr
17	937	90.3	787	24	AAAL47187	Human rheumatoid a
18	738	71.1	4825	24	AAAL47185	Human DR3 gene ass
19	738	71.1	10797	23	ABK42690	Genomic sequence #
20	564	54.3	1251	19	AAV28701	Mouse apoptosis in
21	214	20.6	2130	24	ABK63694	Rat sequence diffe
22	212.5	20.5	1049	18	AAT94007	CDNA for TBP(20-16
23	211	20.3	5870	21	AAA15044	Nucleotide sequenc
24	205.5	19.8	1301	18	AAT94022	CDNA for TBP(20-19
25	203.5	19.6	1202	18	AAT94008	CDNA for TBP(20-16
26	203	19.6	608	13	AAQ24441	Encodes truncated
27	203	19.6	1334	11	AAQ06282	Plasmid Tumour Nec
28	203	19.6	1368	14	AAQ49332	Lambda-derived TNF
29	203	19.6	1368	21	AAA95105	Human TNFRI coding
30	203	19.6	2062	13	AAQ20973	TNF-alpha binding
31	203	19.6	2062	13	AAQ24440	Encodes TNF-alpha
32	203	19.6	2088	12	AAQ10883	30kd TNF inhibitor
33	203	19.6	2088	22	AAC83946	Human 30 kda TNF 1
34	203	19.6	2111	12	AAQ10955	Encodes human 55kd
35	203	19.6	2111	20	AAQ09170	Human tumour necro
36	203	19.6	2111	22	AAH48859	Human TNFBP-assoc1
37	203	19.6	2111	24	ABK84039	Human CDNA differe
38	203	19.6	2111	24	ABN95862	Gene #2360 used to
39	203	19.6	2141	11	AAQ06285	Human Tumour Necro
40	203	19.6	2161	21	AAZ48475	Human tumour necro
41	203	19.6	2161	24	ABK13194	Human tumour necro
42	203	19.6	2175	16	AAQ90513	p55 TNF-R gene. H
43	203	19.6	6889	17	AAT15931	DHFR/Inttron (WTIR
44	203	19.6	6926	18	AAV04431	Vector pCDNA3-IgG1
45	202	19.5	2170	14	AAQ50870	p55 Tumour necrosi

ALIGNMENTS

RESULT 1		
ID	AAT89427	
XX	AAT89427	standard; cDNA; 1254 BP.
XX	AAT89427;	
DT	02-MAR-1998	(first entry)
XX		
DE	Death domain	containing receptor DR3 cDNA.
XX		
KW	Death domain	containing receptor; DR3; human; apoptosis;
KW	inflammation; NF-kappaB;	ds.
XX		
OS	Homo sapiens.	
XX		
FH	key	Location/Qualifiers
FT	sig_peptide	1..72
FT		/*tag= a

FT mat_peptide 73..1251
FT /+tag= b
XX
PN WO9733904-A1.
XX
PD 18-SEP-1997.
XX
PF 17-OCT-1996; 96WO-US16849.
XX
PR 12-MAR-1996; 96US-0013285.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX (UNMI) UNIV MICHIGAN.
PI Dillon PJ, Dixit VM, Gentz RL, Ni J, Yu G;
XX
DR WPI; 1997-470812/43.
DR P-PSDB; AAW31517.
XX

Death domain containing receptor polypeptide(s) DR3 and DR3-V1
PT for activation of apoptosis and NF-kappab, antagonists can be used
PT to treat inflammatory diseases

PS Claim 6; Page 75-77; 108pp; English.

XX This cDNA clone codes for human death domain containing receptor
CC DR3 (see AAW31517), a novel member of the tumour necrosis factor
CC receptor family. It was isolated from a HUVEC cDNA library.
CC Related death domain containing receptor DR3-V1 cDNA (see AAT89426)
CC was isolated from a human testis tumour cDNA library. The genes
CC have also been identified in cDNA libraries of foetal liver,
CC foetal brain, tonsil and leukocyte. Nucleic acids encoding full-
CC length or mature DR3, or the extracellular, transmembrane,
CC intracellular or especially the death domain of DR3, can be used to
CC produce recombinant polypeptides in transformed host cells. These
CC polypeptides can be used to treat diseases and disorders associated
CC with the inhibition of apoptosis. Antagonists can be used to treat
CC diseases and disorders associated with increased apoptosis and for
CC treating inflammatory diseases and disorders.

XX Sequence 1254 BP; 201 A; 420 C; 407 G; 226 T; 0 other;

Alignment Scores:
Pred. No.: 7.96e-72 Length: 1254
Score: 1038.00 Matches: 174
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-09-993-234-6_COPY_25_198 (1-174) x AAT89427 (1-1254)

QY 1 GINGLYGLYThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGly 20
DB 73 CAGGGCGGCACTCGTAGCCCCAGGTGTGACTGTGCCGGTGACTTCCACAGAAGATTGGT 132
QY 21 LeupheCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
DB 133 CTGTTTGTGACAGAGGCTGCCAGCGGGGCACTAAGGAGGCCCTTGACAGAGGCC 192
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
DB 193 TCGGGCAACTCCACCTGCTGTGTGCCCAAGACACCTTCTTGCCCTGGGAGAACCAC 252
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
DB 253 CATAAATCTGAATGTGCCGCTGCCAGGCTGTGATGAGCAGAGGCCCTCCAGGTGGCGCTG 312
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTyrPheValGlu 100
DB 313 GAGAACTGTTCAGCAGAGTGCCGACACCCGCTGTGGCTGAAGCCAGGCTGTTTGTGAG 372
QY 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120

DB 373 TGGCAGGTGACCAATGTGTACAGAGTTCAACCTTCTACTGCCAACCATGCTAGACTGC 432
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
DB 433 GGGGCCCTGCACCCGCCACACACAGGCTACTCTGTTCGCCAGAGTACTGACTGTGGACC 492
QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
DB 493 TGGCTGCTGCTTCTATGAACATGCGATGCGCTGCGTGTCTGCCCCACGAGACCCCTG 552
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTyrArg 174
DB 553 GGGAGCTGTCCAGAGCGCTGTGCCGCTGTGTGCTGGAGG 594

RESULT 2
AAX00925
ID AAX00925 standard; cDNA; 1254 BP.
XX
XX AAX00925;
AC
XX 25-MAR-1999 (first entry)
DT
XX
DE Death domain containing receptor polypeptide (DR3) encoding cDNA.
XX
KW Death domain; receptor; DR3-V1; DR3; recombinant; ds.
XX
OS Homo sapiens.

XX Key Location/Qualifiers
FH CDS 1..1254
FT /+tag= a
FT /product= "Death domain containing receptor DR3"
FT sig_peptide 1..72
FT /+tag= b
FT mat_peptide 73..1251
FT /+tag= c
XX JP11000170-A.

XX 06-JAN-1999.
XX
XX 12-MAR-1997; 97JP-0057503.
XX
XX 06-FEB-1997; 97US-0037341.
PR 12-MAR-1996; 96US-0013285.
PR 17-OCT-1996; 96US-0028711.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (UNMI) UNIV MICHIGAN.
XX
DR WPI; 1999-124390/11.
DR P-PSDB; AAW95538.
XX
XX New death domain containing receptor and recombinant vector -
PT optionally comprising leader sequence
PT
XX
PS Claim 6; Fig 3; 50pp; Japanese.

CC The invention provides nucleotide sequences encoding death domain
CC containing receptor polypeptides DR3-V1 and DR3. The DR3-V1 cDNA clone
CC is contained in ATCC deposition No. 97456 and the DR3 cDNA clone is
CC contained in ATCC deposition No. 97757. Recombinant vectors comprising
CC the nucleic acid sequences and optionally the leader sequences are
CC used for the recombinant production of the proteins. The present
CC sequence represents a cDNA encoding the death domain containing
CC receptor polypeptide (DR3).

SQ Sequence 1254 BP; 201 A; 420 C; 407 G; 226 T; 0 other;

Alignment Scores:
Pred. No.: 7.96e-72 Length: 1254
Score: 1038.00 Matches: 174

Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 20 Gaps: 0

US-09-993-234-6_COPY_25_198 (1-174) x AAX00925 (1-1254)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGly 20
DB 73 CAGGGCGGCACTCGTAGCCCCAGAGTGTGACTGTGCCGGTGACTTCCACAAGAATTGGT 132
QY 21 LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
DB 133 CTGTTTGTGTGACAGAGCGTGCCACGGGGGCACTACCTGAAGGCCCTTGACAGGAGCC 192
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
DB 193 TGGCGGCACTCCACCTGCGCTGTGTGTCCCAAGACACCTTCTTGCGCTGGGAGAACCC 252
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
DB 253 CATAATCTGTAATGTGCCCGCTGACAGCGCTGTGATGAGCAGGCGCTCCAGGTGGCGCTG 312
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
DB 313 GAGAACTGTTCAGACAGTGCGCCAGACCGCTGTGGCTGTAAAGCCAGCGTGTGGAG 372
QY 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120
DB 373 TGGCAGGTCAAGCAATGTGTACAGAGTTCACCTTCTACTGCCAACCATGCGTAGACTGC 432
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
DB 433 GGGGCCCTGCACCGCCACACACGGCTACTGTTCGCCGACAGATACTGACTGTGGAGCC 492
QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
DB 493 TGCCTGCTGGCTTCTATGAACATGGCGATGGCTGCTGCTGCTGCCACGAGCACCCTG 552
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArg 174
DB 553 GGGAGCTGTCCAGAGCGCTGTGCCGCTGTCTGTGGCTGAGG 594

RESULT 3

AAC68777
ID AAC68777 standard; cDNA; 1254 BP.
XX AAC68777;
AC
XX 20-FEB-2001 (first entry)
DT
XX Human death domain containing receptor DR3 coding sequence.
DE
XX Human; death domain containing receptor; DR3; cancer;
KW autoimmune disorder; inflammation; cardiovascular disorder; infection;
KW neurodegenerative disease; angiogenesis; ss.
XX Homo sapiens.
OS
XX WO200064465-A1.
PN
XX 02-NOV-2000.
PD
XX 21-APR-2000; 2000WO-US10741.
PF
XX 22-APR-1999; 99US-0130488.
PR 28-MAY-1999; 99US-0136741.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (UNMI) UNIV MICHIGAN.
PA (YUGG/) YU G.
PA (NIJ/) NI J.
PA (GENT/) GENTZ R L.

PA (DILL/) DILLON P J.
PA (DIXI/) DIXIT V M.
XX
XX Yu G, Ni J, Gentz RL, Dillon PJ, Dixit VM;
DR MPI; 2000-687263/67.
DR P-PSDB; AAB36265.

PT Treating graft-versus-host disease, cancer, immunodeficiency or an
PT autoimmune disease comprising administering an antibody to Death Domain
PT Containing Receptor proteins and a second therapeutic agent -
XX
XX Example 2B; Fig 2; 273pp; English.

CC The present invention provides the protein and coding sequences for two
CC death domain containing receptors, designated DR3 and DR3-V1. These
CC receptors are involved in apoptosis, and the sequences given can be used
CC in the treatment of cancers, infections, cardiovascular disorders such as
CC arrhythmias, ischemia, aneurysms, arterial occlusive diseases, embolisms
CC and congenital heart defects, neurodegenerative diseases including
CC Alzheimer's and Parkinson's diseases, autoimmune diseases such as multiple
CC sclerosis, arthritis, diabetes, Graves' disease, asthma and psoriasis,
CC and to promote angiogenesis and wound healing.

XX SQ Sequence 1254 BP; 201 A; 420 C; 407 G; 226 T; 0 other;

Alignment Scores:
Pred. No.: 7.96e-72 Length: 1254
Score: 1038.00 Matches: 174
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-09-993-234-6_COPY_25_198 (1-174) x AAC68777 (1-1254)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGly 20
DB 73 CAGGGCGGCACTCGTAGCCCCAGAGTGTGACTGTGCCGGTGACTTCCACAAGAATTGGT 132
QY 21 LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
DB 133 CTGTTTGTGTGACAGAGCGTGCCACGGGCACTACCTGAAGGCCCTTGACAGGAGCC 192
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
DB 193 TGGCGCAACTCCACCTGCGCTGTGTGTGCCCAAGACACCTTCTTGCGCTGGGAGAACCC 252
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
DB 253 CATAATCTGTAATGTGCCCGCTGCGCCAGGCTGTGATGAGCAGGCGCTCCAGGTGGCGCTG 312
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
DB 313 GAGAACTGTTCAGACAGTGCGCCAGACCGCTGTGGCTGTAAAGCCAGGCTGTGGAGCC 372
QY 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120
DB 373 TGCAGGTCAAGCAATGTGTACAGAGTTCACCTTCTACTGCCAACCATGCGTAGACTGC 432
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
DB 433 GGGGCCCTGCACCGCCACACACGGCTACTGTTCGCCGACAGATACTGACTGTGGAGCC 492
QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
DB 493 TGCCTGCTGGCTTCTATGAACATGGCGATGGCTGCTGCTGCCACGAGCACCCTG 552
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArg 174
DB 553 GGGAGCTGTCCAGAGCGCTGTGCCGCTGTCTGTGGCTGAGG 594

RESULT 4

AA91180
ID AAT91180 standard; cDNA; 1634 BP.
XX
AC AAT91180;
XX
DT 14-APR-1998 (first entry)
XX
DE Human apoptosis protein Apo-3 cDNA clone FH20.57.
XX
KW Apo-3; apoptosis; human; therapy; drug screening; ss.
XX
OS Homo sapiens.
XX
FH Key
FT CDS Location/Qualifiers
FT sig_peptide 89..160
FT /tag= a
FT /tag= b
FT /note= "determined by hydropathy analysis"
FT mat_peptide 161..1339
FT /tag= c
XX
PN WO9737020-A1.
XX
PD 09-OCT-1997.
XX
PF 31-MAR-1997; 97WO-0605230.
XX
PR 23-SEP-1996; 96US-0710802.
PR 01-APR-1996; 96US-0625328.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ;
XX
DR WPI; 1997-503105/46.
XX
PT Polypeptide(s) Apo-3 and Apo-2LI - useful for regulating apoptosis
PT in mammalian cells
XX
PS Example 1; Page 45-46; 70pp; English.
XX
XX cDNA clone FH20.57 (ATCC 55820) codes for a novel polypeptide (see
CC W26709), designated Apo-3, that stimulates or induces apoptotic
CC activity in mammalian cells. It was isolated from a human foetal
CC heart cDNA library by screening with probes (see T91183-84) based
CC on an EST sequence (GenBank locus W71984) that showed homology to
CC the intracellular domain of human TNFRI and CD95. Amino acid
CC residues 1-181 of Apo-3 are identical to another novel apoptosis
CC polypeptide, Apo-2LI (see W26708). Nucleic acids encoding Apo-3
CC can be used diagnostically for tissue-specific typing and to
CC produce recombinant Apo-3 polypeptides, especially the
CC extracellular domain (amino acids 1-198) or death domain (amino
CC acids 338-417). Apo-3 can be used to induce apoptosis or
CC NF-kappa-N- or JNK-mediated gene expression for therapeutic
CC purposes. Non-human transgenic animals containing cells that
CC express Apo-3 nucleic acid, and knockout animals containing
CC cells that have an altered Apo-3 gene, can be used in drug
CC screening and development.
XX
SQ Sequence 1634 BP; 300 A; 528 C; 519 G; 287 T; 0 other;

Alignment Scores:
Pred. No.: 1.08e-71 Length: 1634
Score: 1038.00 Matches: 174
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-09-993-234-6_COPY_25_198 (1-174) x AAT91180 (1-1634)
QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGly 20

Db 161 CAGGGCGGCACTCGTAGCCCCAGGTGTGACTGTGCCGGTACTTCCACAGAGATGTGT 220
QY 21 LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
Db 221 CTGTTTGTGTCAGAGGCTGCCAGCGGGGACACTACCTGAAGGCCCTTGCACGGAGCCC 280
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db 281 TGGCGCACTCCACCCTGCTGTGTGTCCCAAGACACCTTCTTGCCCTGGAGAACAC 340
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db 341 CATATTTCTGAATGTGCCCTGCTGCCAGGCTGTGATGAGCAGGCCCTCCAGGTGGCTG 400
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
Db 401 GAGAACTGTTACAGAGTGGCCGACACCCGCTGTGGCTGTAAAGCCAGCTGGTTGGAG 460
QY 101 CysGlnValSerGlnCysValSerSerSerProPheTyrCysGlnProCysLeuAspCys 120
Db 461 TGCCAGGTACAGCCAAATGTGTGACAGAGTTCACCCCTTCTACTGCCAACCATGCTGACTGC 520
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 521 GGGGCCCTGCACCGCCACACAGGCTACTCTGTTCGCCGACAGATACTGACTGTGGACCC 580
QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db 581 TGCCCTGCTGCTTCTATGACATGCGGATGGCTGGCTGCTCTGCCCCACGACACCCCTG 640
QY 161 GlySerCysProGlnArgCysAlaAlaValCysGlyTrpArg 174
Db 641 GGGAGCTGTCCAGAGCGCTGTGCCGCTGTCTGTGCTGGAGG 682

RESULT 5
AAH27782
ID AAH27782 standard; DNA; 1634 BP.
XX
XX AAH27782;
AC
XX
DT 15-AUG-2001 (first entry)
XX
DE Human genomic DNA encoding a rheumatoid arthritis associated protein.
XX
KW Rheumatoid arthritis; transmembrane protein; human; ds.
XX
OS Homo sapiens.
XX
FH Key
FT CDS Location/Qualifiers
FT CDS 89..1342
FT /tag= a
FT /product= "Rheumatoid arthritis associated protein"
XX
PN WO200132921-A2.
XX
PD 10-MAY-2001.
XX
PF 01-NOV-2000; 2000WO-JP07690.
XX
PR 01-NOV-1999; 99JP-0310805.
XX
PA (SHIO/) SHIOZAWA S.
XX
PI Shiozawa S, Konishi Y;
XX
DR WPI; 2001-308750/32.
DR P-PSDB; AAB97370.
XX
PT Diagnosing rheumatoid arthritis by probing digested human genomic DNA
PT or comparing expression of mRNA or polypeptide of a region of
PT transmembrane protein
XX

PS Claim 1; Page 14-18; 21pp; Japanese.

XX This invention relates to a method of diagnosing chronic rheumatoid
CC arthritis by digesting human genomic DNA with EcoRI and hybridizing it
CC with a probe containing a fragment of the present sequence which
CC represents DNA encoding a transmembrane protein. The method is used for
CC the diagnosis of chronic rheumatoid arthritis, and for developing new
CC treatments.

XX
SQ Sequence 1634 BP; 300 A; 528 C; 519 G; 287 T; 0 other;

Alignment Scores:

Pred. No.:	1.08e-71	Length:	1634
Score:	1038.00	Matches:	174
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	22	Gaps:	0

US-09-993-234-6_COPY_25_198 (1-174) x AAL47186 (1-1634)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
|||
Db 161 CAGGGCGCACTCGTAGCCCCAGGTGTGACTGTGCCGGTGACTTCACAGAAGATTGGT 220
QY 21 LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
|||
Db 221 CTGTTTGTGTGACAGAGGCTGCCAGGGGGGCACTACCTGAAGGCCCTTGACAGGAGCCC 280
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
|||
Db 281 TGGCGCACTCCACCTGCTGTGTGTCTCCCAAGACACACCTTCTTGCGCTGGAGAACCCAC 340
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
|||
Db 341 CATAAATTCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCGCTCCAGGTGGCGCTG 400
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
|||
Db 401 GAGAACTGTTCAGCAGTGGCCGACACCGCTGTGGCTGTAAAGCCAGGCTTGTGTGAG 460
QY 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120
|||
Db 461 TGCCAGGTCAAGCAATGTGTCAAGCACTTCTACTGCCAACCATTGCTAGACTGC 520
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
|||
Db 521 GGGGCCCTGCACCGCCACACACGGCTACTGTTCGCCGACAGATGACTGTGGAGCC 580
QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
|||
Db 581 TGCCTGCTGCTTCTATGAACATGGCGATGGCTGCGTGTCTGCTGCCCCACGAGCACCTG 640
QY 161 GlySerCysProGluArgCysAlaValCysGlyTrpArg 174
|||
Db 641 GGGAGCTGTCCAGAGCGCTGTGCCGTGTGTGGCTGAGG 682

RESULT 6

AAL47186

ID AAL47186 standard; cDNA; 1634 BP.

XX AC AAL47186;

XX DT 22-AUG-2002 (first entry)

DE Human rheumatoid arthritis associated DR3 gene related cDNA #1.

KW Human; DR3; rheumatoid arthritis; antirheumatic; antiarthritic;

XX gene therapy; gene; ss.

OS Homo sapiens.

XX Key

Key Location/Qualifiers

FT CDS 89..1342
FT /*tag- a
FT /product- "AAO17879"

PN WO200234912-A1.

PD 02-MAY-2002.

PF 24-OCT-2001; 2001WO-JP09313.

PR 24-OCT-2000; 2000JP-0324296.

PR 27-MAR-2001; 2001JP-0090546.

PR 30-MAR-2001; 2001JP-0099990.

PA (NEWI-) NEW IND RES ORG.

PA (SHIO/) SHIOZAWA S.

PI Shiozawa S, Konishi Y;

DR WPI; 2002-417132/44.

DR P-PSDB; AAO17879.

XX Genomes, particularly DR3 genomic DNA, participating in rheumatoid
XX arthritis via mutation, useful in evaluating disease onset and its
XX possibility and providing therapy and remedies -
XX Example 1; Page 66-69; 84pp; Japanese.

CC The present invention relates to the human DR3 gene, which is associated
CC with rheumatoid arthritis. Certain mutations in the gene can be linked to
CC the disease. The sequences can be used to evaluate disease onset and its
CC possibility and to provide therapy and remedies. The present sequence is
CC a coding sequence described in the exemplification of the invention.

SQ Sequence 1634 BP; 300 A; 528 C; 519 G; 287 T; 0 other;

Alignment Scores:

Pred. No.:	1.08e-71	Length:	1634
Score:	1038.00	Matches:	174
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	24	Gaps:	0

US-09-993-234-6_COPY_25_198 (1-174) x AAL47186 (1-1634)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
|||
Db 161 CAGGGCGCACTCGTAGCCCCAGGTGTGACTGTGCCGGTGACTTCACAGAAGATTGGT 220
QY 21 LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
|||
Db 221 CTGTTTGTGTGACAGAGGCTGCCAGGGGGGCACTACCTGAAGGCCCTTGACAGGAGCCC 280
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
|||
Db 281 TGGGGCACTCCACCTGCTGTGTGTCTCCCAAGACACACTTCTTGCGCTGGGAGAACCCAC 340
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
|||
Db 341 CATAAATTCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCGCTCCAGGTGGCGCTG 400
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
|||
Db 401 GAGAACTGTTCAGCAGTGGCCGACACCGCTGTGGCTGTAAAGCCAGGCTTGTGTGAG 460
QY 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120
|||
Db 461 TGCCAGGTCAAGCAATGTGTCAAGCACTTCTACTGCCAACCATTGCTAGACTGC 520
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
|||
Db 521 GGGGCCCTGCACCGCCACACACGGCTACTGTGTCTGCCGACAGATGACTGTGGAGCC 580

OY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrIleu 160
Db 581 TGCCTGCCTGGCTTCTATGAACATGGCGATGGCTGCGTGTCTGCTGGCCACGAGACCCCTG 640
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArg 174
Db 641 GGGAGCTGTCCAGAGCGCTGTGCCGCTGTCTGTGGCTGAGG 682
RESULT 7
AAC91477
ID AAC91477 standard; cDNA; 1662 BP.
XX
AC AAC91477;
XX 21-MAR-2001 (first entry)
DT Human PRO779 cDNA.
XX
DE Human; PRO; antiinflammatory; dermatological; antiarthritic;
KW antirheumatic; cardiant; antianaemic; immunosuppressive; antithyroid;
KW antidiabetic; nootropic; neuroprotective; hepatotropic; virucide;
KW antiallergic; antiasthmatic; immune related disorder;
KW hepatobiliary disease; autoimmune disease; allergy; ss.
XX
OS Homo sapiens.
XX
PN WO200073452-A2.
XX
PD 07-DEC-2000.
XX
PF 02-JUN-2000; 2000WO-US15264.
XX
PR 02-JUN-1999; 99WO-US12252.
PR 20-JUL-1999; 99US-0144732.
PR 20-JUL-1999; 99US-0144758.
PR 28-JUL-1999; 99US-0146222.
PR 01-SEP-1999; 99WO-US20111.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 29-OCT-1999; 99US-0162506.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28634.
PR 09-DEC-1999; 99US-0170262.
PR 20-DEC-1999; 99WO-US30911.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Chan B, Goddard A, Godowski PJ, Gurney AL;
PI Hebert C, Henzel W, Kabakoff RC, Shelton DL, Tumas D, Watanabe CK;
PI Wood WI;
XX
DR WPI; 2001-025253/03.
DR P-PSDB; AAB50918.
XX
PT Thirty three nucleic acids encoding PRO polypeptides which are useful
PT in the diagnosis and treatment of immune related disorders, e.g.
PT systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
PT thyroiditis and diabetes mellitus -
XX

PS Claim 48; Fig 33; 218bp; English.
XX The present sequence is one of thirty three nucleic acids encoding PRO
CC polypeptides. The PRO polypeptides, anti-PRO antibodies, agonists and
CC antagonists are useful for treating and diagnosing immune related
CC disorders such as systemic lupus erythematosus, rheumatoid arthritis,
CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
CC systemic scleriosis, idiopathic inflammatory myopathies, Sjogren's
CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,
CC immune-mediated renal disease, demyelinating diseases of the central
CC and peripheral nervous systems (such as multiple sclerosis, idiopathic
CC demyelinating polyneuropathy or Guillain-Barre syndrome, and chronic
CC inflammatory demyelinating polyneuropathy), hepatobiliary diseases
CC (such as infectious, autoimmune chronic active hepatitis, primary
CC biliary cirrhosis, granulomatous hepatitis and sclerosing cholangitis),
CC inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's
CC disease, autoimmune or immune-mediated skin diseases (such as bullous
CC skin diseases, erythema multiforme, contact dermatitis, psoriasis),
CC allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,
CC food hypersensitivity and urticaria), immunological diseases of the
CC lung (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis
CC and hypersensitivity pneumonitis), transplantation associated diseases
CC including graft rejection and graft-versus-host diseases.
XX
SQ Sequence 1662 BP; 302 A; 540 C; 531 G; 289 T; 0 other;

Alignment Scores:
Pred. No.: 1.1e-71 Length: 1662
Score: 1038.00 Matches: 174
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0

US-09-993-234-6_COPY_25_198 (1-174) x AAC91477 (1-1662)
QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGly 20
Db 175 CAGGGCGGCACATCGTAGCCCCAGGTGTGACTGTGCCGGTGACTTCCACAAGAATTGGT 234
QY 21 LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
Db 235 CTGTTTGTGTGCAGAGGCTGCCACAGCGGGGCACTACTGAAGGCCCTTGACAGGAGCCC 294
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db 295 TCGGGCAACTTCACCTGCTGTGTGTCCCAAGACACACTTCTTGCCCTGGGAGAACCAC 354
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db 355 CATATTCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGAGGCTCCACAGTGGCGCTG 414
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
Db 415 GAGAACTGTTCAGCAGTGGCCGACACCGCTGTGGCTGTAAAGCCAGGCTGTTGTGAG 474
QY 101 CysGlnValSerGlnCysValSerSerSerProPheTyrCysGlnProCysLeuAspCys 120
Db 475 TGCCAGGTTCAGCCAATGTGTACAGCACTTCACCCCTTACTGCCCAACCATGCTAGACTGC 534
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 535 GGGGCCCTGCACCGCCACACACGGCTACTCTGTTCGCCGACAGATACTGACTGTGGACC 594
QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrIleu 160
Db 595 TGCCTGCCTGGCTTCTATGAACATGGCGATGGCTGCGTGTCTGCTGGCCACGAGACCCCTG 654
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArg 174
Db 655 GGGAGCTGTCCAGAGCGCTGTGCCGCTGTCTGTGGCTGAGG 696

RESULT 8
ABK40265
ID ABK40265 standard; cDNA; 1662 BP.
XX
AC ABK40265;
XX
DT 15-JUL-2002 (first entry)
XX
DE cDNA encoding human PRO779 polypeptide.
XX
KW Human; PRO; benign tumour; malignant tumour; lymphoid malignancy;
KW leukaemia; neuronal disorder; stromal disorder; blastocoelec disorder;
KW inflammatory disorder; immune disorder; angiogenic disorder;
KW gene therapy; cytostatic; neuroprotective; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200153486-A1.
XX
PD 26-JUL-2001.
XX
PF 11-FEB-2000; 2000WO-US03565.
XX
PR 08-MAR-1999; 99WO-US05028.
PR 11-MAR-1999; 99US-123972P.
PR 11-MAY-1999; 99US-133459P.
PR 02-JUN-1999; 99WO-US12252.
PR 22-JUN-1999; 99US-140650P.
PR 22-JUN-1999; 99US-140653P.
PR 20-JUL-1999; 99US-144758P.
PR 26-JUL-1999; 99US-145698P.
PR 28-JUL-1999; 99US-146222P.
PR 17-AUG-1999; 99US-149395P.
PR 31-AUG-1999; 99US-151689P.
PR 01-SEP-1999; 99WO-US20111.
PR 15-SEP-1999; 99WO-US21090.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.
PR 05-JAN-2000; 2000WO-US00219.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL, Hillan KJ;
PI Marsters SA, Pan J, Pittl RM, Roy MA, Smith V, Stone DM;
PI Watanabe CK, Wood WI;
XX
DR WPI; 2002-205567/26.
DR P-PSDB; AAU86139.
XX
PT Thirty five nucleic acids encoding PRO polypeptides, useful for
PT treating benign or malignant tumours, leukaemias and lymphoid
PT malignancies, inflammatory, angiogenic and immunologic disorders -
XX
PS Claim 50; Fig 23; 302pp; English.
XX
CC The present invention relates to the isolation of novel human PRO
CC polypeptides and the polynucleotide sequences encoding them. The
CC PRO polypeptides, agonists, antagonists or anti-PRO antibodies are
CC useful for treating benign or malignant tumours (e.g. renal, kidney,
CC bladder, breast, etc), leukaemias and lymphoid malignancies, other
CC disorders such as neuronal, gliol, astrocytal, hypothalamic, glandular,
CC macrophagal, stromal and blastocoelec disorders, inflammatory, immune
CC and angiogenic disorders. The polynucleotide sequences are also
CC useful in gene therapy. ABK40254-ABK40288 encode for the human PRO
CC polypeptides of the invention.
XX
SQ Sequence 1662 BP; 302 A; 540 C; 531 G; 289 T; 0 other;

Alignment Scores:
Pred. No.: 1.1e-71
Score: 1038.00
Percent Similarity: 100.00%

Length: 1662
Matches: 174
Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 24 Gaps: 0
US-09-993-234-6_COPY_25_198 (1-174) x ABK40265 (1-1662)
QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
DB 175 CAGGCGCGACCTGTAAGCCAGGCTGTGACTGTCCGGTGACTTCCACAGAAGATTGGT 234
QY 21 LeupheCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
DB 235 CTGTTTGTGAGAGGCTGCCAGCGGGGACTACCTGAAGGCCCTTGACAGAGGCC 294
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
DB 295 TGGCGCACTGCCACTGCTGTGTGTCCCAAGACACACTTCTTGCCCTGGAGAACCCAC 354
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
DB 355 CATATTTCTGAATGTGCCCCGCTGCCAGGCTGTGATGACAGAGCCCTCCAGGTGGCGCTG 414
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
DB 415 GAGAACTGTTCAGACAGTGGCCGACACCCGCTGTGGCTGTAAGCCAGGCTGTGGAG 474
QY 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120
DB 475 TGCCAGGTCAAGCAATGTGTACAGACAGTACCTTACTGACCAACCAATGCTAGACTGC 534
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
DB 535 GGGGCCCTGCACCCACACACACAGGCTACTGTCTTCCCGCAGAGATACTACTGTGGACC 594
QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
DB 595 TGCCGTGCTGCTTCTATGACATGCGGATGCGTGCCTGCTGCCCGCAGAGCACCCCTG 654
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArg 174
DB 655 GGGAGCTGTCCAGAGCGCTGTGCGCTGTGTGTGGAGG 696
RESULT 9
ABL64119
ID ABL64119 standard; DNA; 1743 BP.
XX
AC ABL64119;
XX
DT 15-MAY-2002 (first entry)
XX
DE Breast cancer related gene sequence SEQ ID NO:2456.
XX
KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW gene; ds.
XX
OS Homo sapiens.
XX
PN WO200194629-A2.
XX
PD 13-DEC-2001.
XX
PF 30-MAY-2001; 2001WO-US10838.
XX
PR 05-JUN-2000; 2000US-209473P.
PR 05-JUN-2000; 2000US-209531P.
PR 18-SEP-2000; 2000US-233133P.
PR 18-SEP-2000; 2000US-233617P.
PR 20-SEP-2000; 2000US-234009P.
PR 20-SEP-2000; 2000US-234034P.
PR 20-SEP-2000; 2000US-234052P.
PR 22-SEP-2000; 2000US-234509P.

PR 22-SEP-2000; 2000US-234567P.
PR 25-SEP-2000; 2000US-234923P.
PR 25-SEP-2000; 2000US-234924P.
PR 25-SEP-2000; 2000US-235077P.
PR 25-SEP-2000; 2000US-235082P.
PR 25-SEP-2000; 2000US-235134P.
PR 25-SEP-2000; 2000US-235280P.
PR 26-SEP-2000; 2000US-235637P.
PR 26-SEP-2000; 2000US-235638P.
PR 27-SEP-2000; 2000US-235711P.
PR 27-SEP-2000; 2000US-235720P.
PR 27-SEP-2000; 2000US-235840P.
PR 27-SEP-2000; 2000US-235863P.
PR 28-SEP-2000; 2000US-236028P.
PR 28-SEP-2000; 2000US-236032P.
PR 28-SEP-2000; 2000US-236033P.
PR 28-SEP-2000; 2000US-236034P.
PR 28-SEP-2000; 2000US-236109P.
PR 28-SEP-2000; 2000US-236111P.
PR 29-SEP-2000; 2000US-236842P.
PR 29-SEP-2000; 2000US-236891P.
PR 02-OCT-2000; 2000US-237172P.
PR 02-OCT-2000; 2000US-237173P.
PR 02-OCT-2000; 2000US-237278P.
PR 02-OCT-2000; 2000US-237294P.
PR 02-OCT-2000; 2000US-237295P.
PR 02-OCT-2000; 2000US-237316P.
PR 03-OCT-2000; 2000US-237425P.
PR 03-OCT-2000; 2000US-237598P.
PR 03-OCT-2000; 2000US-237604P.
PR 03-OCT-2000; 2000US-237606P.
PR 03-OCT-2000; 2000US-237608P.
PR 01-NOV-2000; 2000US-244867P.
PR 01-NOV-2000; 2000US-245084P.
PA (AVAL-) AVALON PHARM.
XX
PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppet DR, Weaver Z;
XX
DR WPI; 2002-188264/24.
XX
PT Screening for anti-neoplastic agent involves exposing cells to a
PT chemical agent to be tested for anti-neoplastic activity, and
PT determining a change in expression of a gene of a signature gene set -
XX
PS Claim 1; SEQ ID 2456; 44pp; English.
XX
CC The present invention describes a method (M1) for screening for an
CC anti-neoplastic agent. The method involves exposing cells to a chemical
CC agent to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)'
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening
CC an anti-neoplastic agent, and can be used for producing a product which
CC is the data collected with respect to the anti-neoplastic agent as a
CC result of M1, and the data is sufficient to convey the chemical
CC structure and/or properties of the agent. M1 can be used in the
CC treatment of cancer such as colon, breast, stomach, lung, thyroid,
CC oesophageal, ovarian, kidney, prostate or pancreatic cancer,
CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
CC carcinoma, papillary carcinoma and Wilm's tumour.
XX
SQ Sequence 1743 BP; 347 A; 543 C; 549 G; 304 T; 0 other;

Alignment Scores:
Pred. No.: 1.17e-71 Length: 1743
Score: 1038.00 Matches: 174
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0
DB: 24 Gaps: 0
US-09-993-234-6_COPY_25_198 (1-174) x ABL64119 (1-1743)
QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
DB 141 CAGGGCGGCACTCGTAGCCCGCAGGTGTGACTGTGCCGGTGACTTCCACAGAAGATGTGT 200
QY 21 LeupheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
DB 201 CTGTTTGTGTGACAGAGGCTGCCAGCGGGGACACTACCTGAAGGCCCTTGACAGGAGCCC 260
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
DB 261 TGGGGCAACTCCACCTGCCCTGTGTGTGCCCAAGACACCTTCTTGCCCTGGAGAACCTAC 320
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
DB 321 CATATTTCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCTCCACAGGTGGCGCTG 380
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
DB 381 GAGAACTGTTACAGCAGTGGCCGACACCCGCTGTGGCTGTAAAGCAGGCTGGTTGTGAG 440
QY 101 CysGlnValSerGlnCysValSerSerSerProPheTyrCysGlnProCysLeuAspCys 120
DB 441 TGCCAGGTCAGCCAAATGTGTCAAGCAGTTCACTCCCTTCTACTGCCAACCATGCTTACACTGC 500
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
DB 501 GGGGCCCTGCACCGCCACACACGGCTACTGTGTCCCGCAGAGATACTGACTGTGGAGCC 560
QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
DB 561 TGCCCTGCTGCTTCTATGAACATGGGATGGCTGTGCTGCTGCCCGCAGAGACACCTCG 620
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTyrArg 174
DB 621 GGGAGCTGTCCAGAGCGCTGTGCCGCTGTCTGTGGCTGGAGG 662
RESULT 10
AAT89426
ID AAT89426 standard; cDNA: 1783 BP.
XX
AC AAT89426;
XX
DT 02-MAR-1998 (first entry)
XX
DE Death domain containing receptor DR3-V1 cDNA.
XX
KW Death domain containing receptor; DR3-V1; human; apoptosis;
KW inflammation; NF-kappaB; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 198..1484
FT sig_peptide 198..302 /*tag= a
FT mat_peptide 304..1481 /*tag= b
FT /*tag= c
PN WO9733904-A1.
XX
PD 18-SEP-1997.
XX
PF 17-OCT-1996; 96WO-US16849.
XX
PR 12-MAR-1996; 96US-0013285.
XX
PA (HUMA-) HUMAN GENOME SCI INC.

PA (UNMI) UNIV MICHIGAN.
XX
PI Dillon PJ, Dixit VM, Gentz RL, Ni J, Yu G;
XX
DR WPI; 1997-470812/43.
DR P-PSDB; AAW31516.
XX
PT Death domain containing receptor polypeptide(s) DR3 and DR3-V1
PT for activation of apoptosis and NF-kappaB, antagonists can be used
PT to treat inflammatory diseases
XX
PS Claim 2; Page 71-73; 108pp; English.
XX
CC This cDNA clone, deposited as ATCC 97456, codes for human death
CC domain containing receptor DR3-V1 (see AAW31516), a novel member of
CC the tumour necrosis factor receptor family. It was isolated from a
CC cDNA library derived from cells of a human testis tumour. Related
CC death domain containing receptor DR3 cDNA (see AAT89427) was isolated
CC from a HUVEC cDNA library. The genes have also been identified in
CC cDNA libraries of foetal liver, foetal brain, tonsil and leukocyte.
CC Nucleic acids encoding full-length or mature DR3-V1 can be used to
CC produce recombinant polypeptides in transformed host cells. These
CC polypeptides can be used to treat diseases and disorders associated
CC with the inhibition of apoptosis. Antagonists, such as antibodies
CC raised against DR3-V1, can be used to treat diseases and disorders
CC associated with increased apoptosis and for treating inflammatory
CC diseases and disorders.
XX
SQ Sequence 1783 BP; 330 A; 562 C; 564 G; 327 T; 0 other;

Alignment Scores:
Pred. No.: 1.2e-71 Length: 1783
Score: 1038.00 Matches: 174
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-09-993-234-6_COPY_25_198 (1-174) x AAT89426 (1-1783)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
Db 303 CAGGGCGGCACTCGTAGCCCCCAGGTGTGACTGTGCCGGTGACTTCCACAAGAAGATTGGT 362
QY 21 LeupheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
Db 363 CTGTTTGTGTGACAGAGGCTGCCAGCGGGGCACTACTGAGGCCCTTGACAGGAGCC 422
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db 423 TGGCGCACTCCACCTGCTGTGTGTCCCAAGACACCTTCTTGCGCTGGAGAACCAC 482
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db 483 CATAAATTCTGAATGTGCCCGCTGCCAGGCCCTGTGATGAGCAGGCCCTCCAGGTGGCGCTG 542
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTyrPheValGlu 100
Db 543 GAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGGCTGTAAAGCCAGGCTGTTGTGAG 602
QY 101 CysGlnValSerGlnCysValSerSerSerProPheTyrCysGlnProCysLeuAspCys 120
Db 603 TGCCAGGTCAGCCAATGTGTGACAGAGTTCACCTTCTACTGCCAACCATGCGCTAGACTGC 662
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 663 GGGGCCCTGCACCGCCACACAGGCTACTGTGTTCCCGAGAGATACTGACTGTGGAGCC 722
QY 141 CysLeuProGlyPheTyrGlnHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db 723 TGCCCTGGCTGGCTTCTATGAACAATGGCGATGGCTGCGTCTGCTGCCCCACGAGACCCCTG 782
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTyrParg 174

Db 783 GGGAGCTGTCCAGAGCGCTGTGCGCTGTGTGGCTGAGG 824

RESULT 11
ID AAX00924
XX AAX00924 standard; cDNA; 1783 BP.
XX
AC AAX00924;
XX
DT 25-MAR-1999 (first entry)
XX
DE Death domain containing receptor polypeptide (DR3-V1) encoding cDNA.
XX
KW Death domain; receptor; DR3-V1; DR3; recombinant; ds.
XX
OS Homo sapiens.
XX

Key Location/Qualifiers
FT CDS 198..1484
FT /tag= a
FT /product= "Death domain containing receptor DR3-V1"
FT sig_peptide 198..300
FT mat_peptide 301..1481
FT /tag= c
XX
PN JP11000170-A.
XX
PD 06-JAN-1999.
XX
PE 12-MAR-1997; 97JP-0057503.
XX
PR 06-FEB-1997; 97US-0037341.
PR 12-MAR-1996; 96US-0013285.
PR 17-OCT-1996; 96US-0028711.
XX

PA (HUMA-) HUMAN GENOME SCI INC.
PA (UNMI) UNIV MICHIGAN.
XX
XX
DR WPI; 1999-124390/11.
DR P-PSDB; AAW95537.
XX
XX

PT New death domain containing receptor and recombinant vector -
PT optionally comprising leader sequence
XX
PS Claim 2; Fig 1, 2; 50pp; Japanese.
XX

CC The invention provides nucleotide sequences encoding death domain
CC containing receptor polypeptides DR3-V1 and DR3. The DR3-V1 cDNA clone
CC is contained in ATCC deposition No. 97456 and the DR3 cDNA clone is
CC contained in ATCC deposition No. 97757. Recombinant vectors comprising
CC the nucleic acid sequences and optionally the leader sequences are
CC used for the recombinant production of the proteins. The present
CC sequence represents a cDNA encoding the death domain containing
CC receptor polypeptide (DR3-V1).
XX

SQ Sequence 1783 BP; 330 A; 562 C; 564 G; 327 T; 0 other;

Alignment Scores:
Pred. No.: 1.2e-71 Length: 1783
Score: 1038.00 Matches: 174
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 20 Gaps: 0

US-09-993-234-6_COPY_25_198 (1-174) x AAX00924 (1-1783)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
Db 303 CAGGGCGGCACTCGTAGCCCCCAGGTGTGACTGTGCCGGTGACTTCCACAAGAAGATTGGT 362
QY 21 LeupheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40

DB 363 CTGTTTGTTCAGAGGCTGCCAGCGGGCACTACCTGAAGGCCCTTGACAGGACCC 422 .

QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60

DB 423 TGGCGCACTCCACCTGCTGTGTGTCCTCCCAAGACACCTTCTTGCGCTGGAGAACCC 482

QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80

DB 483 CATATTTCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGAGCCCTCCAGGTGGCCCTG 542

QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100

DB 543 GAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGGCTGTAAAGCCAGGCTGTTGTGAG 602

QY 101 CysGlnValSerGlnCysValSerSerProPheTyrcysGlnProCysLeuAspCys 120

DB 603 TGGCAGGTCAGCCAATGTGTACAGAGTTCACCCCTTCTACTGCCAACCATTGCTAGACTGC 662

QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140

DB 663 GGGGCCCTGCACCGCCACACAGCGCTACTCTGTCCCGCAGAGATACTGACTGTGGGACC 722

QY 141 CysLeuProGlyPheTyrcysGlnHisGlyAspGlyCysValSerCysProThrSerThrLeu 160

DB 723 TGCCTGCCTGGCTCTATGACATGGCGATGGCTGCTGCTGCCCGCCAGCAGACCCCTG 782

QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArg 174

DB 783 GGGAGCTGTCCAGAGCGCTGTGCCCTGTGTGGCTGGAGG 824

RESULT 12

AAC68776

ID AAC68776 standard; cDNA; 1783 BP.

XX AAC68776;

AC

XX 20-FEB-2001 (first entry)

DT

XX Human death domain containing receptor DR3-V1 coding sequence.

DE

XX Human; death domain containing receptor; DR3-V1; cancer;

KW autoimmune disorder; inflammation; cardiovascular disorder; infection;

KW neurodegenerative disease; angiogenesis; ss.

XX Homo sapiens.

OS

XX WO200064465-A1.

PN

XX 02-NOV-2000.

PD

XX 21-APR-2000; 2000WO-US10741.

PF

XX 22-APR-1999; 99US-0130488.

PR 28-MAY-1999; 99US-0136741.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

PA (UNMI) UNIV MICHIGAN.

PA (YUGG/) YU G.

PA (NIJJ/) NI J.

PA (GENTZ/) GENTZ R L.

PA (DILL/) DILLON P J.

PA (DIXI/) DIXIT V M.

XX

PI YU G, NI J, Gentz RL, Dillon PJ, Dixit VM;

XX

DR WPI; 2000-687263/67.

DR P-PSDB; AAB36264.

XX

PT Treating graft-versus-host disease, cancer, immunodeficiency or an

PT autoimmune disease comprising administering an antibody to Death Domain

PT Containing Receptor proteins and a second therapeutic agent -

XX

PS Example 1; Fig 1; 273pp; English.

XX

CC The present invention provides the protein and coding sequences for two

CC death domain containing receptors, designated DR3 and DR3-V1. These

CC receptors are involved in apoptosis, and the sequences given can be used

CC in the treatment of cancers, infections, cardiovascular disorders such as

CC arrhythmias, ischaemia, aneurysms, arterial occlusive diseases, embolisms

CC and congenital heart defects, neurodegenerative diseases including

CC Alzheimer's and Parkinson's diseases, autoimmune disease such as multiple

CC sclerosis, arthritis, diabetes, Graves' disease, asthma and psoriasis,

CC and to promote angiogenesis and wound healing.

XX

SO Sequence 1783 BP; 330 A; 562 C; 564 G; 327 T; 0 other;

Alignment Scores:

Pred. No.: 1.2e-71 Length: 1783

Score: 1038.00 Matches: 174

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 21 Gaps: 0

US-09-993-234-6_COPY_25_198 (1-174) x AAC68776 (1-1783)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGly 20

DB 303 CAGGGCGCAGCTGTCAGGCCCCAGGTGTGACTGTGCCGGTGACTTCCACAGAGATTGGT 362

QY 21 LeuPheCysCysArgGlyCysProAlaGlyHisTyrcysLeuAlaProCysThrGluPro 40

DB 363 CTGTTTGTTCAGAGGCTGCCAGCGGGGCACTAAGAGGCCCTTGCCAGCAGGACCC 422

QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60

DB 423 TGGCGCACTCCACCTGCTGTGTGTGTCCTCCCAAGACACCTTCTTGCGCTGGAGAACCC 482

QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80

DB 483 CATATTTCTGAATGTGCCCGCTGCTGTGTCCTCCCAAGACACCTTCTTGCGCTGGAGAACCC 482

QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100

DB 543 GAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGCTGTAAAGCCAGGCTGTTGTGAG 602

QY 101 CysGlnValSerGlnCysValSerSerProPheTyrcysGlnProCysLeuAspCys 120

DB 603 TGGCAGGTCAGCCAATGTGTACAGAGTTCACCCCTTCTACTGCCAACCATTGCTAGACTGC 662

QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140

DB 663 GGGGCCCTGCACCGCCACACAGCGCTACTGTTCCGACAGATGACTGTGGACC 722

QY 141 CysLeuProGlyPheTyrcysGlnHisGlyAspGlyCysValSerCysProThrSerThrLeu 160

DB 723 TGCCTGCCTGGCTCTATGACATGGCGATGGCTGCTGCTGCCCGCCAGCAGACCCCTG 782

QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArg 174

DB 783 GGGAGCTGTCCAGAGCGCTGTGCCCTGTGTGGCTGGAGG 824

RESULT 13

AAV28700

ID AAV28700 standard; cDNA; 1847 BP.

XX

AC AAV28700;

XX

DT 20-AUG-1998 (first entry)

DT

XX Human apoptosis inducing receptor coding sequence.

DE

XX Apoptosis inducing receptor; AIR protein; human; cell death regulator;

KW Type I transmembrane protein; tumour cell death; autoimmune disease;

KW therapy; ss.

XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT CDS 236..1489
FT /*tag= a
FT /product= AIR
XX
PN W09814565-A1.
XX
XX 09-APR-1998.
PD
XX
PF 03-OCT-1997; 97WO-US17876.
XX
XX 04-OCT-1996; 96US-0044456.
PR
XX (IMMV) IMMUNEX CORP.
PA
XX Perkins PA;
PI
XX
XX WPI; 1998-240077/21.
DR P-PSDB; AAW57045.
DR
XX
PT DNA encoding apoptosis inducing receptor - which is Type I
PT transmembrane protein, useful for regulating cell death
XX
XX
PS Claim 2; Page 28-30; 45pp; English.
XX
XX This sequence encodes the human apoptosis inducing receptor (AIR) of the
CC invention. AIR is a Type I transmembrane protein, soluble forms of which
CC can be used to regulate cell death in a therapeutic setting. Soluble AIR
CC can also be used in vitro to block apoptosis or AIR-expressing cells, or
CC to screen agonists or antagonists of AIR activity. The cytoplasmic domain
CC of AIR can be used to develop assays for inhibitors of AIR-induced cell
CC death, which is useful to regulate cell death in a therapeutic setting as
CC well as in vitro. Agonists of AIR activity can be used to kill tumour
CC cells that express AIR, or T cells expressing AIR in autoimmune diseases.
XX
SQ Sequence 1847 BP; 316 A; 605 C; 579 G; 347 T; 0 other;

Alignment Scores:
Pred. No.: 1.25e-71 Length: 1847
Score: 1038.00 Matches: 174
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 19 Gaps: 0

US-09-993-234-6_COPY_25_198 (1-174) x AAV28700 (1-1847)

OY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
Db 308 CAGGGCGGCACCTGCTAGCCCCAGGTGTGACTGTGCCGGTGACTTCCACAAGAAGATTGGT 367

OY 21 LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
Db 368 CTGTTTGTGTGCAGAGGCTGCCAGCGGGGCACTACCTGAAGGCCCTTGACAGGAGCCC 427

OY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db 428 TGGGGCACTCCACCTGCTGTGTGTCCCAAGACACCTTCTTGGCTGGGAGAACAC 487

OY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db 488 CATTAATCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGAGCCTCCACAGTGGCGCTG 547

OY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
Db 548 GAGAACTGTTCAAGAGTGGCGGACACCGCTGTGGCTGTAAAGCCAGCGCTTGTGTGAG 607

OY 101 CysGlnValSerGlnCysValSerSerSerProPheTyrCysGlnProCysLysLeuAspCys 120
Db 608 TGCAGGTCAAGCAATGTGTCAAGAGTTACCCCTTCTACTGCGCAACCATGCTAGACTGC 667

OY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 668 GGGGCCCTGCACCGCCACACACAGCGCTACTGTGTCCCGCAGAGATACTGACTGTGGACC 727

OY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db 728 TGCCTGCTGGCTTCTATGACATGGCATGGCTGCGTGTCTGCCCCACGAGACACCCTG 787

OY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArg 174
Db 788 GGGAGCTGTCCAGACGCGCTGTGCCGCTGTGTGGCTGAGG 829

RESULT 14
AAAF83770
ID AAFA83770 standard; DNA; 1250 BP.
XX
XX AAFA83770;
AC
XX
DT 06-AUG-2001 (first entry)
XX
DE Nucleotide sequence of human TR3 gene.
XX
KW TR3; cell proliferation; leukemia; immunosuppressive; cytostatic;
KW dermatological; antiarthritic; antidiabetic; neuroprotective; cardiant;
KW antithyroid; antiinflammatory; antiallergic; T-cell-inhibitor; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1250
FT /*tag= a
FT /transl_except- "(pos:481..482, aa:Asp)"
FT /note= "this codon has an apparent 1 nucleotide
FT deletion which alters the reading frame"
FT /transl_except- "(pos:558..559, aa:Cys)"
FT /note= "this codon has an apparent 1 nucleotide
FT deletion which alters the reading frame"
FT /transl_except- "(pos:638..639, aa:Leu)"
FT /note= "this codon has an apparent 1 nucleotide
FT deletion which alters the reading frame"
FT sig_peptide 1..72
FT /*tag= b
FT mat_peptide 73..1247
FT /*tag= c

W0200135995-A2.
PN
XX
XX 25-MAY-2001.
PD
XX
PF 17-NOV-2000; 2000WO-US31692.
PR
XX 19-NOV-1999; 99US-0166583.
PR
XX (TITT/) TITILE T V.
PA (WEGM/) WEGMANN K W.
XX
XX Tittle TV, Wegmann KW;
PI
XX
DR WPI; 2001-343711/36.
DR P-PSDB; AAB84941.
XX
PT Composition for treatment of T-cell mediated disease e.g. arthritis,
PT cancer comprises a biologically active TR3-specific binding agent
PT especially a monoclonal antibody -
XX
PS Disclosure; Page 72; 77pp; English.
XX
CC The invention relates to a composition comprising a biologically active
CC TR3-specific binding agent (I) that binds to TR3 and inhibits the

CC proliferation of cells expressing TR3. (I) identified by the methods are
CC useful for treating a subject suspected of having a disease associated
CC with a proliferation of cells expressing TR3 especially leukemias or
CC lymphomas or a T-cell mediated disease especially autoimmune diseases
CC such as myasthenia gravis, systemic lupus erythematosus, rheumatoid
CC arthritis, diabetes, multiple sclerosis, sarcoidosis, myocarditis,
CC thyroiditis and tumours. (I) is also useful for treating a subject
CC suspected of having graft-versus-host disease, rejection of a
CC transplanted organ such as heart, liver, lung, kidney, pancreas, bowel,
CC skin or an appendage, or inflammatory diseases, allergies and contact
CC dermatitis. The present sequence represents the nucleotide sequence of
CC human TR3 gene.

XX SQ Sequence 1250 BP; 201 A; 419 C; 406 G; 224 T; 0 other;

Alignment Scores:

pred. No.:	3.67e-67	Length:	1250
Score:	978.00	Matches:	172
Percent Similarity:	98.85%	Conservative:	0
Best Local Similarity:	98.85%	Mismatches:	2
Query Match:	94.22%	Indels:	2
DB:	22	Gaps:	0

US-09-993-234-6_COPY_25_198 (1-174) x AAF83770 (1-1250)

QY 1 GINGLYGLYThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
DB 73 CAGGGCGGCACTCGTAGCCCGAGGTGTGACTGTGCGGTGACTTCCACAAGAAGATTGCT 132
QY 21 LeuPheCysCysArgGlyCysProAlaGlyHisLysLysLysAlaProCysThrGluPro 40
DB 133 CTGTTTGTGTGAGAGGCTGCCCCAGCGGGGCACTACTGAAGGCCCTTGACGGAGCC 192
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
DB 193 TCGCGCAACTCCACCTGCTGTGTGTCCCAAGACACCTTCTTGCGCTGGGAGAACAC 252
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
DB 253 CATAAATTCTGAATGTGCCCGCTGCCAGGCTGTGATGACAGCGCTCCAGGTGGCGCTG 312
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
DB 313 GAGAACTGTTCAGCAGGTGGCCGACACCCGCTGTGCTGTAAGCCAGGCTGTTGTGGAG 372
QY 101 CysGlnValSerGlnCysValSerSerProPheThrCysGlnProCysLeuAspCys 120
DB 373 TGCCAGGTACGCCAATGTGTACAGAGTTACCTTCTACTGCCAACCATGCTTAGACTGC 432
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
DB 433 GGGGCCCTGCACCGCACACCGGCTACTGTGTCCCGCAGAGATAC-GACTGTGGGACC 491
QY 141 CysLeuProGlyPheThrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
DB 492 TGCCCTGCTGCTTCTATGAACATGGCGATGGCTGCTCCTGCCCCAGAGACACCTG 551
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArg 174
DB 552 GGGAGCGT-CCAGAGCGCTGTGCCGCTGTGTGGCTGGAGG 592

RESULT 15

ABL67258

ID ABL67258 standard; DNA; 816 BP.

XX ABL67258;

AC ABL67258;

DT 15-MAY-2002 (first entry)

DE Thyroid cancer related gene sequence SEQ ID NO:5595.

XX Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;

KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;

KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW gene; ds.

XX Homo sapiens.

PN WO200194629-A2.

XX 13-DEC-2001.

PF 30-MAY-2001; 2001WO-US10838.

PR 05-JUN-2000; 2000US-209473P.

PR 05-JUN-2000; 2000US-209531P.

PR 18-SEP-2000; 2000US-233133P.

PR 18-SEP-2000; 2000US-233617P.

PR 20-SEP-2000; 2000US-234009P.

PR 20-SEP-2000; 2000US-234034P.

PR 20-SEP-2000; 2000US-234052P.

PR 22-SEP-2000; 2000US-234509P.

PR 22-SEP-2000; 2000US-234567P.

PR 25-SEP-2000; 2000US-234923P.

PR 25-SEP-2000; 2000US-234924P.

PR 25-SEP-2000; 2000US-235077P.

PR 25-SEP-2000; 2000US-235082P.

PR 25-SEP-2000; 2000US-235134P.

PR 25-SEP-2000; 2000US-235280P.

PR 26-SEP-2000; 2000US-235637P.

PR 26-SEP-2000; 2000US-235638P.

PR 27-SEP-2000; 2000US-235711P.

PR 27-SEP-2000; 2000US-235720P.

PR 27-SEP-2000; 2000US-235840P.

PR 27-SEP-2000; 2000US-235863P.

PR 28-SEP-2000; 2000US-236028P.

PR 28-SEP-2000; 2000US-236032P.

PR 28-SEP-2000; 2000US-236033P.

PR 28-SEP-2000; 2000US-236034P.

PR 28-SEP-2000; 2000US-236109P.

PR 28-SEP-2000; 2000US-236111P.

PR 29-SEP-2000; 2000US-236842P.

PR 29-SEP-2000; 2000US-236891P.

PR 02-OCT-2000; 2000US-237172P.

PR 02-OCT-2000; 2000US-237173P.

PR 02-OCT-2000; 2000US-237278P.

PR 02-OCT-2000; 2000US-237294P.

PR 02-OCT-2000; 2000US-237295P.

PR 03-OCT-2000; 2000US-237316P.

PR 03-OCT-2000; 2000US-237425P.

PR 03-OCT-2000; 2000US-237598P.

PR 03-OCT-2000; 2000US-237604P.

PR 03-OCT-2000; 2000US-237606P.

PR 03-OCT-2000; 2000US-237608P.

PR 01-NOV-2000; 2000US-244867P.

PR 01-NOV-2000; 2000US-245084P.

(AVAL-) AVALON PHARM.

Young PE, Augustus M, Carter KC, Edner R, Endress G, Horrigan S;

Soppet DR, Weaver Z;

WPI; 2002-188264/24.

Screening for anti-neoplastic agent involves exposing cells to a
chemical agent to be tested for anti-neoplastic activity, and
determining a change in expression of a gene of a signature gene set

Claim 1; SEQ ID 5595; 44pp; English.

The present invention describes a method (M1) for screening for an
anti-neoplastic agent. The method involves exposing cells to a chemical
agent to be tested for anti-neoplastic activity, determining a change in
expression of at least one gene (I) of a signature gene set, where (I)
comprises a sequence (S) selected from 8447 sequences (given in ABL61664
to ABL70110), or is at least 95% identical to (S), where a change in

CC expression is indicative of anti-neoplastic activity. (1) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening
CC an anti-neoplastic agent, and can be used for producing a product which
CC is the data collected with respect to the anti-neoplastic agent as a
CC result of M1, and the data is sufficient to convey the chemical
CC structure and/or properties of the agent. M1 can be used in the
CC treatment of cancer such as colon, breast, stomach, lung, thyroid,
CC oesophageal, ovarian, kidney, prostate or pancreatic cancer,
CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
CC carcinoma, papillary carcinoma and Wilms' tumour.

XX
SQ Sequence 816 BP; 149 A; 235 C; 264 G; 168 T; 0 other;

Alignment Scores:

Pred. No.:	3.37e-65	Length:	816
Score:	950.00	Matches:	163
Percent Similarity:	93.68%	Conservative:	0
Best Local Similarity:	93.68%	Mismatches:	3
Query Match:	91.52%	Indels:	8
DB:	24	Gaps:	1

US-09-993-234-6_COPY_25_198 (1-174) x ABL67258 (1-816)

```
QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGly 20
Db 57 CAGGGCGGCACACTGTAAGCCCCAGGTGTGACTGTGCCGGTACTTCCACAAGAAGATTGGT 116
QY 21 LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
Db 117 CTGTTTGTGTGACAGAGGCTGCCAGGGGGGACTACCTGAAGGCCCTTGACAGGAGCCC 176
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db 177 TGGCGCACTCCACCTGCTGTGTGTCCCAAGACACCTTGTGGCTGGAGAACCAC 236
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db 237 CATAAATTCTGAATGTGCCCGTGCAGGCCCTGTGATGAGCAGGCCCTCCAGGTGGCGCTG 296
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
Db 297 GAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGGCTGTAAAGCCAGGCTGTTGTGAG 356
QY 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120
Db 357 TGGCAGGTCAAGCAATGTGTACAGAGTTCAACCTTCTACTGCCAACCATGCTAGACTGC 416
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 417 GGGGCCCTGCACCGCACACACAGGCTACTCTGTCCCGCAGAGATTAAGTGTGGAGCC 476
QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db 477 TGGCTGGCTGGCTCTATGACATGGCGATGGCTGCGTCTGCTGCCACGTAATTCCTA 536
QY 161 GlySerCysProGluArgCysAlaValCysGlyTyrParg 174
Db 537 -----GCTGTGCTGGGATGGAG 554
```

Search completed: April 6, 2003, 16:52:37
Job time : 169.014 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 6, 2003, 21:08:18 ; Search time 66.2544 Seconds
(without alignments)
2303.655 Million cell updates/sec

Title: US-09-993-234-6_COPY_25_198
Perfect score: 1038
Sequence: 1 QGGTRSPRCDCAGDFHKKIG.....CPTSTLGSCPERCAAVCGWR 174

Scoring table: BLOSUM62
Xgapop 10.0 , Ygapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 593429 segs, 438583890 residues

Total number of hits satisfying chosen parameters: 1186858

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US09993234/runat_27032003_115459_15466/app_query.fasta_1.2346
-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09993234_@CGN_1_1_249_@runat_27032003_115459_15466
-NCPUP=6 -ICPU=3 -NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCt_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCtUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1038	100.0	1254	10	US-09-333-966-3	Sequence 3, Appl1
2	1038	100.0	1634	9	US-10-081-280-9	Sequence 9, Appl1
3	1038	100.0	1634	9	US-10-112-793-9	Sequence 9, Appl1
4	1038	100.0	1634	9	US-10-112-193-11	Sequence 11, Appl1

5	1038	100.0	1634	10	US-09-993-234-9	Sequence 9, Appl1
6	1038	100.0	1743	9	US-09-954-531-1389	Sequence 1389, Ap
7	1038	100.0	1783	10	US-09-333-966-1	Sequence 1, Appl1
8	950	91.5	816	10	US-09-964-824A-292	Sequence 292, App
9	950	91.5	1438	9	US-10-081-280-5	Sequence 5, Appl1
10	950	91.5	1438	9	US-10-112-793-5	Sequence 5, Appl1
11	950	91.5	1438	9	US-10-112-193-5	Sequence 5, Appl1
12	950	91.5	1438	10	US-09-884-733-5	Sequence 5, Appl1
13	950	91.5	1438	10	US-09-993-234-5	Sequence 5, Appl1
14	738	71.1	10797	9	US-10-092-154-1577	Sequence 1577, Ap
15	738	71.1	10797	10	US-09-764-847-1577	Sequence 1577, Ap
16	666	64.2	433	9	US-10-081-280-2	Sequence 2, Appl1
17	666	64.2	433	9	US-10-112-793-2	Sequence 2, Appl1
18	666	64.2	433	9	US-10-112-193-2	Sequence 2, Appl1
19	666	64.2	433	10	US-09-884-733-2	Sequence 2, Appl1
20	666	64.2	433	10	US-09-993-234-2	Sequence 2, Appl1
21	214	20.6	2130	10	US-09-917-800A-1601	Sequence 1601, Ap
22	212.5	20.5	1049	10	US-09-756-186-1	Sequence 1, Appl1
23	211	20.3	5870	10	US-09-838-718A-8	Sequence 8, Appl1
24	205.5	19.8	1301	10	US-09-756-186-7	Sequence 7, Appl1
25	205	19.7	1674	9	US-09-359-595-12	Sequence 12, Appl1
26	203.5	19.6	1202	10	US-09-756-186-3	Sequence 3, Appl1
27	203	19.6	519	9	US-09-899-429A-15	Sequence 15, Appl1
28	203	19.6	549	9	US-09-899-429A-9	Sequence 9, Appl1
29	203	19.6	603	9	US-09-899-429A-13	Sequence 13, Appl1
30	203	19.6	633	9	US-09-899-429A-7	Sequence 7, Appl1
31	203	19.6	1334	9	US-09-898-234-11	Sequence 11, Appl1
32	203	19.6	1334	9	US-09-792-356-11	Sequence 11, Appl1
33	203	19.6	1334	10	US-09-899-422-11	Sequence 11, Appl1
34	203	19.6	1368	9	US-09-898-234-1	Sequence 1, Appl1
35	203	19.6	1368	9	US-09-899-429A-1	Sequence 1, Appl1
36	203	19.6	1368	9	US-09-792-356-1	Sequence 1, Appl1
37	203	19.6	1368	10	US-09-899-422-1	Sequence 1, Appl1
38	203	19.6	2111	10	US-09-880-107-2360	Sequence 2360, Ap
39	203	19.6	2141	9	US-09-898-234-16	Sequence 16, Appl1
40	203	19.6	2141	9	US-09-899-429A-26	Sequence 26, Appl1
41	203	19.6	2141	9	US-09-792-356-16	Sequence 16, Appl1
42	203	19.6	2141	10	US-09-899-422-16	Sequence 16, Appl1
43	203	19.6	2175	12	US-10-120-397-1	Sequence 1, Appl1
44	202	19.5	1334	9	US-09-899-429A-21	Sequence 21, Appl1
45	201	19.4	1147	10	US-09-756-186-5	Sequence 5, Appl1

ALIGNMENTS

RESULT 1
US-09-333-966-3
; Sequence 3, Application US/09333966
; Patent No. US20020009773A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Dixit, Vishva
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dillon, Patrick J.
; TITLE OF INVENTION: Death Domain Containing Receptors
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/333,966
; FILING DATE:
; CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/815,469
FILING DATE:
APPLICATION NUMBER: No. US20020009773A1 Yet Assigned
FILING DATE: 06-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,711
FILING DATE: 17-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,285
FILING DATE: 12-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1254 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1251
US-09-333-966-3

Alignment Scores:
Pred. No.: 7.16e-99 Length: 1254
Score: 1038.00 Matches: 174
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-993-234-6_COPY_25_198 (1-174) x US-09-333-966-3 (1-1254)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGly 20
Db 73 CAGGGCGGCACTCGTAGCCCCAGGTGTGACTGTCCGGTGACTTCCACAGAAGATTGGT 132
QY 21 LeuPheCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
Db 133 CTGTTTGTGTCAGAGGCTGCCAGCGGGGCACTACCTGAAGGCCCTTGCACGAGCCCC 192
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db 193 TGGCGCACTCCAGCTGCTGTGTGTGTCGCCAAGACACCTTCTGGCCTGGGAGAACCAC 252
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db 253 CATAATTCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCCCTCCAGGTGGCGCTG 312
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
Db 313 GAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGGCTGTAAAGCCAGGCTGTTTGTGAG 372
QY 101 CysGlnValSerGlnCysValSerSerSerProPheTyrCysGlnProCysLeuAspCys 120
Db 373 TGGCAGGTTCAGCCAAATGTGTCAAGAGTTCACCTTCTACTGCCAACCATGCTAGACTGC 432
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 433 GGGGCCCTGCACCGCCACACAGGCTACTCTGTTCGCCGAGAGATACTGACTGTGGAGCC 492
QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db 493 TGCCTGCTGCTGCTTCTATGACATGGCGATGGCTGCTGCTGCTGCCCCACGAGACACCTG 552
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArg 174

Db 553 GGGAGCTGTCCAGAGCGCTGTGCCGCTGTCTGTGGCTGAGG 594

RESULT 2
US-10-081-280-9

Sequence 9, Application US/10081280
Patent No. US20020165157A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/081,280
FILING DATE: 21-Feb-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/829,270
FILING DATE: 31-Mar-1997

ATTORNEY/AGENT INFORMATION:

NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5416
TELEFAX: 415/952-9881
TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:
LENGTH: 1634 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-081-280-9

Alignment Scores:
Pred. No.: 9.85e-99 Length: 1634
Score: 1038.00 Matches: 174
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-993-234-6_COPY_25_198 (1-174) x US-10-081-280-9 (1-1634)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGly 20
Db 161 CAGGGCGGCACTCGTAGCCCCAGGTGTGACTGTGCCGCTGACTTCCACAGAAGATTGGT 220
QY 21 LeuPheCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
Db 221 CTGTTTGTGTCAGAGGCTGCCAGCGGGGCACTACCTGAAGGCCCTTGGCCTGGGAGAACCAC 280
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db 281 TGGCGCACTCCAGCTGCTGTGTGTGCCAAGACACCTTCTTGGCCTGGGAGAACCAC 340
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db 341 CATAATTCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCCCTCCAGGTGGCGCTG 400

QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
Db 401 GAGAACTGTTCAAGCAGTGGCCGACACCCGCTGTGGCTGTAAGCCAGCGCTGTTGTGGAG 460
QY 101 CysGlnValSerGlnCysValSerSerProPheTyrcysGlnProCysLeuAspCys 120
Db 461 TGCAGGTGACCAATGTGTACAGCAATTACCCCTTCTACTGCCAACCATGCTAGACTGC 520
QY 121 GAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 521 GGGGCCCTGCACCGCCACACAGCGGTACTGTGTCCCGCAGAGATACTGACTGTGGACC 580
QY 141 CysLeuProGlyPheTyrgluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db 581 TGCTGCTGCTGCTTCTATGAACAATGGCGATGGCTGCGTGTCTGCCCCACAGACACCTG 640
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArg 174
Db 641 GGGAGCTGTCCAGAGCGCTGTGCCGCTGTCTGTGGCTGGAG 682

RESULT 3

US-10-112-793-9

; Sequence 9, Application US/10112793
; Publication No. US20020192729A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/112,793
FILING DATE: 28-Mar-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/828,683A
FILING DATE: 31-Mar-1997
APPLICATION NUMBER: 08/625328
FILING DATE: 1-Apr-1996
APPLICATION NUMBER: 08/710802
FILING DATE: 23-Sep-1996

ATTORNEY/AGENT INFORMATION:

NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/952-5416
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:
LENGTH: 1634 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-10-112-793-9

Alignment Scores:

Pred. No.: 9.85e-99 Length: 1634
Score: 1038.00 Matches: 174
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

DB: 9 Gaps: 0
US-09-993-234-6_copy_25_198 (1-174) x US-10-112-793-9 (1-1634)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
Db 161 CAGGGCGGACTCGTAGCCGCCAGGTTGACTGTGCCGGTGACTTCACAAAGAATTGGT 220

QY 21 LeuPheCysCysArgGlyCysProAlaGlyHisIstYrLeuLysAlaProCysThrGluPro 40
Db 221 CTGTTTGTGTGCAGAGGCTGCCACGGGGCACACTACCTGAAGGCCCTTGACACGAGCCC 280

QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db 281 TGCGGCACTCCACCTGCTGTGTGTGCCCAAGACACACTTCTGGCCTGGAGAACAC 340

QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db 341 CATTAATTGAAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCGCTGCCAGGTGGCGCTG 400

QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
Db 401 GAGAACTGTTCAAGCAGTGGCCGACACCCGCTGTGGCTGTAAGCCAGCGCTGTTGTGGAG 460

QY 101 CysGlnValSerGlnCysValSerSerProPheTyrcysGlnProCysLeuAspCys 120
Db 461 TGCAGGTGACCAATGTGTACAGCAATTACCCCTTCTACTGCCAACCATGCTAGACTGC 520

QY 121 GAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 521 GGGGCCCTGCACCGCCACACAGCGGTACTGTGTCCCGCAGAGATACTGACTGTGGACC 580

QY 141 CysLeuProGlyPheTyrgluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db 581 TGCTGCTGCTGCTTCTATGAACAATGGCGATGGCTGCGTGTCTGCCCCACAGACACCTG 640

QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArg 174
Db 641 GGGAGCTGTCCAGAGCGCTGTGCCGCTGTCTGTGGCTGGAG 682

RESULT 4

US-10-112-193-11

; Sequence 11, Application US/10112193
; Publication No. US20030004313A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-3 POLYPEPTIDE
NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/112,193
FILING DATE: 28-Mar-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/928,069
FILING DATE: 11-Sep-1997
APPLICATION NUMBER: 60/026943
FILING DATE: 23-Sep-1996

ATTORNEY/AGENT INFORMATION:

NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1052R1

TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1634 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-112-193-11

Alignment Scores:
Pred. No.: 9.85e-99 Length: 1634
Score: 1038.00 Matches: 174
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-993-234-6_COPY_25_198 (1-174) x US-10-112-193-11 (1-1634)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
Db 161 CAGGGCGGCACTCGTAGCCCCAGGTGTGACTGTGCCGGTGACTTCCACAGAAGATTGGT 220
QY 21 LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
Db 221 CTGTTTGTGTGAGAGGCTGCCAGCGGGGCACTACCTGAAGCCCCCTTGACAGGAGCCC 280
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db 281 TGGCGCACTCCACCTGCTGTGTCTCCCAAGACACCTTCTTGCGCTGGAGAACAC 340
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db 341 CATTAATCTGAATGTGCCCGCTGCCAGGCTGTGATGACAGCCCTCCAGGTGGCGCTG 400
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
Db 401 GAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGCTGTAAGCCAGGCTGTTGTGGAG 460
QY 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120
Db 461 TGCCAGGTCAGCCAAATGTGTGACAGATTACCTTCTACTGCCAACCACTGCTAGACTGC 520
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 521 GGGGCCCTGCACCGCACACACGCGTACTCTGTTCCCGCAGAGATACTGACTGTGGAGCC 580
QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db 581 TGCCTGCTGGCTTCTATGAACATGGCGATGGCTGCTGCTGCTGCCCCACGAGACACCTG 640
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArg 174
Db 641 GGGAGCTGTCCAGACGCGCTGTGCGGCTGTGCTGTGGCTGAGG 682

RESULT 5

US-09-993-234-9
Sequence 9, Application US/09993234
Patent No. US20020146768A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/993,234
FILING DATE: 19-NO. US20020146768A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,683
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5416
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1634 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-993-234-9

Alignment Scores:
Pred. No.: 9.85e-99 Length: 1634
Score: 1038.00 Matches: 174
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-993-234-6_COPY_25_198 (1-174) x US-09-993-234-9 (1-1634)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
Db 161 CAGGGCGGCACTCGTAGCCCCAGGTGTGACTGTGCCGGTGACTTCCACAGAAGATTGGT 220
QY 21 LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
Db 221 CTGTTTGTGTGAGAGGCTGCCAGCGGGGCACTACCTGAAGCCCCCTTGACAGGAGCCC 280
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db 281 TGGCGCACTCCACCTGCTGTGTCTCCCAAGACACCTTCTTGCGCTGGAGAACAC 340
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db 341 CATTAATCTGAATGTGCCCGCTGCCAGGCTGTGATGACAGCCCTCCAGGTGGCGCTG 400
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
Db 401 GAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGCTGTAAGCCAGGCTGTTGTGGAG 460
QY 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120
Db 461 TGCCAGGTCAGCCAAATGTGTGACAGATTACCTTCTACTGCCAACCACTGCTAGACTGC 520
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 521 GGGGCCCTGCACCGCACACACGCGTACTCTGTTCCCGCAGAGATACTGACTGTGGAGCC 580
QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db 581 TGCCTGCTGGCTTCTATGAACATGGCGATGGCTGCTGCTGCTGCCCCACGAGACACCTG 640
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArg 174
Db 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArg 174

Db 641 GGGAGCTGTCCAGAGCGCTGTGCCGTGTCTGTGGCTGAGG 682

RESULT 6
US-09-954-531-1389

: Sequence 1389, Application US/09954531

: Patent No. US20020165180A1

: GENERAL INFORMATION:

: APPLICANT: Weaver, Zoe

: TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cand

: TITLE OF INVENTION: Gene Sets

: FILE REFERENCE: 689290-77

: CURRENT APPLICATION NUMBER: US/09/954,531

: PRIOR APPLICATION NUMBER: US/60/233,133

: PRIOR FILING DATE: 2000-09-18

: PRIOR APPLICATION NUMBER: US/60/234,009

: PRIOR FILING DATE: 2000-09-20

: PRIOR APPLICATION NUMBER: US/60/234,034

: PRIOR FILING DATE: 2000-09-20

: PRIOR APPLICATION NUMBER: US/60/234,509

: PRIOR FILING DATE: 2000-09-22

: PRIOR APPLICATION NUMBER: US/60/234,567

: PRIOR FILING DATE: 2000-09-22

: NUMBER OF SEQ ID NOS: 1392

: SOFTWARE: PatentIn version 3.0

: SEQ ID NO 1389

: LENGTH: 1743

: TYPE: DNA

: ORGANISM: Homo sapiens

: US-09-954-531-1389

Alignment Scores:

Pred. No.:	1.06e-98	Length:	1743
Score:	1038.00	Matches:	174
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-993-234-6_COPY_25_198 (1-174) x US-09-954-531-1389 (1-1743)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGly 20

Db 141 CAGGGCGGCACTGTAGCCCAAGGTGTACTGTGCCGTGACTTCCACAAGAATTTGGT 200

QY 21 LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40

Db 201 CTGTTTGTTCAGAGGCTGCCCAAGCGGGCACTACCTGAAGGCCCCCTTGCAAGGAGCCC 260

QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60

Db 261 TCGGGCACTCCACCTGCTGTGTGTCTCCCAAGACACCTTCTTGCCCTGGGAGAACCAC 320

QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80

Db 321 CATAAATCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCGCTCCAGGTGGCGCTG 380

QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100

Db 381 GAGAACTGTTCAGCAGTGGCCGACACCGCTGTGGCTGTAAAGCCAGGCTGTTGTGAG 440

QY 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120

Db 441 TGGCAGGTCAAGCAATGTGTACAGCAGTTCACCTTCTACTGCCAACCATGCTAGACTGC 500

QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140

Db 501 GGGGCCCTGCACCGCCACACACGGCTACTCTGTCCCGCAGAGATGACTGACTGTGGACC 560

QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160

Db 561 TGCCTGCTGCTCTTATGAAACATGGCATGGCTGCGTGTCTGCTGCCACGAGCACCCTG 620

QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArg 174

Db 621 GGGAGCTGTCCAGAGCGCTGTGCCGTGTCTGTGGCTGAGG 662

RESULT 7

US-09-333-966-1

: Sequence 1, Application US/09333966

: Patent No. US20020009773A1

: GENERAL INFORMATION:

: APPLICANT: Yu, Guo-Liang

: APPLICANT: Ni, Jian

: APPLICANT: Dixit, Vishva

: APPLICANT: Gentz, Reiner L.

: APPLICANT: Dillon, Patrick J.

: TITLE OF INVENTION: Death Domain Containing Receptors

: NUMBER OF SEQUENCES: 17

: CORRESPONDENCE ADDRESS:

: ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.

: STREET: 1100 New York Ave., NW, Suite 600

: CITY: Washington

: STATE: DC

: COUNTRY: USA

: ZIP: 20005-3934

: COMPUTER READABLE FORM:

: MEDIUM TYPE: Floppy disk

: OPERATING SYSTEM: PC-DOS/MS-DOS

: SOFTWARE: PatentIn Release #1.0, Version #1.30

: CURRENT APPLICATION DATA:

: APPLICATION NUMBER: US/09/333,966

: FILING DATE:

: CLASSIFICATION:

: PRIOR APPLICATION DATA:

: APPLICATION NUMBER: US/08/815,469

: FILING DATE:

: APPLICATION NUMBER: No. US20020009773A1 Yet Assigned

: FILING DATE: 06-FEB-1997

: PRIOR APPLICATION DATA:

: APPLICATION NUMBER: US 60/028,711

: FILING DATE: 17-OCT-1996

: PRIOR APPLICATION DATA:

: APPLICATION NUMBER: US 60/013,285

: FILING DATE: 12-MAR-1996

: ATTORNEY/AGENT INFORMATION:

: NAME: Steffe, Eric K.

: REGISTRATION NUMBER: 36,688

: REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM

: TELECOMMUNICATION INFORMATION:

: TELEPHONE: 202-371-2600

: TELEFAX: 202-371-2540

: INFORMATION FOR SEQ ID NO: 1:

: SEQUENCE CHARACTERISTICS:

: LENGTH: 1783 base pairs

: TYPE: nucleic acid

: STRANDEDNESS: double

: TOPOLOGY: both

: MOLECULE TYPE: CDNA

: FEATURE:

: NAME/KEY: CDS

: LOCATION: 198..1481

: US-09-333-966-1

Alignment Scores:

Pred. No.:	1.09e-98	Length:	1783
Score:	1038.00	Matches:	174
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-09-993-234-6_COPY_25_198 (1-174) x US-09-333-966-1 (1-1783)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGly 20

```
|||||
Db 303 CAGGGCGGCACTCGTAGCCCGCAGGTGTGACTGTGCGGTGACTTCCACAGAAGATTGGT 362
QY 21 LeuphEcysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
Db 363 CTGTTTGTGTGACAGAGGCTGCCAGCGGGGACACTACTGAAGGCCCTTGACAGGAGCCC 422
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db 423 TCGGGCAACTCCACCTGCTGTGTGTCCCAAGACACCTTCTTGCGCTGGAGAACCCAC 482
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db 483 CATAATTCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCCCTCCAGGTGGCGCTG 542
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
Db 543 GAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGGCTGTAAAGCCAGGCTGGTTGTGAG 602
QY 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120
Db 603 TGCAGGTTCAGCAATGTGTACAGAGTTACACCTTCTACTGCCAACCATGCTGAGACTGC 662
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 663 GGGGCCCTGCACCGCCACACAGGCTACTCTGTCCCGCAGAGATACTGACTGTGGAGCC 722
QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db 723 TGCCTGCCCTGCTTCTATGAACATGGCGATGGCTGCTCTGCCCCACGACAGACCCTG 782
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArg 174
Db 783 GGGAGCTGTCCAGAGCGCTGTGCCGCTGTCTGTGGCTGGAGG 824
```

RESULT 8

```
US-09-964-824A-292
; Sequence 292, Application US/09964824A
; Patent No. US20020102531A1
; GENERAL INFORMATION:
; APPLICANT: Horrigan, Stephen
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-73
; CURRENT APPLICATION NUMBER: US/09/964,824A
; PRIOR APPLICATION NUMBER: US/60/236,033
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,032
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,028
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 583
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 292
; LENGTH: 816
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-824A-292
```

Alignment Scores:

```
Pred. No.: 5,76e-90 Length: 816
Score: 950.00 Matches: 163
Percent Similarity: 93.68% Conservative: 0
Best Local Similarity: 93.68% Mismatches: 3
Query Match: 91.52% Indels: 8
DB: 10 Gaps: 1
```

US-09-993-234-6_copy_25_198 (1-174) x US-09-964-824A-292 (1-816)

```
QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
Db 57 CAGGGCGGCACTCGTAGCCCGCAGGTGTGACTGTGCGGTGACTTCCACAGAAGATTGGT 116
```

```
QY 21 LeuphEcysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
Db 117 CTGTTTGTGTGACAGAGGCTGCCAGCGGGGACACTACTGAAGGCCCTTGACAGGAGCCC 176
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db 177 TCGGGCAACTCCACCTGCTGTGTGTCCCAAGACACCTTCTTGCGCTGGAGAACCCAC 236
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db 237 CATAATTCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCCCTCCAGGTGGCGCTG 296
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
Db 297 GAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGGCTGTAAAGCCAGGCTGGTTGTGAG 356
QY 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120
Db 357 TGCAGGTTCAGCAATGTGTACAGAGTTACACCTTCTACTGCCAACCATGCTGAGACTGC 416
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 417 GGGGCCCTGCACCGCCACACAGGCTACTCTGTCCCGCAGAGATACTGACTGTGGAGCC 476
QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db 477 TGCCTGCCCTGCTTCTATGAACATGGCGATGGCTGCTGCTGCCCCACGTAATTCTTA 536
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArg 174
Db 537 -----GCTGTGCTGGGATGGAGG 554
```

RESULT 9

```
US-10-081-280-5
; Sequence 5, Application US/10081280
; Patent No. US20020165157A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/081,280
; FILING DATE: 21-Feb-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/829,270
; FILING DATE: 31-Mar-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1007R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5416
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1438 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
```



```

:
: TOPOLOGY: Linear
: SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-081-280-5

Alignment Scores:
Pred. No.: 1.14e-89 Length: 1438
Score: 950.00 Matches: 163
Percent Similarity: 93.68% Conservative: 0
Best Local Similarity: 93.68% Mismatches: 3
Query Match: 91.52% Indels: 8
DB: 9 Gaps: 1

US-09-993-234-6_COPY_25_198 (1-174) x US-10-081-280-5 (1-1438)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
Db 449 CAGGGCGGCACTCGTAGCCCGCAGGTGTGACTGTGCCGTGACTTCCACAAGAAGATTGGT 508
QY 21 LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
Db 509 CTGTTTGTGTCAGAGGCTGCCAGCGGGGCACTACCTGAAGGCCCTTGCCACGGAGCCC 568
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db 569 TGGGGCACTCCACCTGCTGTGTGTCCCAAGACACCTTCTTGCCCTGGGAGAACCCAC 628
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db 629 CATAAATCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGAGCCCTCCACGAGTGGCGCTG 688
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
Db 689 GAGAACTGTTCAGACAGTGGCCGACACCGCTGTGGCTGTAAGCCAGGCTGTTGTGGAG 748
QY 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120
Db 749 TGGCAGGTCAAGCCATGTGTACAGACATCACTTCTACTGCCAACCATGCTAGACTGC 808
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 809 GGGGCCCTGCACCGCCACACACGCGTACTGTTCGCCGACAGATACTGACTGTGGAGCC 868
QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db 869 TGCCTGCTGGCTTCTATGAACATGGCGATGGCTGCTGCTGCCGCCACGTAATTCCTA 928
QY 161 GlySerCysProGluArgCysAlaValCysGlyTrpArg 174
Db 929 -----GCTGTGCTGGATGGAGG 946

RESULT 10
US-10-112-793-5
: Sequence 5, Application US/10112793
: Publication No. US20020192729A1
:
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi J.
: TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
: NUMBER OF SEQUENCES: 28
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 1 DNA Way
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 Inch, 1.44 Mb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Winpatin (Genentech)
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/10/112,793
: FILING DATE: 28-Mar-2002
```

```

:
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/828,683A
: FILING DATE: 31-Mar-1997
: APPLICATION NUMBER: 08/625328
: FILING DATE: 1-Apr-1996
: APPLICATION NUMBER: 08/710802
: FILING DATE: 23-Sep-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Mairschang, Diane L.
: REGISTRATION NUMBER: 35,600
: REFERENCE/DOCKET NUMBER: P1007P1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650/225-5416
: TELEFAX: 650/952-9881
:
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1438 base pairs
: TYPE: Nucleic Acid
: STRANDEDNESS: Single
: TOPOLOGY: Linear
:
: SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-112-793-5

Alignment Scores:
Pred. No.: 1.14e-89 Length: 1438
Score: 950.00 Matches: 163
Percent Similarity: 93.68% Conservative: 0
Best Local Similarity: 93.68% Mismatches: 3
Query Match: 91.52% Indels: 8
DB: 9 Gaps: 1

US-09-993-234-6_COPY_25_198 (1-174) x US-10-112-793-5 (1-1438)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
Db 449 CAGGGCGGCACTCGTAGCCCGCAGGTGTGACTGTGCCGTGACTTCCACAAGAAGATTGGT 508
QY 21 LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
Db 509 CTGTTTGTGTCAGAGGCTGCCAGCGGGGCACTACCTGAAGGCCCTTGCCACGGAGCCC 568
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db 569 TGGGCAACTCCACCTGCTGTGTGTCCCAAGACACCTTCTTGCCCTGGGAGAACCCAC 628
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db 629 CATAAATCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCTGCCAGGTGGCGCTG 688
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
Db 689 GAGAACTGTTCAGACAGTGGCCGACACCGCTGTGGCTGTAAGCCAGGCTGTTGTGGAG 748
QY 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120
Db 749 TGGCAGGTCAAGCCATGTGTACAGACATCACTTCTACTGCCAACCATGCTAGACTGC 808
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 809 GGGGCCCTGCACCGCCACACACGCGTACTGTTCGCCGACAGATACTGACTGTGGAGCC 868
QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db 869 TGCCTGCTGGCTTCTATGAACATGGCGATGGCTGCTGCTGCCGCCACGTAATTCCTA 928
QY 161 GlySerCysProGluArgCysAlaValCysGlyTrpArg 174
Db 929 -----GCTGTGCTGGATGGAGG 946

RESULT 11
US-10-112-193-5
: Sequence 5, Application US/10112193
```


QY 21 LeupheCysArGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
Db 509 CTGTTTGTGCAGAGGCTGCCAGCGGGGCACTACCTGAAGGCCCTTGACGAGACCC 568
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db 569 TGGCGCACTCCACCTGCCCTGTGTGTCCCAAGACACACCTTCTTGCCCTGGAGAACAC 628
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db 629 CATAAATCTGAATGTGCCCGCTGCCAGCCCTGTGATGAGCAGGCCCTCCACAGTGGCGCTG 688
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
Db 689 GAGAACTGTTCAGCAGTGGCCGACACCGCTGTGCTGTAAAGCCAGCGCTTGTGAGAG 748
QY 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120
Db 749 TGCCAGGTCAAGCAATGTGTCAAGAGTTCAACCTTCTACTGCCAACCATGCTAGACTGC 808
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 809 GGGGCCCTGCACCGCCACACACGGCTACTCTGTTCGCCGACAGAACTGACTGTGGAGCC 868
QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db 869 TGCCTGCTGGCTTCTATGAACATGGCGATGGCTGCGTCTGCTGCCACGTAATTCCTA 928
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArg 174
Db 929 -----GCTGTCGTGGATGGAGG 946

RESULT 13
US-09-993-234-5
; Sequence 5, Application US/09993234
; Patent No. US20020146768A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/993,234
FILING DATE: 19-NO. US20020146768A1-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,683
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.

REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007P1

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5416

TELEFAX: 415/952-9881
TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:

LENGTH: 1438 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-09-993-234-5

Alignment Scores:

Pred. No.: 1.14e-89 Length: 1438
Score: 950.00 Matches: 163
Percent Similarity: 93.68% Conservative: 0
Best Local Similarity: 93.68% Mismatches: 3
Query Match: 91.52% Indels: 8
DB: 10 Gaps: 1

US-09-993-234-6_COPY_25_198 (1-174) x US-09-993-234-5 (1-1438)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
Db 449 CAGGGCGCACTCGTAGCCGCCAGGCTGTGACTGTGCCGGTGACTTCACAAAGAATTGGT 508
QY 21 LeupheCysArGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
Db 509 CTGTTTGTGCAGAGGCTGCCAGCGGGGCACTACCTGAAGGCCCTTGACGAGACCC 568
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db 569 TGGCGCACTCCACCTGCCCTGTGTGTCCCAAGACACACCTTCTTGCCCTGGAGAACAC 628
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db 629 CATAAATCTGAATGTGCCCGCTGCCAGCCCTGTGATGAGCAGGCCCTCCACAGTGGCGCTG 688
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
Db 689 GAGAACTGTTCAGCAGTGGCCGACACCGCTGTGCTGTAAAGCCAGCGCTTGTGAGAG 748
QY 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120
Db 749 TGCCAGGTCAAGCAATGTGTCAAGAGTTCAACCTTCTACTGCCAACCATGCTAGACTGC 808
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 809 GGGGCCCTGCACCGCCACACACGGCTACTCTGTTCGCCGACAGAACTGACTGTGGAGCC 868
QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db 869 TGCCTGCTGGCTTCTATGAACATGGCGATGGCTGCGTCTGCTGCCACGTAATTCCTA 928
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArg 174
Db 929 -----GCTGTCGTGGATGGAGG 946

RESULT 14

US-10-092-154-1577
; Sequence 1577, Application US/10092154
; Publication No. US20030054375A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC009C1

CURRENT APPLICATION NUMBER: US/10/092,154
CURRENT FILING DATE: 2002-03-07

NUMBER OF SEQ ID NOS: 2003

Prior Application removed - See file wrapper or Palm

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1577

LENGTH: 10797

TYPE: DNA

ORGANISM: Homo sapiens

US-10-092-154-1577

Alignment Scores:

Pred. No.: 1.29e-66 Length: 10797
Score: 738.00 Matches: 161
Percent Similarity: 39.95% Conservative: 0
Best Local Similarity: 39.95% Mismatches: 5

Query Match: 71.10% Indels: 239
DB: 9 Gaps: 4
US-09-993-234-6_COPY_25_198 (1-174) x US-10-092-154-1577 (1-10797)
QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGly 20
DB 5268 CAGGGCGGCACTCGTAGCCCAAGCTGACTGTGCGGTGACTTCCACAAGAAGATTGGT 5327
QY 21 LeuPheCysCysArgGlyCysProAla----- 29
DB 5328 CTGTTTGTTCAGAGGCTGCCACGGGGTAAGTGCCACAGGGGTGGAGAGGCATGGG 5387
QY 29 ----- 29
DB 5388 GCAGGCAAGGCTGAGAGGTGGGGCAGCCCCGGAGGTAGAGAGAGGCTGGCAGGGGA 5447
QY 29 ----- 29
DB 5448 GGTAGGGTAGGCTGACAGAGAGTAGGAGCTGGAGAGAAAGAGGAGGAGGCGAGGG 5507
QY 29 ----- 29
DB 5508 TGGAAACAGGTCGGGGGTGCTGGGGCAGCCCCCTGCTGCTGACCCCTGCTGTTTC 5567
QY 30 ----GlyHisTyrLeuLysAlaProCysThrGluProCysGlyAsnSerThrCysLeuVa 48
DB 5568 CACAGGGCACTACTGTAAGGCCCTTGACAGGAGCCCTGGGCAACTCCACCTGCTGTGT 5627
QY 48 lCysProGlnAspThrPheLeuAlaTrpGluAsnHisAsnSerGluCysAlaArgCy 68
DB 5628 GTGTCCCAAGACACCTTCTGGCCTGGGAGAAACACCAATTAATCTGAATGTGCCCGCTG 5687
QY 68 sGlnAlaCysAspGlu----- 73
DB 5688 CCAGGCTGTGATGAGCAGAGGTGAGGGGCTTCTCAGTGCCTTGGCAGGAGTTCCTAAGA 5747
QY 73 ----- 73
DB 5748 CAGGCTTCTTGAAGAGAGTGGCTGGCTGGGGCCAAACTTGGGGTGTGAGGGTCTGCA 5807
QY 73 ----- 73
DB 5808 CCCACCCCTTGCAGAACCCCTCCACCCCTGATCTCTCTTCAGGGGTGCCCTTGCCTTCTCT 5867
QY 73 ----- 73
DB 5868 CTTCCTGGTGACCTTCCATCTCTCATGTGCTTGGCCTTGTGCTGCGCTTAATCTCTG 5927
QY 73 ----- 73
DB 5928 AGCTTCTCTCTTTTAAAGGTAAGCCCTGTACTGTCTCTTTCGCTATTTCTGTCTCC 5987
QY 73 ----- 73
DB 5988 ATTATCTTGGATAATGCTCTGCTCTCCATGGAGGACCTTGGCCCTGACTTAATCTCTCC 6047
QY 74 -----GlnAlaSerGlnValAlaLeuGluAsnCysSerAl 85
DB 6048 ACTCCCATCTCCCTGACACCCCAACAGCC-TCACAGGTGGCGCTGGAGAACTGTTCAGC 6106
QY 85 aValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGluCysGlnValSerG 105
DB 6107 AGTGGCCGACACCCGCTGTGGCTGTAAGCCAGGCTGTGTTGTGGAGTGCAGGTCAGCCA 6166
QY 105 nCysValSerSerSerProPheTyrCysGlnProCysLeuAspCysGlyAlaLeuHisAr 125
DB 6167 ATGTGTACAGCAGTTCACCTTCTACTGCCAACCATTAGACTGCGGGGCCCTGCACCG 6226
QY 125 gHisThrArgLeuLeuCysSer----- 132
DB 6227 CCACACACAGGCTACTCTGTGA-GTACCCCAACCCAGGGCTCTCTACTCCAGACCCCTT 6285

QY 132 ----- 132
DB 6286 CTCCCTGCTGACCCACTCTCTGTCATGCTGACGACATGCTCTCTGATTCAGGTTTC 6345
QY 133 -ArgArgAspThrAspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCy 152
DB 6346 CCGCAGAGATACTGACTGTGGACCTGCTGCTGCTTCTATGAACATGGCGATGGCTG 6405
QY 152 sValSerCysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysG 172
DB 6406 CGTGTCTGCCCCACGTAATTCCTA-----GCTGTCTGGG 6441
QY 172 YTrpArg 174
DB 6442 ATGAGG 6448

RESULT 15
US-09-764-847-1577
; Sequence 1577, Application US/09764847
; Patent No. US20020132767A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009
; CURRENT APPLICATION NUMBER: US/09/764,847
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2003
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1577
; LENGTH: 10797
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-847-1577

Alignment Scores:
Pred. No.: 1.29e-66 Length: 10797
Score: 738.00 Matches: 161
Percent Similarity: 39.95% Conservative: 0
Best local Similarity: 39.95% Mismatches: 5
Query Match: 71.10% Indels: 239
DB: 10 Gaps: 4

US-09-993-234-6_COPY_25_198 (1-174) x US-09-764-847-1577 (1-10797)
QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGly 20
DB 5268 CAGGGCGGCACTCGTAGCCCAAGCTGACTGTGCGGTGACTTCCACAAGAAGATTGGT 5327
QY 21 LeuPheCysCysArgGlyCysProAla----- 29
DB 5328 CTGTTTGTTCAGAGGCTGCCAGCGGGTAAGTGCCACAGGGGTGGAGAGGCATGGG 5387
QY 29 ----- 29
DB 5388 GCAGGCAAGGCTGAGAGAGGTGGCGGACGCCCGGAGGTAAGAGAGAGGCTGGCAGGGGA 5447
QY 29 ----- 29
DB 5448 GGTAGGGTAGGCTGACAGAGAGTAGGAGCTGAGAGAAAGAGGAGGAGGCGAGGG 5507
QY 29 ----- 29
DB 5508 TGGAAAGCAGTGGGGGTGCTGGGCAAGCCCTTGCCTGCTGACCCCTGCTGTTTC 5567
QY 30 ----GlyHisTyrLeuLysAlaProCysThrGluProCysGlyAsnSerThrCysLeuVa 48
DB 5568 CACAGGGCACTACTGTAAGGCCCTTGACAGGAGACCCCTGGGCAACTCCACCTGCTGTGT 5627
QY 48 lCysProGlnAspThrPheLeuAlaTrpGluAsnHisAsnSerGluCysAlaArgCy 68
DB 5628 GTGTCCCAAGACACCTTCTTGGCCTGGGAGAAACACCATTAATCTGAATGTGCCCGCTG 5687

QY 68 sGlnAlaCysAspGlu----- 73
 |||||
Db 5688 CCAGGCTGTGATGAGCAGGGGTGAGGGCTTCTCAGTGCCTGGCAGGGAGTTCCTAAGGA 5747
QY 73 ----- 73
Db 5748 CAGGCTTCTGAAGGAAGTGGCTGGCTCGGGCCCAACTGGGGGTGTAGGGTCTGCA 5807
QY 73 ----- 73
Db 5808 CCCACCCTTGCAGAACCTCCACCCCTGATCCTCTTCAGGGGTGCCCTTGCCCCCTCTCT 5867
QY 73 ----- 73
Db 5868 CTTCCTGGTGACCTTCCCATCTCCATGTGCTTGCCCTGTGGCTTGGCCTTAATCTCTG 5927
QY 73 ----- 73
Db 5928 AGCTTCTCTTTTATAGGGTACCCCTGTACCTGTCTGTCTTTCGCCCTATTCTGTCTCC 5987
QY 73 ----- 73
Db 5988 ATTAATCTTGGGATAATGCCCTGTGCTCTCCATGGGAGCCCTTGGCCCTGACTAATCTCTCC 6047
QY 74 -----GlnAlaSerGlnValAlaLeuGluAsnCysSerAl 85
 ||| |||
Db 6048 ACTCCCATCTCCCTGCACCCCAACAGCC-TCCAGAGTGGCGCTGGAAGAACTGTTCAGC 6106
QY 85 aValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGluCysGlnValSerG 105
 |||||
Db 6107 AGTGGCCGACACCCGCTGTGGCTGAAGCAGGCTGTTGTGGAGTGCAGGTCAGCCA 6166
QY 105 ncysValSerSerProPheThrCysGlnProCysLeuAspCysGlyAlaLeuHisAr 125
 |||||
Db 6167 ATGTGTCAAGCATTCACCCCTTCTACTGCCAACCATGCTAGACTGGGGCCCTGCACCG 6226
QY 125 gHisThrArgLeuLeuCysSer----- 132
 |||||
Db 6227 CCACACAGGCTACTCTGTGA-GTACCCCAACCAAGGCTCTCTACTCCACAGACCCCTT 6285
QY 132 ----- 132
Db 6286 CTCCCTGCCCTGACCCACACTCTGTCCCATGTGTGACGCGCATGCCCTCTCTGATTGCAGGTTC 6345
QY 133 -ArgArgAspThrAspCysGlyThrCysLeuProGlyPheTyrcGluHisGlyAspGlyCy 152
 |||||
Db 6346 CCGCAGAGATACTGACTGTGGGACCTGCCTGCGCTTCTATGAACATGGCGATGGCTG 6405
QY 152 sValSerCysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysG 172
 |||||
Db 6406 CGTGTCTTGCCTGCCCCACGTAATTCCTA-----GCTGTCTGTGGG 6441
QY 172 yTrpArg 174
 |||||
Db 6442 ATGGAGG 6448

Search completed: April 7, 2003, 03:58:46
Job time : 80.2544 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.4-p5-4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 6, 2003, 16:19:54 ; Search time 1088.39 Seconds

(without alignments)
2589.161 Million cell updates/sec

Title: US-09-993-234-6_COPY_25_198
Perfect score: 1038
Sequence: 1 QGGRSPRCDCAGDFHKKIG.....CPTSTLGSCPERCAAVCGWR 174

Scoring table:
BLOSUM62
Xgapop 10.0, Ygapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-O=/cgn2_1/USPTO_spool/US09993234/runat_27032003_115456_15362/app_query.fasta_1.2346
-DB=EST -QFMT=fastap -SUFFIX=first -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS-human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09993234_@CGN_1_1_4749_@runat_27032003_115456_15362 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
EST:*
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_man:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1025	98.7	767	13	BI909448
2	1019	98.2	632	10	AW268610
3	1014	97.7	688	9	AI424936
4	1009	97.2	698	9	AI807913
5	979	94.3	562	9	AI140043
6	950	91.5	552	14	BM783972
7	950	91.5	585	10	AW517358
8	941	90.7	565	14	BM744307
9	937	90.3	514	14	BM756372
10	937	90.3	514	14	BM783979
11	932	89.8	492	14	BM741016
12	916	88.2	508	9	AI203624
13	893	86.0	488	14	BM770798
14	862	83.0	1010	14	BQ068309
15	798.5	76.9	478	10	AW002222
16	781	75.2	427	12	BE965772
17	680	65.5	422	9	AI700459
18	666	64.2	433	14	H41522
19	639	61.6	572	10	BE668836
20	591	56.9	432	14	N71143
21	580.5	55.9	434	14	BM826048
22	517	49.8	345	9	AA934992
23	516.5	49.8	443	14	H46211
24	470.5	45.3	755	13	BI555045
25	461	44.4	468	14	H46374
26	443	42.7	673	13	BM251737
27	436.5	42.1	775	12	BG867742
28	420.5	40.5	322	9	AA971249
29	416	40.1	330	14	N71141
30	405	39.0	316	14	H49675
31	395.5	38.1	639	10	BB636341
32	389.5	37.5	393	14	H41851
33	360.5	34.7	418	14	H46662
34	323	31.1	397	14	H46378
35	296	28.5	246	14	H46424
36	292	28.1	246	14	H19739
37	277.5	26.7	517	14	BM692368
38	268.5	25.9	368	10	BB872434
39	214	20.6	252	14	BM695862
40	211	20.3	725	12	BG863025
41	210	20.2	779	9	AI119338
42	209.5	20.2	984	12	BF164835
43	207.5	20.0	775	13	BI555040
44	206	19.8	872	13	BI769006
45			556	10	AV664984

ALIGNMENTS

RESULT 1
BI909448
LOCUS 767 bp mRNA linear EST 16-OCT-2001
DEFINITION 603065172F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5214568 5', mRNA sequence.
ACCESSION BI909448
VERSION BI909448.1 GI:16172666
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 767)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL COMMENT

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://lml.nhl.gov>
Plate: L1AM1538 row: 0 column: 17
High quality sequence stop: 754.
Location/Qualifiers
1. 767

FEATURES source

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5214568"
/clone_lib="NIH_MGC_118"
/tissue_type="Leukocyte"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH_MGC Library."
BASE COUNT 122 a 243 c 241 g 161 t
ORIGIN

Alignment Scores:
Pred. No.: 1.11e-88 length: 767
Score: 1025.00 Matches: 174
Percent Similarity: 99.43% Conservative: 0
Best Local Similarity: 99.43% Mismatches: 0
Query Match: 98.75% Indels: 1
DB: 13 Gaps: 0

US-09-993-234-6_COPY_25_198 (1-174) x BI909448 (1-767)

OY 1 gln gly l y t h r a r g s e r p r o a r g c y s a s p c y s a l a g l y a s p h e i s l y s i l e g l y 20
Db 109 CAGGGCGGCACTCGTAGCCCCAGGTGTGACTGTGCCGGTGACTTCCACAGAAGATTGGT 168
OY 21 leu p h e c y s a r g l y c y s p r o a l a - g l y h i s t y r l e u l y s a l a p r o c y s t h r g l u p r 40
Db 169 CTGTTTGTGTCAGAGGCTGCCAGCTGGGGCACTGAAAGGCCCTTGCCACAGGAGCC 228
OY 40 o c y s g l y a s n s e r t h r c y s l e u v a l c y s p r o g l i n a s p t h r p h e l e u a l a t r p g l u a s n h i 60
Db 229 CTGCGGCACTCCACTGCTGTGTGTCCCAAGACACCTTCTTGCGCTGGGAGAACCA 288
OY 60 s h i s a s n s e r g l u c y s a l a a r g c y s g l i n a l a c y s a s p g l u g l i n a l a s e r g l i n a l a l e 80
Db 289 CCATATTCTGATGTGCCCGCTGCAGGCTGTGATGAGCAGGCTCCCAAGTGGCGCT 348
OY 80 u g l u a s n c y s s e r a l a v a l a a s p t h r a r g c y s g l y c y s l y s p r o g l y t r p h e v a l g l 100
Db 349 GGAGAACTGTTCAGCAGTGGCCGACACCGCTGTGGCTGTAAGCCAGCGCTGTGTGGA 408
OY 100 u c y s g l i n v a l s e r g l i n c y s v a l s e r s e r p r o p h e t y r c y s g l i n p r o c y s l e u a s p c y 120
Db 409 GTGCCAGGTCAAGCAGTGTGTACAGCTTACCTTCTACTGCCAACCATGCTAGACTG 468
OY 120 s g l y a l a l e u h i s a r g h i s t h r a i g l e u l e u c y s s e r a r g a r g a s p t h r a s p c y s g l y t h 140
Db 469 CGGGGCCCTGCACCGCCACACAGGCTACTGTTCGCCGAGAGATACTGACTGTGGGAC 528
OY 140 r c y s l e u p r o g l y p h e t y r g l u h i s g l y a s p g l y c y s v a l s e r c y s p r o t h r s e r t h r l e 160
Db 529 CTGCTGCTGCTGCTTCTATGAACATGGCGATGGCTGCTGTCTGCTGCCACAGACACCT 588

OY 160 u g l y s e r c y s p r o g l u a r g c y s a l a l a v a l c y s g l y t r p a r g 174
Db 589 GGGAGCTGTCCAGAGCGGCTGTGCCCTGTCTGTGGCTGAGG 631

RESULT 2
LOCUS AW268610
DEFINITION xvalb12.x1 Soares_NFL_T_GBC_S1 Homo sapiens CDNA clone
IMAGE:2815679 3' similar to SW:WSL1_HUMAN Q93038 WSL-1 PROTEIN
PRECUSOR ;, mRNA sequence.
AW268610 632 bp mRNA linear EST 03-JAN-2000
AW268610
AW268610.1 GI:6655640
EST.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 632)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Possible reversed clone: polyT not found
Seq primer: -40UP from Gibco
High quality sequence stop: 455.
Location/Qualifiers
1. 632

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Possible reversed clone: polyT not found
Seq primer: -40UP from Gibco
High quality sequence stop: 455.
Location/Qualifiers
1. 632

FEATURES source

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2815679"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI-CGAP-GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo."
BASE COUNT 102 a 194 c 192 g 143 t 1 others
ORIGIN

Alignment Scores:
Pred. No.: 3.16e-88 length: 632
Score: 1019.00 Matches: 172
Percent Similarity: 98.85% Conservative: 0
Best Local Similarity: 98.85% Mismatches: 2
Query Match: 98.17% Indels: 0
DB: 10 Gaps: 0

US-09-993-234-6_COPY_25_198 (1-174) x AW268610 (1-632)

OY 1 gln gly l y t h r a r g s e r p r o a r g c y s a s p c y s a l a g l y a s p h e i s l y s i l e g l y 20
Db 27 CAGGGCGGCACTCGTAGCCCCAGGTGTGACTGTGCCGGTGACTTCCACAGAAGATTGGT 86
OY 21 leu p h e c y s a r g l y c y s p r o a l a g l y h i s t y r l e u l y s a l a p r o c y s t h r g l u p r o 40
Db 87 CTGTTTGTGTCAGAGGCTGCCAGCGGGCACTGAAAGGCCCTTGCCAGGAGCC 146
OY 41 c y s g l y a s n s e r t h r c y s l e u v a l c y s p r o g l i n a s p t h r p h e l e u a l a t r p g l u a s n h i 60
|||||

Seq primer: -40UP from Gibco
High quality sequence stop: 459.
Location/Qualifiers
1. 698

FEATURES
SOURCE
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:2359204"
/lab_host="DH10B"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI-CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo."
BASE COUNT 111 a 218 c 214 g 155 t
ORIGIN

Alignment Scores:
Pred. No.: 3.37e-87 Length: 698
Score: 1009.00 Matches: 170
Percent Similarity: 97.70% Conservative: 0
Best Local Similarity: 97.70% Mismatches: 4
Query Match: 97.21% Indels: 0
DB: 9 Gaps: 0

US-09-993-234-6_COPY_25_198 (1-174) x A1807913 (1-698)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGly 20
Db 36 CAGGGGGGGGCTCGATGCCAGGCTGTGACTGTGCCGGTGACTTCCACAGAAGATTGGT 95
QY 21 LeupheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
Db 96 CTGTTTGTGTCAGAGGCTGCCAGCGGGGACTTGAAGGCCCTTGACGAGCC 155
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTyrGluAsnHis 60
Db 156 TCGGGCACTCCACCTGCTGTGTGCCCAAGACACTTCTTGCCCTGGAGAACAC 215
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGlnAlaSerGlnValAlaLeu 80
Db 216 CATTAATTCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCTCCACAGTGGCCTG 275
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTyrPheValGlu 100
Db 276 GAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGCTGTAAGCCAGGCTGTTGTGGAG 335
QY 101 CysGlnValSerGlnCysValSerSerSerProPheTyrCysGlnProCysLeuAspCys 120
Db 336 TGGCAGGTACAGCCATGTGTCAGCAGTTCACCTTCTACTGCCAACCATGCTAGACTGC 395
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 396 GGGGCCCTGCACCGCACACACGGCTACTCTGTTCGCCAGAGATAGTACTGTGGAGCC 455
QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db 456 TGCCTGCTGCTTCTATGAAATGGCGAGTGGCTGCTGCTGCTGCATCAGACACCCCTG 515
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTyrParg 174
Db 516 TGGAGCTGTTCAGAGCGCTGTGCCGCTGTCTGTGGCTGAGG 557
RESULT 5
A1140043
LOCUS A1140043 562 bp mRNA linear EST 13-APR-1999

DEFINITION qa87a04.x1 Soares_fetal_heart_NbHL19W Homo sapiens cDNA clone
IMAGE:1693710 3' similar to SW:WSL1_HUMAN Q93038 WSL-1 PROTEIN
PRECUSOR ;, mRNA sequence.
ACCESSION A1140043 GI:3647500
VERSION A1140043.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 562)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1640 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 494.
Location/Qualifiers

FEATURES
source
1. 562
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:1693710"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: heart; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTACCAATCTGAAGTGGAGCGGCCGCATCTTTTGTGTGTGT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NbHL19W."
BASE COUNT 88 a 182 c 180 g 111 t 1 others
ORIGIN

Alignment Scores:
Pred. No.: 1.9e-84 Length: 562
Score: 979.00 Matches: 165
Percent Similarity: 99.40% Conservative: 0
Best Local Similarity: 99.40% Mismatches: 1
Query Match: 94.32% Indels: 0
DB: 9 Gaps: 0

US-09-993-234-6_COPY_25_198 (1-174) x A1140043 (1-562)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGly 20
Db 65 CAGGGGGGCACTCGTAGCCCAAGGTGACTGTGCCGGTACTTCCACAAGAATTGGT 124
QY 21 LeupheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
Db 125 CTGTTTGTGTCAGAGGCTGCCAGGGGGCACTACCTGAAGGCCCTTGACAGAGCCC 184
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTyrGluAsnHis 60
Db 185 TGGCGCACTCCACCTGCTGTGTGTGCCCAAGACACCTTCTTGCCCTGGAGAACAC 244
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGlnAlaSerGlnValAlaLeu 80
Db 245 CATTAATTCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCCCTCCAGGTGGCCTG 304
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTyrPheValGlu 100

|||||
Db 305 GAGAACTGTTTCAGCAGTGGCCGACACCCGCTGTGCTGTAAAGCCAGCGCTGTTGTGGAG 364
Qy 101 CysglnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120
Db 365 TGCAGGTTCAGCCAAATGTGTACAGAGTTCACCCCTTCTACTGCAACCATGCGCTAGACTGC 424
Qy 121 GtAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 425 GGGGCCCTGCACCGCCACACACAGGCTACTGTCTCCGACAGATGACTGTGGACC 484
Qy 141 CysLeuProGlyPheTyrGlnHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db 485 TGCCGTGCTGGCTTCTATGACATGGCGATGGCTGCTGCTGCCCCACGAGCACCCTG 544
Qy 161 GlySerCysProGluArg 166
Db 545 NGAGCTGTCCAGACGCC 562
RESULT 6
BM783972
LOCUS / BM783972 552 bp mRNA linear EST 05-MAR-2002
DEFINITION K-EST0062019 S6SNU620 Homo sapiens cDNA clone S6SNU620-31-H06 5',
mRNA sequence.
ACCESSION BM783972
VERSION BM783972
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 552)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: Yongsung@email.kribb.re.kr
Plate: 31 row: H column: 06
High quality sequence stop: 552.
Location/Qualifiers
1. 552
FEATURES
source
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="S6SNU620-31-H06"
/clone_lib="S6SNU620"
/sex="F"
/tissue_type="Ascites"
/cell_type="Scattering floating"
/cell_line="SND-620"
/lab_host="Top10F"
/note="Organ: Stomach; Vector: pcNS; Site_1: EcoRI;
Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tobacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transforamation of
competent cells E. coli Top10F' by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."

BASE COUNT 92 a 172 c 173 g 115 t
ORIGIN
Alignment Scores:
Pred. No.: 1.15e-81 Length: 552
Score: 950.00 Matches: 163
Percent Similarity: 93.68% Conservative: 0
Best Local Similarity: 93.68% Mismatches: 3
Query Match: 91.52% Indels: 8
DB: 14 Gaps: 1
US-09-993-234-6_COPY_25_198 (1-174) x BM783972 (1-552)
Qy 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
Db 38 CAGGGCGGCACTGCTGAGCCCGCAGGTTGACTGTGCCGTTGACTTCACAGAAATTGGT 97
Qy 21 LeupheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
Db 98 CTGTTTGTTCAGAGAGGCTGCGCCAGCGGGGCACTACCTGAAGGCCCTTGACACGAGCC 157
Qy 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db 158 TCGCGCAACTCCACCTGCGCTTGTGTGCCCAAGACACCTTCTTGCGCTGGAGAACAC 217
Qy 61 HisAsnSerGlnCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db 218 CATATTCGTGATGTGCCCGCTGCGCCAGGCCCTGTGATGAGCAGAGCCCTCCAGGTGG 277
Qy 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTyrPheValGlu 100
Db 278 GAGAACTGTTCACAGATGGCCGACACACCCGCTGTGCTGAAGCCAGGCTGTTGTGGAG 337
Qy 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120
Db 338 TGCCAGGTTCAGCAATGTGTTCAGCAGTTACCTTCTACTGCCAACCATGCTTAGACTGC 397
Qy 121 GtAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 398 GGGGCCCTGCACCGCCACACACGCTACTGTGTCCCGACAGATACTGATGGGACC 457
Qy 141 CysLeuProGlyPheTyrGlnHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db 458 TGCCGTGCTGGCTTCTATGACATGGCGATGGCTGCTGCTGCCCCACGTAATTCTTA 517
Qy 161 GlySerCysProGluArgCysAlaAlaValCysGlyTyrArg 174
Db 518 -----GCTGTCTGGGATGGAGG 535
RESULT 7
AW517358 585 bp mRNA linear EST 03-MAR-2000
LOCUS AW517358
DEFINITION xp939g02.x1 Soares_NHCE_cervix Homo sapiens cDNA clone IMAGE:2747954
3' similar to TR:000276 000276 LYMPHOCYTE ASSOCIATED RECEPTOR OF
DEATH 2. ;, mRNA sequence.
ACCESSION AW517358
VERSION AW517358
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 585)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
possible reversed clone: polyT not found

Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 32 row: A column: 05
High quality sequence stop: 514.

FEATURES

source

1. 514
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="S6SNU620-32-A05"
/clone_lib="S6SNU620"
/sex="F"
/tissue_type="Ascites"
/cell_type="Scattering floating"
/cell_line="SNU-620"
/lab_host="Top10F"
/note="Organ: Stomach; Vector: pcNS; Site_1: EcoRI;
Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tobacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including Ecor
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F' by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."

BASE COUNT 86 a 166 c 153 g 109 t
ORIGIN

Alignment Scores:

Pred. No.: 1.85e-80 Length: 514
Score: 937.00 Matches: 157
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 90.27% Indels: 0
DB: 14 Gaps: 0

US-09-993-234-6_COPY_25_198 (1-174) x BM783979 (1-514)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGly 20
|||||
Db 38 CAGGGCGGCACTGTAGCCGCCAGGTGTGACTGTGCCGGTGACTTCCACAGAAGATTGGT 97
QY 21 LeupheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
|||||
Db 98 CTGTTTGTGTGAGAGGCTGCCAGCGGGGCACTACTGAAGGCCCTTGCGGAGAACCCC 157
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
|||||
Db 158 TCGGCAACTGTCCACCTGCTGTGTGTCCCAAGACACACTTCTTGCGCTGGGAGAACCCAC 217
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
|||||
Db 218 CATAATCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCTCTCCACAGGTGGCGCTG 277
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
|||||
Db 278 GAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGCTGAAGCCAGGCTGTTGTGAG 337
QY 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120
|||||
Db 338 TGCCAGGTCAAGCAATGTGTACAGCAGTTTCAACCTTCTACTGCCAACCATGCTAGACTGC 397
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
|||||
Db 398 GGGGCCCTGCACCGCCACACACAGGCTACTGTGTCCCGCAGAGATACTGACTGTGGACC 457
QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThr 157

Db 458 TGCCTGCCTGCGCTTCTATGACATGCGATGGCTGCGTGCCTGCCCCACG 508

RESULT 11
BM741016 492 bp mRNA linear EST 01-MAR-2002
LOCUS K-EST0013376 S6SNU620 Homo sapiens cDNA clone S6SNU620-2-C03 5',
DEFINITION mRNA sequence.
ACCESSION BM741016
VERSION BM741016.1 GI:19062345
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 492)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 2 row: C column: 03
High quality sequence stop: 492.

TITLE
JOURNAL
COMMENT

FEATURES

source

1. 492
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="S6SNU620-2-C03"
/clone_lib="S6SNU620"
/sex="F"
/tissue_type="Ascites"
/cell_type="Scattering floating"
/cell_line="SNU-620"
/lab_host="Top10F"
/note="Organ: Stomach; Vector: pcNS; Site_1: EcoRI;
Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tobacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including Ecor
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F' by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."

BASE COUNT 85 a 157 c 146 g 104 t
ORIGIN

Alignment Scores:

Pred. No.: 5.26e-80 Length: 492
Score: 932.00 Matches: 156
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 89.79% Indels: 0
DB: 14 Gaps: 0

US-09-993-234-6_COPY_25_198 (1-174) x BM741016 (1-492)

QY 2 GlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGlyLeu 21
|||||
Db 19 GCGGCACTGTAGCCCGAGGTGTGACTGTGCCGTTGACTTCCACAGAAGATTGTCTG 78

OY 22 pheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluProCys 41
|||||
DB 79 TTTGTTCAGAGAGCTGCCAGCGGGCACTACCTGAAGGCCCTTGACAGGAGCCCTGC 138
OY 42 GlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHisHis 61
|||||
DB 139 GGCACCTCCACCTGCTGTGTGTGCCAAGACACCTTCTTGCCCTGGGAGAACCACCAT 198
OY 62 AsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeuGlu 81
|||||
DB 199 AATTCGAAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCCCTCCAGGTGGCGCTGGAG 258
OY 82 AsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGluCys 101
|||||
DB 259 AACTGTTACAGCAGTGGCCGACACCCGCTGTGGCTGTAAGCCAGGCTGGTTGTGAGAGTGC 318
OY 102 GlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCysGly 121
|||||
DB 319 CAGGTCAGCCAATGTGTACAGCAGTTCACCTTCTACTGCCAACCAATGCTAGACTGCGGG 378
OY 122 AlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThrCys 141
|||||
DB 379 GCCCTGCACCGCACACACAGCGCTCTGTGCCGACAGAGATGACTGTGGAGCCTGC 438
OY 142 LeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThr 157
|||||
DB 439 CTGCCCTGCTCTATGACATGGCGATGGCTGCTGCTGCCCCACG 486

RESULT 12
AI203624 508 bp mRNA linear EST 29-OCT-1998
LOCUS 9e75f02.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone
DEFINITION IMAGE:1744827 3' similar to SW:WSL1_HUMAN Q93038 WSL-1 PROTEIN
PRECURSOR ; , mRNA sequence.
AI203624
AI203624.1 GI:3756230
EST.

ACCESSION AI203624
VERSION AI203624
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 508)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Insert Length: 1699 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 442.

FEATURES
Source
1..508
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1744827"
/clone_lib="Soares_fetal_lung_NbHL19W"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: lung; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer
[5'-TGTTACCAATCTGACAGTGGAGCGGCCGCAATTTTCTTTTCTTTT-3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M.Fatima Bonaldo. This library was constructed
from the same fetus as the fetal heart library, Soares

BASE COUNT 82 a 161 c 159 g 106 t fetal heart NbHL19W."
ORIGIN
Alignment Scores:
Pred. No.: 1,92e-78 Length: 508
Score: 916.00 Matches: 154
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 88.25% Indels: 0
DB: 9 Gaps: 0
US-09-993-234-6_COPY_25_198 (1-174) x AI203624 (1-508)

OY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
|||||
DB 47 CAGGGCGGCACTCGTAGCCCCAGGCTGTGACTGTGCCGGTGACTTCCACAGAAGATTGGT 106
OY 21 LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
|||||
DB 107 CTGTTTGTTCAGAGAGGCTGCCAGCGGGGCACCTACCTGAAGGCCCTTGACAGGAGCCC 166
OY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
|||||
DB 167 TGCGGCAACTCCACCTGCTGTGTGTGCCAAGACACCTTCTTGCCCTGGGAGAACCAC 226
OY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
|||||
DB 227 CATAAATTCGAAATGTGCCCGCTGCCAGGCTGTGATGAGCAGAGGCCCTCCAGGTGGCGCTG 286
OY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
|||||
DB 287 GAGAACTGTTCAGCAGTGGCCGACACACCCGCTGTGGCTGTAAGCCAGGCTGTGTGGAG 346
OY 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120
|||||
DB 347 TGCCAGGTCAGCCAATGTGTACAGCAGTTCACCTTCTACTGCCAACCAATGCTAGACTGC 406
OY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
|||||
DB 407 GGGGCCCTGCACCGCCACACACAGCGTACTGTCTTCCCGACAGAGATACTGCTGGGACC 466
OY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSer 154
|||||
DB 467 TGCCCTGCTGCTCTATGACATGGCGATGGCTGCTGCTGCC 508

RESULT 13
BM770798 488 bp mRNA linear EST 04-MAR-2002
LOCUS K-EST0054419 S6SNU620s1 Homo sapiens cDNA clone S6SNU620s1-21-D12
DEFINITION 5', mRNA sequence.
ACCESSION BM770798
VERSION BM770798
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 488)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@email.kribb.re.kr
Plate: 21 row: D column: 12
High quality sequence stop: 488.

FEATURES
source

Location/Qualifiers
1. .488
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="S6SNU62051-21-D12"
/clone_lib="S6SNU62051"
/sex="F"
/tissue_type="Ascites"
/cell_type="Scattering floating"
/cell_line="SNU-620"
/lab_host="Top10F"
/note="Organ: Stomach; Vector: pcns; Site_1: EcoRI; Site_2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library. After analyzing and sequencing about 2,000 ~ 3,000 colonies in original cDNA library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including T7 promoter as 5' primer and N(OT)14 as 3' primer. The PCR products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original library and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted cDNA libraries were constructed by transformation of the remaining DNA into competent cells E. coli Top10F' with electroporation method."

BASE COUNT 83 a 156 c 147 g 102 t
ORIGIN

Alignment Scores:
Pred. No.: 2.98e-76 Length: 488
Score: 893.00 Matches: 150
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 86.03% Indels: 0
DB: 14 Gaps: 0

US-09-993-234-6_COPY_25_198 (1-174) x BW770798 (1-488)

OY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
Db 38 CAGGGCGGCACTCGTAGCCGCCAGGTGTGACTGTGCCGTGACTTCCACAGAAGATTGGT 97
OY 21 LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
Db 98 CTGTTTGTGTGCAGAGGCTGCCAGCGGGGACTACTGAAGGCCCTTGACAGGAGCCC 157
OY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db 158 TGGCGCACTCCACCTGCTGTGTGTCCCAAGACACCTTCTTGCGCTGGAGAACCAC 217
OY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db 218 CATTAATTCGTAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCTCCAGGTGGCGCTG 277
OY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
Db 278 GAGAACTGTTCAGCAGTGGCGCCGACCCGCTGTGGCTGTAAAGCCAGGCTGTTGTGAG 337

OY 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120
Db 338 TGGCAGGTTCAGCCATGTGTACAGAGTTCACCCCTTCTACTGCTCAACCATGCTAGACTGC 397
OY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 398 GGGGCCCTGCACCCGCCACACAGGCTACTCTGTTCGCCGAGAGATACTGACTGTGGACC 457
OY 141 CysLeuProGlyPheTyrGluHisGlyAsp 150
Db 458 TGGCTGGCTGGCTTCTATGACATGGCGAT 487
RESULT 14
BQ068309
LOCUS
DEFINITION BQ068309 1010 bp mRNA linear EST 02-APR-2002
AGENCOURT_6794093 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5770562
5', mRNA sequence.
ACCESSION BQ068309
VERSION BQ068309.1 GI:19897355
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 1010)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L1AM12833 row: n column: 03
High quality sequence stop: 689.

FEATURES
source

Location/Qualifiers
1. .1010
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5770562"
/clone_lib="NIH_MGC_121"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH_MGC Library."

BASE COUNT 179 a 353 c 287 g 191 t
ORIGIN

Alignment Scores:
Pred. No.: 8.46e-73 Length: 1010
Score: 862.00 Matches: 145
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 83.04% Indels: 0
DB: 14 Gaps: 0

US-09-993-234-6_COPY_25_198 (1-174) x BQ068309 (1-1010)

OY 30 GlyHisTyrLeuLysAlaProCysThrGluProCysGlyAsnSerThrCysLeuValCys 49
Db 50 GGGCACTACCTGAAGGCCCTTGACAGGAGCCCTGCGCAACTCCACCTGCTGTGTGT 109

QY 50 ProGlnAspThrPheLeuAlaTrpGluAsnHisAsnSerGluCysAlaArgCysGln 69
Db 110 CCCCAGACACCTTCTTGCCCTGGAGAACCATATATCTGAATGTGCCCGCTGCCAG 169
QY 70 AlaCysAspGluGlnAlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThr 89
Db 170 GCCTGTGATGAGCAGGCGCTCCAGGTGGCGCTGGAGAAGTGTTCAGCAGTGGCCGACACC 229
QY 90 ArgCysGluCysLysProGlyTrpPheValGluCysGlnValSerGlnCysValSerSer 109
Db 230 CGCTGTGGCTGTAAAGCCAGGCTGGTTGTGGAGTGCACAGTCACCAATGTGTCCAGCAGT 289
QY 110 SerProPheTyrCysGlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeu 129
Db 290 TCACCCCTTCTACTGCCAACCATGCTGAGCTGCGGGCCCTGCACCGCCACACACGCGCTA 349
QY 130 LeuCysSerArgArgAspThrAspCysGlyThrCysLeuProGlyPheTyrGluHisGly 149
Db 350 CTCTGTTCCTCCGACAGATAGTACTGAGTGGGACCTGCCCTGGCTCTATGAACATGGC 409
QY 150 AspGlyCysValSerCysProThrSerThrLeuGlySerCysProGluArgCysAlaAla 169
Db 410 GATGGCTGGGTGCTCTGCCCCACGACACCCCTGGGAGCTGTCCAGACGCGCTGTGCCGCT 469
QY 170 ValCysGlyTrpArg 174
Db 470 GTCTGTGGCTGGAGG 484

RESULT 15
LOCUS AW002222 478 bp mRNA linear EST 09-MAR-2000
DEFINITION wt85c09.x1 Soares_thymus_NHFTb Homo sapiens cDNA clone
IMAGE:2514256 3' similar to TR:014866 014866 SOLUBLE DEATH RECEPTOR
3 BETA.; mRNA sequence.
ACCESSION AW002222 GI:5849138
VERSION AW002222
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
COMMENT Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov

FEATURES
source
1.478
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2514256"
/clone_lib="Soares_thymus_NHFTb"
/dev_stage="fetal"
/lab_host="DH10B (phage-resistant)"
/note="Organ: thymus, pooled; Vector: pT7T3D-Pac
(Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo(dT) primer 15',
TGTTACCAATCTGAAGTGGAGCGGCGGCAACGTTTCTTTTCTTTT 3'},
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M. Fatima Bonaldo.

BASE COUNT 76 a 152 c 150 g 100 t
ORIGIN

Alignment Scores:
Pred. No.: 3.67e-67
Score: 798.50
Percent Similarity: 97.93%
Best Local Similarity: 97.93%
Query Match: 76.93%
DB: 10
Length: 478
Matches: 142
Conservative: 0
Mismatch: 3
Indels: 3
Gaps: 0

US-09-993-234-6_COPY_25_198 (1-174) x AW002222 (1-478)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
Db 47 CAGGGCGGCACTGCTAGCCGCCAGGTGTGACTGTGCCGCTTCCACAGAAGATTGGT 106
QY 21 LeupheCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
Db 107 CTGTTTGTGTCAGAGGCTGCCCCAGCGGGGCACTAACCTGAAGGCCCTTGACACGAGCC 166
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db 167 TGGCGCACTCCACCTGCCCTGTGTGTGCCCAAGACACCTTCTTGCCCTGGGAGAACCAC 226
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluAlaSerGlnValAlaLeu 80
Db 227 CATATTTCTGATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCTCCCGAGTGGCGCTG 286
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
Db 287 GAGAACTGTTCAGCAGTGGCCGACACCCCGCTGTGGCTGTAAAGCCAGGCTGTGTGGAG 346
QY 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120
Db 347 TGGCAGGTCAAGCAATGTGTACAGAGTTCACCTTCTACTGCCAACCAATGCCCTAAGTGC 406
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 407 GGGGCCCTGCACCGCACAA-CGGCTACTCTGTTC-CGACAGAGATCT-GACTGTGGGACC 463
QY 141 CysLeuProGlyPhe 145
Db 464 TGCCTGCCCTGGCTTT 478

Search completed: April 6, 2003, 23:25:18
Job time : 1093.39 secs

14

THIS PAGE BLANK (USPTO)

GenCore version 5.1.4-p5-4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 6, 2003, 16:28:24 ; Search time 66.3429 Seconds

(without alignments)
1816.682 Million cell updates/sec

Title: US-09-993-234-6_COPY_25_417

Perfect score: 2209
Sequence: 1 QGGTRSPRCDCAGDHRKKG.....ERMGLDGCVEDLRSLQRC 393

Scoring table: BLOSUM62

Xgapop	10.0	Xgapext	0.5
Ygapop	10.0	Ygapext	0.5
Fgapop	6.0	Fgapext	7.0
Delop	6.0	Delext	7.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US09993234/runat_27032003_115457_15378/app_query.fasta_1.2346
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=biosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09993234@cgn2_1_116@runat_27032003_115457_15378 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*

- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2209	100.0	1254	3	US-08-815-469-3 Sequence 3, Appli
2	2209	100.0	1634	4	US-08-928-069-11 Sequence 11, Appli
3	2209	100.0	1634	4	US-08-828-683A-9 Sequence 9, Appli
4	2209	100.0	1783	3	US-08-815-469-1 Sequence 1, Appli
5	952	43.1	1438	4	US-08-928-069-5 Sequence 5, Appli
6	952	43.1	1438	4	US-08-828-683A-5 Sequence 5, Appli
7	666	30.1	433	4	US-08-928-069-2 Sequence 2, Appli
8	666	30.1	433	4	US-08-828-683A-2 Sequence 2, Appli
9	393.5	17.8	1956	2	US-08-762-308-10 Sequence 10, Appli
10	383.5	17.4	2440	4	US-09-513-007-1 Sequence 1, Appli
11	371	16.8	2062	1	US-08-050-319B-24 Sequence 24, Appli
12	371	16.8	2062	2	US-08-465-982-24 Sequence 24, Appli

13	369	16.7	2161	3	US-09-106-038A-1	Sequence 1, Appli
14	369	16.7	2161	4	US-09-505-250-3	Sequence 3, Appli
15	369	16.7	2175	1	US-08-321-668-1	Sequence 1, Appli
16	369	16.7	2175	1	US-08-837-941-1	Sequence 1, Appli
17	369	16.7	2175	1	US-08-126-016-1	Sequence 1, Appli
18	369	16.7	2175	4	US-08-054-970-1	Sequence 1, Appli
19	227.5	10.3	1724	5	PCT-US96-12374-1	Sequence 1, Appli
20	226.5	10.3	1724	4	US-08-509-024-1	Sequence 1, Appli
21	226.5	10.3	1724	4	US-09-333-279-1	Sequence 1, Appli
22	214	9.7	1202	4	US-08-804-166-3	Sequence 3, Appli
23	214	9.7	1202	4	US-08-910-991-3	Sequence 3, Appli
24	213.5	9.7	6889	1	US-08-286-740-2	Sequence 2, Appli
25	213.5	9.7	6889	5	PCT-US95-09576-2	Sequence 2, Appli
26	213	9.6	1049	4	US-08-804-166-1	Sequence 1, Appli
27	213	9.6	1049	4	US-08-910-991-1	Sequence 1, Appli
28	212.5	9.6	1929	4	US-09-146-950-1	Sequence 1, Appli
29	212	9.6	1301	4	US-08-804-166-7	Sequence 7, Appli
30	212	9.6	1301	4	US-08-910-991-7	Sequence 7, Appli
31	205	9.3	600	1	US-08-050-319B-47	Sequence 47, Appli
32	205	9.3	600	2	US-08-465-982-47	Sequence 47, Appli
33	205	9.3	6896	3	US-08-627-151A-6	Sequence 6, Appli
34	203.5	9.2	1323	2	US-08-883-036A-1	Sequence 1, Appli
35	201	9.1	1147	4	US-08-804-166-5	Sequence 5, Appli
36	201	9.1	1147	4	US-08-910-991-5	Sequence 5, Appli
37	200.5	9.1	483	4	US-09-326-394-1	Sequence 1, Appli
38	200.5	9.1	1478	4	US-09-149-922-6	Sequence 6, Appli
39	199.5	9.0	1167	5	PCT-US95-17083-1	Sequence 1, Appli
40	199.5	9.0	2534	2	US-08-219-237B-1	Sequence 1, Appli
41	199.5	9.0	2534	4	US-08-468-560C-1	Sequence 1, Appli
42	199.5	9.0	2534	4	US-09-180-100-16	Sequence 16, Appli
43	199.5	9.0	2551	4	US-09-290-640-1	Sequence 1, Appli
44	193.5	8.8	1596	4	US-09-146-950-17	Sequence 17, Appli
45	192.5	8.7	1480	4	US-09-290-640-65	Sequence 65, Appli

ALIGNMENTS

RESULT 1
US-08-815-469-3
Sequence 3, Application US/08815469
Patent No. 6153402
GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang
APPLICANT: N1, Jian
APPLICANT: Dixit, Vishva
APPLICANT: Gentz, Reiner L.
APPLICANT: Dillon, Patrick J.
TITLE OF INVENTION: Death Domain Containing Receptors
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/815,469
FILING DATE: HEREWITH
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: No. 6153402 Yet Assigned
FILING DATE: 06-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,711
FILING DATE: 17-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,285

FILING DATE: 12-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Steife, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1254 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1251
US-08-815-469-3

Alignment Scores:
Pred. No.: 1.18e-174 Length: 1254
Score: 2209.00 Matches: 393
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-993-234-6_COPY_25_417 (1-393) x US-08-815-469-3 (1-1254)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
Db 73 CAGGGCGGCACTCGTAGCCCGCAGGGTGTGACTGTGCCGGTGACTTCCACAGAAGATTGGT 132
QY 21 LeuphCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
Db 133 CTGTTTGTGGCAGAGGCTGCCAGCGGGGCACTACTGGAAGCCCCCTTGCACGGAGCCC 192
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTyrGluAsnHis 60
Db 193 TGGGGCAACTCCACCTGCTGTGTGTCCCAAGACACTTCTTGGCCTGGAGAACCCAC 252
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db 253 CATAATTCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCCCTCCAGGTGGCGCTG 312
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTyrPheValGlu 100
Db 313 GAGAACTGTTCAGCAGTGGCCGACACCCCGTGTGGCTGTAAGCCAGGCTGTGTGGAG 372
QY 101 CysGlnValSerGlnCysValSerSerSerProPheTyrCysGlnProCysLeuAspCys 120
Db 373 TGCAGGTCCAGCAATGTGTCCAGAGTTCACCTTCTACTGCCAACCAATGCTAGACTGC 432
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 433 GGGGCCCTGCACCCGACACACAGGCTACTGTGTCCCGCAGAGATACTGCTGGGACC 492
QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db 493 TGCCTGCTGCTCTATGAAATGGGCGTGGCTGTCTCTGCTGCCCAAGACACCTGTG 552
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTyrPargGlnMetPheTyrValGln 180
Db 553 GGGAGCTGTCCAGAGCGCTGTGCCGCTGTGTGTGGCTGAGGCGAGATGTCTGGTCCAG 612
QY 181 ValLeuLeuAlaGlyLeuValValProLeuLeuGlyAlaThrLeuThrTyrThrTyr 200
Db 613 GTGCTCTGTGGCTGGCTTGTGTGCCCTCTGTGGGGCCACCTGACCTACACATAC 672
QY 201 ArgHisCysTyrProHisLysProLeuValThrAlaAspGluAlaGlyMetGluAlaLeu 220
Db 673 CGCCACTGCTGGCTCACAAGCCCGCTGTACTGCAGATGAAGCTGGGATGAGGCTCTG 732

QY 221 ThrProProAlaThrHisLeuSerProLeuAspSerAlaHisThrLeuLeuAlaPro 240
Db 733 ACCCCACACCGGCCACCCATCTGTACCTTGGACAGCGCCACACCCCTTCTAGACACT 792
QY 241 ProAspSerSerGluLysIleCysThrValGlnLeuValGlyAsnSerTyrThrProGly 260
Db 793 CCGTACAGCAGTGAAGAATCTGCACCGCTCCAGTTGGTGGTAAACAGCTGGACCCCTGCC 852
QY 261 TyrProGluThrGlnGluAlaLeuCysProGlnValThrTyrSerTyrPargLysPro 280
Db 853 TACCCGAGAGCCAGAGAGCGCTGTGCCCGCAGGTGACATGTCTCTGGAGCACAGTGGCC 912
QY 281 SerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSerProAlaGlySer 300
Db 913 AGCAGACTCTTGGCCCGCTGTCTGCCCGCACACTCTGCCACAGAGTCCCGACCGGCTCG 972
QY 301 ProAlaMetMetLeuGlnProGlyProGlnLeuTyrAspValMetAspAlaValProAla 320
Db 973 CCAGCCATGATGCTGCAGCGCGGCCCGCAGCTCTACGACGTGATGAGCGGCTGCCAGCG 1032
QY 321 ArgArgTyrLysGluPheValArgThrLeuGlyLeuArgGluAlaGluIleGluAlaVal 340
Db 1033 CGGGCTGGAAGAGTGTCTGCGCACAGCTGTGGGCTGTGGCGGAGCAGAGATGAGCCGTG 1092
QY 341 GluValGluIleGlyArgPheArgAspGlnGlnTyrGluMetLeuLysArgTyrPargLys 360
Db 1093 GAGGTGAGATCGGCCGCTTCCGAGACACAGCAGCAGATGATGCTCAAGCGCTGGCGCCAG 1152
QY 361 GlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMetGlyLeuAspGly 380
Db 1153 CAGCAGCCCGCGGCTCGGAGCGCTTACGCGGCGCTGAGCGCATGGGCTGGACGGC 1212
QY 381 CysValGluAspLeuArgSerArgLeuGlnArgGlyPro 393
Db 1213 TGCCTGGAAGACTTGCAGCGCCCTGACGCGGCGCCG 1251

RESULT 2
US-08-928-069-11
Sequence 11, Application US/08928069
Patent No. 6462176

GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-3 POLYPEPTIDE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,069
FILING DATE: 11-Sep-1997
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/026943
FILING DATE: 09/23/1996
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1052R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:

LENGTH: 1634 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
US-08-928-069-11

Alignment Scores:

Pred. No.:	1.75e-174	Length:	1634
Score:	2209.00	Matches:	393
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-09-993-234-6_COPY_25_417 (1-393) x US-08-928-069-11 (1-1634)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
DB 161 CAGGGCGGCACTCGTAGCCCCAGGTGTGACTGTGCCGGTGACTTCCACAAGAAGATTGGT 220
QY 21 LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
DB 221 CTGTTTGTTCAGAGGCTGCCCGCGGGGCACTACCTGAAGGCCCCCTTGACAGGAGCCC 280
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
DB 281 TGGGGCACTCCACCTGCTGTGTGTCCTCCCAAGACACCTTCTTGCGCTGGAGAACCCAC 340
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
DB 341 CATAACTCTGAATGTGCCCCGCTGCGAGGCTGTGATGAGCAGGCTCCACAGGTGGCGCTG 400
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
DB 401 GAGAACTGTTCAGAGTAGGCGGACACCGCTGTGCTGTAAGCCAGGCTGGTTGTGAG 460
QY 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120
DB 461 TGGCAGGTCAGCCAATGTGTACAGCAGTTACACCTTCTACTGCCAACCAATGCCCTAGACTGC 520
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
DB 521 GGGGCCCTGCACCGCCACACAGGGCTACTCTGTCCCGCAGAGATACTGACTGTGGAGCC 580
QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
DB 581 TGCCTGCTGGCTTCTATGAACATGGCGATGGCTGCTGCTGCCGCCACGAGCACCCCTG 640
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArgGlnMetPheTrpValGln 180
DB 641 GGGAGCTGTCCAGAGCGCTGTGCCCTGTCTGTGGCTGAGGCGAGATGTCTGGGTCCAG 700
QY 181 ValLeuLeuAlaGlyLeuValValProLeuLeuGlyAlaThrLeuThrTyrThrTyr 200
DB 701 GTGCTCTGGCTGGCTGTGTGCTCCCTCTGCTGTGGGCCACCTGACCTACACATAC 760
QY 201 ArgHisCysTrpProHisLysProLeuValThrAlaAspGluAlaGlyMetGluAlaLeu 220
DB 761 CGCCACTGTGCTGAGAGCGCTGTGCCCTGTCTGTGGCTGAGGCGAGATGGAGGCTCTG 820
QY 221 ThrProProAlaThrHisLeuSerProLeuAspSerAlaHisThrLeuLeuAlaPro 240
DB 821 ACCCCACACCGGGCCACCCATCTGTACACCTTGACAGGCGCCACACCCCTTCTAGCACCT 880
QY 241 ProAspSerSerGluLysIleCysThrValGlnLeuValGlyAsnSerTrpThrProGly 260
DB 881 CCTGACAGCAGTGAGAAGATCTGCACGCTCCAGTTGGTGGTAACAGCTGGACCCCTGGC 940
QY 261 TyrProGluThrGlnGluAlaLeuCysProGlnValThrTrpSerTrpAspGlnLeuPro 280
DB 941 TACCCCGAGACCCAGAGGCGCTGTGCCCGCAGGTGACATGTCTCTGGGACACAGTTGCC 1000
QY 281 SerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSerProAlaGlySer 300

DB 1001 AGCAGAGCTCTGGCCCCCGCTGTGCGGCCACACTCTCGCCAGAGTCCCCAGCGGCTCG 1060
QY 301 ProAlaMetLeuLeuGlnProGlyProGlnLeuTyrAspValMetAspAlaValProAla 320
DB 1061 CCAGCCATGATGCTGCAGACCGGGCCCGCAGCTCTACGACGTGATGACCGCGCTCCAGCG 1120
QY 321 ArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGluAlaGluIleGluAlaVal 340
DB 1121 CGGCGCTGGAAGAGATTGCTGCGCAGCGCTGGGGCTGCGCGAGGCGAGAGATCGAAGCCGTG 1180
QY 341 GluValGluIleGlyArgPheArgAspGlnGlnTyrGluMetLeuLysArgTrpArgGln 360
DB 1181 GAGGTGAGATCGCGCGCTTCCGAGACAGCAGTACGAGATGCTCAAGCGCTGGCGCCAG 1240
QY 361 GlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMetGlyLeuAspGly 380
DB 1241 CAGCAGCCCCGGGCGCTCGAGCGCTTTCACCGCGCCCTGAGCGCGCATGGCGCTGAGCGGC 1300
QY 381 CysValGluAspLeuArgSerArgLeuGlnArgGlyPro 393
DB 1301 TGGTGGAAGACTTGGCAGCGCGCTGACGGCGGCGCCG 1339

RESULT 3

US-08-828-683A-9
; Sequence 9, Application US/08828683A
; Patent No. 6469144

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/828,683A
FILING DATE: 31-Mar-1997
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/625328
FILING DATE: 1-Apr-1996
APPLICATION NUMBER: 08/710802
FILING DATE: 23-Sep-1996

ATTORNEY/AGENT INFORMATION:

NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:
LENGTH: 1634 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-08-828-683A-9

Alignment Scores:

Pred. No.:	1.75e-174	Length:	1634
Score:	2209.00	Matches:	393
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0

Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-09-993-234-6_COPY_25_417 (1-393) x US-08-828-683A-9 (1-1634)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
DB 161 CAGGGCGGCGACTGTAACCCAGGTGTAAGTGTGCGGGTACTTCCACAAGAAGATTGGT 220
QY 21 LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
DB 221 CTGTTTGTGTCAGAGGCTGCCAGCGGGGCACTTGAAGGCCCTTGACAGGAGCC 280
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
DB 281 TGGCGCACTCCACCTGCTGTGTGTGTCACAGACACCTTCTTGCGCTGGAGAACCC 340
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
DB 341 CATTAATCTGAATGTGCCCGCTGCGCAGGCTGTGATGAGCAGGCGCTCCAGGTGGCGCTG 400
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
DB 401 GAGAACTGTTCAGCAGTGGCGGACACCGCGCTGTGGCTGTAGCCAGGCTGTTGTGGAG 460
QY 101 CysGlnValSerGlnCysValSerSerSerProPheTyrCysGlnProCysLeuAspCys 120
DB 461 TGGCAGGTTCAGCCATGTGTACAGAGTTCACCCCTTCTACTGCCAACCATGCTAGACTGC 520
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
DB 521 GGGGCGCTGCACCGCCACACAGGCTACTCTGTTCGCCGAGAGATACTGACTGTGGGACC 580
QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
DB 581 TGCCTGCTGCTGCTTATGACATGGCGATGGCTGCTGCTGCCACAGACACCGCTG 640
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArgGlnMetPheTrpValGln 180
DB 641 GGGAGCTGTCCAGAGCGCTGTGCGCTGTGTGGCTGGAGGACAGATGTTCTGGGTCCAG 700
QY 181 ValLeuLeuAlaGlyLeuValValProLeuLeuGlyAlaThrLeuThrTyrThrTyr 200
DB 701 GTGCTCTGCTGGCTGTGTGCTGCCCTCTGCTTGGGGCCACCGCTGACCTACACATAC 760
QY 201 ArgHisCysTrpProHisLysProLeuValThrAlaAspGluAlaGlyMetGluAlaLeu 220
DB 761 CGCCACTGTGCGCTTACACAAGCCCTGTGTACTGCAGATGAAGCTGGGATGGAGGCTCTG 820
QY 221 ThrProProAlaThrHisLeuSerProLeuAspSerAlaHisThrLeuLeuAlaPro 240
DB 821 ACCCCACACCGGCGCCACCATCTGTACACCTTGGACAGCGCCACACCGCTTCTAGCACCT 880
QY 241 ProAspSerSerGluLysIleCysThrValGlnLeuValGlyAsnSerTrpThrProGly 260
DB 881 CCTGACAGCAGTGAAGAATCTGCACCGCTCAGTTGTTGGTTAACAGCTGGACCCCTGGC 940
QY 261 TyrProGluThrGlnGluAlaLeuCysProGlnValThrTrpSerTrpAspGlnLeuPro 280
DB 941 TACCCCGAGACCGAGGAGCGCTGTGCGCAGAGTGCATGTCTGTGGAGCACAGTTGCC 1000
QY 281 SerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSerProAlaGlySer 300
DB 1001 AGCAGAGCTCTTGCCCGCTGTGCTGCCACACTCTCGCCAGAGTCCCCAGCGGCTCG 1060
QY 301 ProAlaMetLeuGlnProGlyProGlnLeuTyrAspValMetAspAlaValProAla 320
DB 1061 CCAGCCATGATGCTGCAGCGCGGCGGAGCTTACGACGTGATGAGCGCGGTCCAGCG 1120
QY 321 ArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGluAlaGluIleGluAlaVal 340
DB 1121 CGGCGCTGGAAGAGTCTGTCGCGCACGCTGGGGCTGCGCGAGCGAGAGATCGAAGCGCTG 1180

QY 341 GluValGluIleGlyArgPheArgAspGlnGlnTyrGluMetLeuLysArgTrpArgGln 360
DB 1181 GAGGTGAGATCGCGCGCTTCCGAGACACAGCAGTACGAGATGCTCAAGCGCTGCCCGCAG 1240
QY 361 GlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMetGlyLeuAspGly 380
DB 1241 CAGCAGCCCGCGGCGCTCGAGCGCGTTTACGCGCGCCCTGGAGCGCATGGGGCTGACGCG 1300
QY 381 CysValGluAspLeuArgSerArgLeuGlnArgGlyPro 393
DB 1301 TGGGTGAAGACTTGGCGACCGCGCTGCAGCGCGCGCCG 1339

RESULT 4

US-08-815-469-1
Sequence 1, Application US/08815469
Patent No. 6153402

GENERAL INFORMATION:

APPLICANT: Yu, Guo-Liang
APPLICANT: Ni, Jian
APPLICANT: Dixit, Vishva
APPLICANT: Gentz, Reiner L.
APPLICANT: Dillon, Patrick J.
TITLE OF INVENTION: Death Domain Containing Receptors
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/815,469
FILING DATE: HERewith

CLASSIFICATION: 435

Prior Application DATA:
APPLICATION NUMBER: No. 6153402 yet Assigned
FILING DATE: 06-FEB-1997
Prior Application DATA:
APPLICATION NUMBER: US 60/028,711
FILING DATE: 17-OCT-1996

Prior Application DATA:
APPLICATION NUMBER: US 60/013,285
FILING DATE: 12-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488, 0310003/EKS/KRM

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 1783 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:

NAME/KEY: CDS
LOCATION: 198..1481
US-08-815-469-1

Alignment Scores:

Pred. No.: 1.99e-174 Length: 1783
Score: 2209.00 Matches: 393
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0 Gaps: 0
DB: 3
US-09-993-234-6_COPY_25_417 (1-393) x US-08-815-469-1 (1-1783)
QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
Db 303 CAGGGCGGCACTGCTAGCCCGCAGGTGTGACTGTGCCGGTACTTCCACAGAAGATTGGT 362
QY 21 LeuPheCysCysArgGlyCysProAlaGlyHisIleuLysAlaProCysThrGluPro 40
Db 363 CTGTTTGTGTCAGAGGCTGCCAGCGGGGCACTACTGAGGGCCCTTGCACGGAGGCC 422
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db 423 TCGGGCACTCCACCTGCTGTGTGTCGCCAGACACCTTCTTGGCTGGAGAACCCAC 482
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db 483 CATTAATTCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCCCTCCAGGTGGCGCTG 542
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
Db 543 GAGAACTGTTCAAGCAGTGGCCGACACCCGCTGTGGCTGTAAGCCAGGCTGTGGAG 602
QY 101 CysGlnValSerGlnCysValSerSerSerProPheTrpCysGlnProCysLeuAspCys 120
Db 603 TGCCAGGTCAAGCAATGTTTCAGACAGTTCACCCCTTCTACTGCCAACCATGCCCTAGACTGC 662
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 663 GGGGGCCCTGCACCGCCACACAGGCTACTCTGTTCGCCGACAGATACTGACTGTGGACCC 722
QY 141 CysLeuProGlyPheTrpGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db 723 TGCTTGCTGCTGCTTCTATGACATGGCGATGGCTGCTGCTGCCACGAGCACCTG 782
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArgGlnMetPheTrpValGln 180
Db 783 GGGAGCTGTCCAGAGCGCTGTGCCGCTGTGTGGCTGAGGACAGATGTTCTGGTCCAG 842
QY 181 ValLeuLeuAlaGlyLeuValValProLeuLeuLeuGlyAlaThrLeuThrTrpTyr 200
Db 843 GTGCTCTGCTGGCTGTGTGTCCTCCCTCTGCTGGGGCCACCTGACCTACACATAC 902
QY 201 ArgHisCysTrpProHisLysProLeuValThrAlaAspGluAlaGlyMetGluAlaLeu 220
Db 903 CGCCACTGCTGGCTTCAAGAGCCCTGTGTACTGCAAGTGAAGCTGGATGGAGGCTCTG 962
QY 221 ThrProProProAlaThrHisLeuSerProLeuAspSerAlaHisThrLeuLeuAlaPro 240
Db 963 ACCCCACACCGGCCCATCTGTACCCCTTGGACAGCGCCACACACCTTCTAGCACCT 1022
QY 241 ProAspSerSerGlyLysIleCysThrValGlnLeuValGlyAsnSerTrpThrProGly 260
Db 1023 CCGTACAGCAGTGAAGATCTGCACCGTCCAGTGTGGGTAAACAGCTGAGCCCTGCG 1082
QY 261 TyrProGluThrGlnGluAlaLeuCysProGlnValThrTrpSerTrpAspGlnLeuPro 280
Db 1083 TACCCCGAGACCCAGAGCGCTCTGCGCCGACAGTGCATGTCTGTGAGCACAGTGGCC 1142
QY 281 SerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSerProAlaGlySer 300
Db 1143 AGCAGAGCTCTGGCCCGCTGCTGCGCCACACTCTGCCACAGAGTCCCCAGCGGCTCG 1202
QY 301 ProAlaMetMetLeuGlnProGlyProGlnLeuTrpAspValMetAspAlaValProAla 320
Db 1203 CCAGCCATGATGCTGCAGCGGGGGCCGACAGCTTACGACGTGATGGACGGGCTCCACGG 1262
QY 321 ArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGluAlaGluIleGluAlaVal 340
Db 1263 CGCGCGTGAAGAGATTCTGCGCACGCTGGGGCTGGCGAGGACAGAGATCGAAGCCGCTG 1322

QY 341 GluValGluIleGlyArgPheArgAspGlnGlnIleTyrGluMetLeuLysArgTrpArgGln 360
Db 1323 GAGGTGAGATCGGCCGCTTCCAGAGACAGACAGTACGAGATGCTCAAGCGCTGCCCGCAG 1382
QY 361 GlnGlnProAlaGlyLeuGlyAlaValIleTyrAlaAlaLeuGluArgMetGlyLeuAspGly 380
Db 1383 CAGCAGCCCCGGGGCTCGAGCCGTTTACGCGGCCCTGAGCGCATGGGGCTGGAGCGC 1442
QY 381 CysValGluAspLeuArgSerArgLeuGlnArgGlyPro 393
Db 1443 TGGCTGAAGACTTGGCAGCGCCCTGACGCGCGGCCG 1481

RESULT 5

US-08-928-069-5

Sequence 5, Application US/08928069

Patent No. 6462176

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

TITLE OF INVENTION: Apo-3 POLYPEPTIDE

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/928,069

FILING DATE: 11-Sep-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/026943

FILING DATE: 09/23/1996

ATTORNEY/AGENT INFORMATION:

NAME: Marschang, Diane L.

REGISTRATION NUMBER: 35,600

REFERENCE/DOCKET NUMBER: P1052R1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-5416

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 1438 base pairs

TYPE: Nucleic Acid

STRANDEDNESS: Single

TOPOLOGY: Linear

US-08-928-069-5

Alignment Scores:

Pred. No.: 4.25e-70

Score: 952.00

Percent Similarity: 93.71%

Best Local Similarity: 93.14%

Query Match: 43.10%

DB: 4

Length: 1438

Matches: 163

Conservative: 1

Mismatches: 3

Indels: 8

Gaps: 1

US-09-993-234-6_COPY_25_417 (1-393) x US-08-928-069-5 (1-1438)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
Db 449 CAGGGCGGCACTGCTAGCCCGCAGGTGTGACTGTGCCGGTACTTCCACAGAAGATTGGT 508
QY 21 LeuPheCysCysArgGlyCysProAlaGlyHisIleuLysAlaProCysThrGluPro 40
Db 509 CTGTTTGTGTCAGAGGCTGCCACAGCGGGGCACTACTGTAAGGCCCTTGCACGGAGGCC 568
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60

```

Db      569  TCGGGCAACTCCACCTGCTGTGTGTCCTCCAGACACACCTTCTGGCTGGAGAACAC 628
QY      61  HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db      629  CATATTTCTGAATGTGCCCTGCTCCAGGCTGTGATGAGCAGGCTCCAGGCTGGCGCTG 688
QY      81  GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
Db      689  GAGAACTGTTACAGAGTGCGCCGACACCCGCTGTGGCTGTAGCCAGGCTGTTGTGGAG 748
QY      101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120
Db      749  TCCAGGTCAGCCAATGTGTACAGAGTTCACCTTCTACTGCCAACCATGCTAGACTGC 808
QY      121 GAlaAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db      809  GGGGCCCTGCACCGCCACACACGGCTACTGTCTCCCGCAGAGATACTGACTGTGGGACC 868
QY      141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db      869  TGCCTGCTGCTTCTATGAACATGGCGATGGCTGCTGCTCTGCTCCCGCAGCTAATTCCTA 928
QY      161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArgGln 175
Db      929  -----GCTGTCGTGGATGAGGGGAA 949

RESULT 6
US-08-828-683A-5
; Sequence 5, Application US/08828683A
; Patent No. 6469144
; GENERAL INFORMATION:
;   APPLICANT: Ashkenazi, Avi J.
;   TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
;   NUMBER OF SEQUENCES: 28
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Genentech, Inc.
;     STREET: 1 DNA Way
;     CITY: South San Francisco
;     STATE: California
;     COUNTRY: USA
;     ZIP: 94080
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/828, 683A
;   FILING DATE: 31-Mar-1997
;   CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/625328
;   FILING DATE: 1-Apr-1996
;   APPLICATION NUMBER: 08/710802
;   FILING DATE: 23-Sep-1996
; ATTORNEY/AGENT INFORMATION:
;   NAME: Marschang, Diane L.
;   REGISTRATION NUMBER: 35,600
;   REFERENCE/DOCKET NUMBER: P1007P1
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 650/225-5416
;   TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 5:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 1438 base pairs
;     TYPE: Nucleic Acid
;     STRANDEDNESS: Single
;     TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-08-828-683A-5
```

Alignment Scores:

```

Pred. No.: 4.25e-70
Score: 952.00
Percent Similarity: 93.71%
Best Local Similarity: 93.14%
Query Match: 43.10%
DB: 4
Gaps: 1

US-09-993-234-6_COPY_25_417 (1-393) x US-08-828-683A-5 (1-1438)

QY      1  GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
Db      449  CAGGGCGGCACTCGTAGCCCGCAGGTGTGACTGTGCCGGTGACTTCCACAAGAGATTGGT 508
QY      21  LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
Db      509  CTGTTTGTGTGACAGAGGCTGCCAGCGGGGCACTTGAAGGCCCTTGACGAGGCC 568
QY      41  CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db      569  TCGGGCAACTCCACCTGCTGTGTGTCCCAAGACACCTTCTTGCGCTGGAGAACAC 628
QY      61  HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db      629  CATATTTCTGAATGTGCCCTGCTCCAGGCTGTGATGAGCAGGCTCCAGGCTGGCGCTG 688
QY      81  GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
Db      689  GAGAACTGTTACAGAGTGCGCCGACACCCGCTGTGGCTGTAGCCAGGCTGTTGTGGAG 748
QY      101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120
Db      749  TCCAGGTCAGCCAATGTGTACAGAGTTCACCTTCTACTGCCAACCATGCTAGACTGC 808
QY      121 GAlaAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db      809  GGGGCCCTGCACCGCCACACACGGCTACTGTCTCCCGCAGAGATACTGACTGTGGGACC 868
QY      141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db      869  TGCCTGCTGCTTCTATGAACATGGCGATGGCTGCTGCTCTGCTCCCGCAGCTAATTCCTA 928
QY      161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArgGln 175
Db      929  -----GCTGTCGTGGATGAGGGGAA 949

RESULT 7
US-08-928-069-2
; Sequence 2, Application US/08928069
; Patent No. 6462176
; GENERAL INFORMATION:
;   APPLICANT: Ashkenazi, Avi J.
;   TITLE OF INVENTION: Apo-3 POLYPEPTIDE
;   NUMBER OF SEQUENCES: 15
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Genentech, Inc.
;     STREET: 1 DNA Way
;     CITY: South San Francisco
;     STATE: California
;     COUNTRY: USA
;     ZIP: 94080
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/928, 069
;   FILING DATE: 11-Sep-1997
;   CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 60/026943
;   FILING DATE: 09/23/1996
; ATTORNEY/AGENT INFORMATION:
```


NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1052R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 433 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-928-069-2

Alignment Scores:
Pred. No.: 4.25e-47 Length: 433
Score: 666.00 Matches: 127
Percent Similarity: 93.48% Conservative: 2
Best Local Similarity: 92.03% Mismatches: 5
Query Match: 30.15% Indels: 5
DB: 4 Gaps: 0

US-09-993-234-6_COPY_25_417 (1-393) x US-08-928-069-2 (1-433)

QY 2 GlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGlyLeu 21
DB 22 GCGGCACTCGTAGCCCAAGGTGACTGTGCCGGTGACTTCACAAGAAGATTGGTCTG 81
QY 22 PheCysCysArgGlyCysProAla-glyHisTyrLeuLysAlaProCysThrGluProCys 41
DB 82 TTTTGTTCAGAGGCTGCCAGCGGGCACTACCTGAAGGCCCTTGCACGAGCCCTG 141
QY 41 sGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHisH 61
DB 142 CGC-AACTCCACCTGCTGTGTCTCCCAAGACACCTTGTGGCTGGAGAACACCA 200
QY 61 sAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeuG 81
DB 201 TAATTCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCTCCAGGTGGCGCTGA 260
QY 81 uAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGluC 101
DB 261 GAACGTGTACAGAGTGGCCGACACCCGCTGTGGCTGTAAAGCAGGCGTGTGTGAGTG 320
QY 101 sGln-ValSerGlnCysValSerSer-SerProPheTyrCysGlnProCysLeuAspCys 120
DB 321 CCAGGGTCAGCCAATGTGTACAGAGTTTCACCCCTTCTAATGCCAACCATGCTAGACTGC 380
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCys-SerArgArgAsp 135
DB 381 GGGGCCCTGCACACGCAACACAGGCTAATNTGTTCCCGCAGAGAT 426

RESULT 8
US-08-828-683A-2
Sequence 2, Application US/08828683A
Patent No. 6469144

GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/828, 683A
FILING DATE: 31-Mar-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/625328
FILING DATE: 1-Apr-1996
APPLICATION NUMBER: 08/710802
FILING DATE: 23-Sep-1996
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 433 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-08-828-683A-2

Alignment Scores:
Pred. No.: 4.25e-47 Length: 433
Score: 666.00 Matches: 127
Percent Similarity: 93.48% Conservative: 2
Best Local Similarity: 92.03% Mismatches: 5
Query Match: 30.15% Indels: 5
DB: 4 Gaps: 0

US-09-993-234-6_COPY_25_417 (1-393) x US-08-828-683A-2 (1-433)

QY 2 GlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGlyLeu 21
DB 22 GCGGCACTCGTAGCCCAAGGTGACTGTGCCGGTGACTTCACAAGAAGATTGGTCTG 81
QY 22 PheCysCysArgGlyCysProAla-glyHisTyrLeuLysAlaProCysThrGluProCys 41
DB 82 TTTTGTTCAGAGGCTGCCAGCGGGCACTACCTGAAGGCCCTTGCACGAGCCCTG 141
QY 41 sGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHisH 61
DB 142 CGC-AACTCCACCTGCTGTGTCTCCCAAGACACCTTGTGGCTGGAGAACACCA 200
QY 61 sAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeuG 81
DB 201 TAATTCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCTCCAGGTGGCGCTGA 260
QY 201 TAATTCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCTCCAGGTGGCGCTGA 260
QY 81 uAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGluC 101
DB 261 GAACGTGTACAGAGTGGCCGACACCCGCTGTGGCTGTAAAGCAGGCGTGTGTGAGTG 320
QY 101 sGln-ValSerGlnCysValSerSer-SerProPheTyrCysGlnProCysLeuAspCys 120
DB 321 CCAGGGTCAGCCAATGTGTACAGAGTTTCACCCCTTCTAATGCCAACCATGCTAGACTGC 380
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCys-SerArgArgAsp 135
DB 381 GGGGCCCTGCACACGCAACACAGGCTAATNTGTTCCCGCAGAGAT 426

RESULT 9
US-08-762-308-10

Sequence 10, Application US/08762308
Patent No. 592548
GENERAL INFORMATION:
APPLICANT: Beutler, Bruce A.
APPLICANT: Bazzone, Flavio M.
TITLE OF INVENTION: MODIFIED RECEPTORS THAT CONTINUOUSLY
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/762,308
FILING DATE: 09-DEC-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/224,593
FILING DATE: 05-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: UTSD:335--1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 418-3000
TELEFAX: 474-7577
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1956 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-762-308-10
Alignment Scores:
Pred. No.: 1,75e-23 Length: 1956
Score: 393.50 Matches: 123
Percent Similarity: 39.50% Conservative: 52
Best Local Similarity: 27.77% Mismatches: 183
Query Match: 17.81% Indels: 85
DB: 2 Gaps: 18
US-09-993-234-6_COPY_25_417 (1-393) x US-08-762-308-10 (1-1956)
QY 3 GlyThrArgSerProArg-----CysAspCysAlaGlyAspPheHisLysIle 19
DB 198 GGTGACCGGAGAGAGGATAGCTGTGTGCCCAAGAAAGTATGTCATCTAAGAAC 257
QY 20 GlyLeuPheCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGlu 39
DB 258 AATTCATCTGTGACCAAGTGCACAAAGAACTACTGTGTGAGTGCATGTCGAGC 317
QY 40 ProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTyrGluAsn 59
DB 318 CCAGGCGGATACAGTCTGCAGGAGTGTGAAGGACACCTTTACGGCTTCCAGAAAT 377
QY 60 HisHisAsnSerGlyCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAla 79
DB 378 TACCTCAG--CAGTGTCTCAGTTCGACAGACATGTCGGAAGAAATGTCGAGGTGAG 434
QY 80 LeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTyrPheVal 99
DB 435 ATCTCTCTTCCCAAGCTGACAAAGACAGGCTGTGTGCTGTAG-----479
QY 100 GluCysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAsp 119
DB 480 GAGAACCAAGTTCACACGCTACGTGAGACACACTTCAGTGCCTGAGTGCAGCCCC 539
QY 120 CysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGly 139
DB 540 TGC-----TTCAACGGCACCCTGACAAATCCCTGTAAAGAGACTCAGAACACCGTGT 593
QY 140 ThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThr 159

DB 594 AACTGCCATGCAGGGTCTTTCTGAGAGAAAGTGAGTGCCTCCCTTGC-----641
QY 160 LeuGlySerCysPro-----GluArgCysAlaAlaValCys-----171
DB 642 ---AGCCACTGCAGAAATAAGAGAGAGTGTATGAAGTGTGCTTACCTCCCTCCGTTGCA 698
QY 172 -----GlyTyrArgGlnMetPheTyrValGlnValLeuAla 184
DB 699 AATGTCACAAACCCCGAGACTCAGGTACTGCGGTGCTGTGCCCCCTGTATCTTGTCTA 758
QY 185 GlyLeuValValProLeuLeuGlyAlaThrLeuThrTyrThrTyrArgHisCysTyr 204
DB 759 GGTCTTTCCTTCTATCTTATCTTCATCATCAGTTTAATGCGCATATCCCCGGTGGAG 818
QY 205 Pro-----HisLysProLeuValThrAlaAspGluAlaGlyMet 217
DB 819 CCCGAAGTCTACTCCATCATTTGTAGGGATCCCGTGCCTGTCAAGAGAGAGAGGCTGGA 878
QY 218 GluAlaLeuThrProProProAlaThrHisLeuSerProLeuAspSerAlaHisThrLeu 237
DB 879 AAGCCCTTAAGTCCAGCCCTTCCAGCCCTTCCAGCCCTCCGCTTCAACCCCACT 938
QY 238 Leu-----AlaProProAspSerSerGluLysIleCysThrVal 250
DB 939 CTGGGCTTCAGACCCCGAGCTTGTAGTTCTCTGTCTTCAGTACCCCATCAGCCCATC 998
QY 251 GlnLeuValGlyAsnSerTyr-----ThrPro 259
DB 999 ---TTGGTCTCTAGTAACTGGCACTTCATGCACCTGTCACTGAGTAGTCCCAACCCAG 1055
QY 260 GlyTyr---ProGluThrGlnGluAlaLeuCys-----ProGlnValThrTyr 274
DB 1056 GGAGCTGACCCCTGTCTCTACGAATCACTGTGCTGCCAGCCCGACCTGTCTCAG 1115
QY 275 SerTyrAspGlnLeuProSerArgAlaLeuGlyProAlaAlaProThrLeuSerPro 294
DB 1116 AAATGGGAAGAC-----TCCGCCAACCCG 1139
QY 295 GluSerProAlaGlySerProAlaMetMetLeuGlnProGlyProGlnLeuTyrAspVal 314
DB 1140 CAACGTCCTGACAAATGCAGACCTTGCATT-----CTGTATGCTGTG 1181
QY 315 MetAspAlaValProAlaArgTyrTyrPheValArgThrLeuGlyLeuArgGlu 334
DB 1182 GTGATGGCGGTGCTTCCAGCGCGCTGGAAGAGTTCATGCGTTCATGGGCTGAGCGAG 1241
QY 335 AlaGluIleGluAlaValGluValGluIleGlyArg---PheArgAspGlnGlnTyrGlu 353
DB 1242 CACGAGATCGAGAGGTGAGATGCAGAACGGGCGCTGCTGCGGAGGCTCAGTACAGC 1301
QY 354 MetLeuLysArgTyrPargGlnGlnGlnProAla-----GlyLeuGlyAlaValTyr 370
DB 1302 ATGCTGGAAGCCTGGCGGCGCGCCGACGCCGCCAGAGACACCGCTGGAAGTATGTTGGC 1361
QY 371 AlaAlaLeuGluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGln 390
DB 1362 CTCGTGCTTCCACATGAACCTGGCTGGGTGCTGAGAAATATCTCGAGGCTCTG---1418
QY 391 ArgGlyPro 393
DB 1419 AGAAATCCC 1427
RESULT 10
US-09-513-007-1
; Sequence 1, Application us/09513007
; Patent No. 6406907
; GENERAL INFORMATION:
; APPLICANT: Taylor, J. Michael
; APPLICANT: Kehrli, Jr., Marcus
; APPLICANT: Lee, Eun-Kyung
; APPLICANT: Mwangi, Simon
; TITLE OF INVENTION: BOVINE TUMOR NECROSIS FACTOR RECEPTOR-1
; TITLE OF INVENTION: AND METHODS OF USE

FILE REFERENCE: 08411-018001
; CURRENT APPLICATION NUMBER: US/09/513,007
; CURRENT FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 60/122,156
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2440
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (294)...(1706)
; US-09-513-007-1

Alignment Scores:
Pred. No.: 1.64e-22 Length: 2440
Score: 383.50 Matches: 120
Percent Similarity: 37.56% Conservative: 46
Best Local Similarity: 27.15% Mismatches: 173
Query Match: 17.36% Indels: 103
DB: 4 Gaps: 16

US-09-993-234-6_COPY_25_417 (1-393) x US-09-513-007-1 (1-2440)

QY 16 HisLysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAla 35
||| ::| ||||| ||| ||| |||||
Db 444 CACCCGCAAAATAGCACCATTTGCTGCACCAAGTGCACAAAGGTACCTATCTGTACAAAT 503

QY 36 ProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeu 55
||| ||| ::| ||| ||||| ||| |||
Db 504 GACTGTCCGGGTCCAGGGGAGACAGGACTGCAGGGTGTGTGCCCCCTGGCACCCTACACT 563

QY 56 AlaTrpGluAsnHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAla 75
||| ||||| ||| ||| ||| ||| ::| |||
Db 564 GCCTTGAGAGAACCATCTCAGA--CGATGCCCTGAGCTGCCAGGTGCCGGGAGCAAAATG 620

QY 76 SerGlnValAlaLeuGluAsnSerAlaValAlaAspThrArgCysGlyCysLysPro 95
||||| ::| ||| ||||| ||||| ||||| |||||
Db 621 TTCACAGTGGAGATTTCGCCCTGTGTAGTGAGCCGGGACACTGTGTGCGGCTGCAGGAAG 680

QY 96 GlyTrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCysGln 115
||| ||| ::| ||| ||| ||| ||| |||
Db 681 AAC-----CAGTACCGGGAATACTGGGGTGAATGCGCTTCCGGTGTCTG 725

QY 116 ProCysLeuAspCys-----GlyAlaLeuHisArgHisThrArgLeuLeuCys---Ser 132
||| ||| ||| ::| ||| ||| ||| |||
Db 726 AACTGCAGCCTCTGTCCCAATGGCAGCTGAAT-----ATCCCTGCCAGAG 773

QY 133 ArgArgAspThrAspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCys 152
|||::| ||||| ||| ||| |||||::| ||| |||
Db 774 AGACAGGACACCATCTGC--CACTGCCATATGGGCTTCTTTAAAGGCCCAAGTGC 830

QY 153 ValSerCysProThrSerThrLeuGlySerCysProGluArg---CysAlaAlaValCys 171
::| ||||| ||| ||| ||| ::| ||| |||
Db 831 ATCTCTGT-----CATGATTGTAGAACAAGAGTGCAGAGATTATGT 875

QY 172 GlyTrpArg-----GlnMetPheTrpVal 179
||| ||| ::| ||| ||| ||| |||
Db 876 CCAACCCGACCTTCACTGTGAAGACTCTCAGAGCCAGGCACTACAGTACTATTACCC 935

QY 180 GlnValLeuLeuAlaGlyLeuValAlaProLeuLeuGlyAlaThrLeuThrTyrThr 199
|||::| ||||| ||| ||| ||| ||| |||
Db 936 CTGTGATTGTCTTGGGCTTGCCATGCACTTCGCTGTGTCTTAGCATGTGCG 995

QY 200 TyrArgHisCysTrpProHisLys----- 207
|||::| ||| ||| ||| ||| ||| |||
Db 996 TACAGCGG---TGGAAGCCCAAGTCTACTCCATCATTTGGGGCAGTCGACTCTGTA 1052

QY 207 ----- 207
1053 AAAGAGGGGAGCCAGAACTCTGTGTCGGGGCCAGGCTTCAACCCCAACCAACCATC 1112

QY 208 -----ProLeuValThrAlaAsp 213
Db 1113 TGCTTACAGTCCACCCCAAGTTCACGTCTGTCTCCATTCGCCCTTACATCTCTGTGAC 1172

QY 214 GluAlaGlyMetGluAlaLeuThrProProAlaThrHisLeuSerProLeuAspSer 233
::| ||| ||| ||| |||
Db 1173 CGGTCCACTTCGGAGCGGCTCGCATCTCCCTCCAGCGAGAGCGGCCGCCCATCTAAAG 1232

QY 234 AlaHisThrLeuLeuAlaProProAspSerSerGluLysIleCysThrValGlnLeuVal 253
||| ::| ||| ||| ||| ||| |||
Db 1233 GCTGGCCCCATCTCCCGGGGCTCGGCTCCACCCACCTCTGTACCCCGGGGCTCCG 1292

QY 254 GlyAsnSer-----TrpThrProGlyTyrProGluThrGlnGluAlaLeuCysProGln 271
::| ||| ||| ||| ||| ||| |||
Db 1293 GCCTCCACCACCTCTGTACCCCGGGGCTCCGCTCCACCCACCTCTGCACCCAGTT 1352

QY 272 ValThrTrpSerTrpAspGlnLeuProSerArgAlaLeuGlyProAlaAlaProThr 291
||| ||| ||| ||| ||| ||| |||
Db 1353 CAGAAGTGG-----GAAGCCAGCGCCCGCCAGCGCCCGATCAG 1391

QY 292 LeuSerProGluSerProAlaGlySerProAlaMetMetLeuGlnProGlyProGlnLeu 311
|||::| ||||| ||| ||| ||| |||
Db 1392 CTCGGGATGCCGACCCCGG-----ACCTG 1418

QY 312 TyrAspValMetAspAlaValProAlaArgTrpLysGluPheValArgThrLeuGly 331
||| |||::| ||||| ||||| ||||| ||||| |||||
Db 1419 TACGGGTGTGAGCGGCGGTGCCCGCTGCCCTGGAAGAGTTGTGCGGGCTGGA 1478

QY 332 LeuArgGluAlaGluIleGluAlaValGluValGluIleGlyArg---PheArgAspGln 350
||| ||| ||||| ||| ||| ||| ||| ||| |||
Db 1479 CTGAGCGAGCAGAGATCGAGCGGCTGAGAGTGGAGAACGGGCGCACCTGCGGAGCG 1538

QY 351 GlnTyrGluMetLeuLysArgTrpArgGlnGlnPro-----AlaGlyLeuGly 367
||||| ||||| ||||| |||||::| ||| ||| |||
Db 1539 CAGTACAGCATGCTGGCGGCTGGCGGCGCACGCGCGCGGAGGCCACGCTGAG 1598

QY 368 AlaValTyrAlaAlaLeuGluArgMetGlyLeuAspGlyCysValGluAspLeuArgSer 387
::| ||| ||| ||| ||| ||| ||| ||| |||
Db 1599 CTGCTGGGCGCGTGTCTCAGGAGCATGGACCTGTGGTTGCGTGAACATAGAGAG 1658

QY 388 ArgLeu 389
||| ||| ||| ||| ||| ||| ||| |||
Db 1659 GCGCTG 1664

RESULT 11
US-08-050-319B-24
; Sequence 24, Application US/08050319B
; Patent No. 5633145

GENERAL INFORMATION:
; APPLICANT: M.Feldmann, P.W. Gray,
; APPLICANT: M.J.C. Turner, F.M.Brennan
; TITLE OF INVENTION: Modified human TNFalpha (Tumor
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reed & Robbins
; STREET: 635 Bryant Street
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94301

COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/050,319B
; FILING DATE: 10-May-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Robbins, Roberta L.

```

: REGISTRATION NUMBER: 33,208
: REFERENCE/DOCKET NUMBER: 5150-0030
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 617-8999
: TELEFAX: (415) 327-3231
: INFORMATION FOR SEQ ID NO: 24:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2062 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA to mRNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 155..1519
: US-08-050-319B-24

Alignment Scores:
Pred. No.: 1.4e-21
Score: 371.00
Percent Similarity: 39.28%
Best Local Similarity: 28.44%
Query Match: 16.79%
Matches: 126
Conservative: 48
Mismatch: 177
Indels: 92
Gaps: 21

US-09-993-234-6_COPY_25_417 (1-393) x US-08-050-319B-24 (1-2062)

QY 3 GlyThrArgSerProArg-----CysAspCysAlaGlyAspPheHisLysIle 19
Db 257 GGGGACAGGAGAGAGAGATGTGTGTCCCAAGAAATATATCCACCCTCAAAAT 316
QY 20 GlyLeuPheCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGlu 39
Db 317 AATTCGATTGTGTGTACCAAGTCCACAAAGAACCTACTGTACATGACTGTCCAGGC 376
QY 40 ProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsn 59
Db 377 CCGGGGACAGATACGAGTCCAGGAGTGTGAGACCGGCTCTTCCACCCTTCAGAAAC 436
QY 60 HisHisAsnSerGlyCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAla 79
Db 437 CACCTCAGA---CACTGCCCTCAGCTGCTCCAAATGCCGAAAGAAATGGGTGAGTGGAG 493
QY 80 LeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTyrPheVal 99
Db 494 ATCTCTTCTTGCACAGTGGACCGGACACCGTGTGTGCTGCAGGAAGAACAGTACCGG 553
QY 100 GluCys-----GlnValSerGlnCysValSerSerProPheTyrCysGlnPro 116
Db 554 CATTAATGAGTGAACCTTTTCCAGTGC-----TTCAATTGCAACCTC 598
QY 117 CysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThr 136
Db 599 TGCCTCAAT---GGGACCGGTGCAC-----CTCTCCTGCCAGAGAAACAGAAC 643
QY 137 AspCysGlyThrCysLeuProGlyPheTyrGlnHisGlyAspGlyCysValSerCysPro 156
Db 644 ACCGTGTGCACCTGCATGCAGGTTCTTCTAAGAGAAACGAGTGTCTCTCTGT--- 700
QY 157 ThrSerThrLeuGlySerCysProGlu-----ArgCysAlaAlaValCys----- 171
Db 701 -----AGTAACGTGAAGAAACCTGGAGTGCACGAGTGTGTGCTTACCCAG 748
QY 172 -----GlyTrrArgGlnMetPheTrpValGlnValLeu 182
Db 749 ATTGAGATGTTAAGGACAGTGAAGTACAGCAGTGTGTGCCCCCTGTCAAT 808
QY 183 LeuAlaGlyLeuValAlaProLeuLeuGlyAlaThrLeuThrTyrThrArgHis 202
Db 809 TTTCTTGTGCTTGCCTTTATCCCTCTCTCATGTGTTAATGATTCGCTACCAACGG 868
QY 203 CysTrpProHisLys-----ProLeuValThrAlaAspGluAla 215
Db 111
```

```

Db 869 ---TGGAAGTCCAAGCTCTACTCCATTGTTGTGGGAATCGACACCTGAAAGAGGGG 925
QY 216 GlyMetGluAlaLeuThrProProProAlaThrHisLeuSerProLeuAspSer----- 233
Db 926 GAGCTTGAAGAACTACTACTAAGCCC-----CTGGCCCCAAACCAAGCTTCACT 976
QY 234 -----AlaHisThrLeuLeuAlaProProAspSerSerGluLysIleCys 248
Db 977 CCGACTCCAGGCTTCACCCCACTGGGCTTCAGTCCCGTCCCAAGTTCACCTTCACC 1036
QY 249 ThrValGlnLeuValGlyAsnSerThrProGlyTyrProGluThrGlnGlnAlaLeu 268
Db 1037 TCC-----AGCTCCACCTATACCCCGGTGAC----- 1063
QY 269 CysProGlnValThrTrpSerTrpAspGlnLeuProSerArgAlaLeuGlyPro----- 286
Db 1064 TGTCCCACTTGGC-----GCTCCCGCAGAGAGGTGGACACCACTAT 1108
QY 287 -----AlaAlaAlaProThrLeuSerPro--- 294
Db 1109 CAGGGGGCTGACCCCATCTTGGACAGCCCTCGCTCCGACCCCATCCCAACCCCTT 1168
QY 295 -----GluSerProAlaGlySerProAlaMetLeuGlnProGlyProGln--- 310
Db 1169 CAGAAAGTGAGAGACAGTCCACCAAGCCACAGAGCCCTAGACACTGATGACCCCGGACG 1228
QY 311 LeuTyrAspValMetAspAlaValProAlaArgArgTyrPlyGluPheValArgThrLeu 330
Db 1229 CTGTACGCCGTGTGTGAGAACGTGCCCCCGTGGCTGGAAGAAATTCGTGGCGCCCTA 1288
QY 331 GlyLeuArgGluAlaGluIleGluAlaValGlnValGluIleGlyArg---PheArgAsp 349
Db 1289 GGGCTGAGCGACCGACAGATCGATCGGCTGAGCTGCAGAACGGCGCTGCTGCGCGAG 1348
QY 350 GlnGlnTyrGlnMetLeuLysArgTyrPargGlnGlnPro-----AlaGlyLeu 366
Db 1349 GCGCAATACAGCATCTGTGCGCAGCTGAGGCGGCGCACCGCGCGGAGGCCACGCTG 1408
QY 367 GlyAlaValTyrAlaAlaLeuGluArgMetGlyLeuAspGlyCysValGluAspLeuArg 386
Db 1409 GAGCTGTGGAGCGGTGCTCCGCGACATGACCTGCTGGCTGCTGAGGAGACATCGAG 1468
QY 387 SerArgLeu 389
Db 1469 GAGGCGCTT 1477

RESULT 12
US-08-465-982-24
: Sequence 24, Application US/08465982
: Patent No. 5863786
: GENERAL INFORMATION:
: APPLICANT: M.Feldmann, P.W. Gray,
: APPLICANT: M.J.C. Turner, F.M. Brennan
: TITLE OF INVENTION: Modified human TNFalpha (Tumor
: TITLE OF INVENTION: Necrosis Factor alpha) Receptor
: NUMBER OF SEQUENCES: 57
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Reed & Robbins
: STREET: 635 Bryant Street
: CITY: Palo Alto
: STATE: California
: COUNTRY: USA
: ZIP: 94301
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/465,982
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
```



```

; FILING DATE: June 26, 1998
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Laurel Spear Bernstein
; REGISTRATION NUMBER: 37,280
; REFERENCE/DOCKET NUMBER: RTS-0004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (760) 931-9200
; TELEFAX: (760) 603-3820
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2161
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-09-106-038A-1

```

Alignment Scores:	
Pred. No.:	2.2e-21
Score:	369.00
Percent Similarity:	39.05%
Best Local Similarity:	28.44%
Query Match:	16.70%
DB:	3
Length:	216
Matches:	126
Conservative:	47
Mismatches:	178
Indels:	92
Gaps:	21

US-09-993-234-6_COPY_25_417 (1-393) x US-09-106-038A-1 (1-2161)

QY	3	GlyThrArgSerProArg-----CysAspCysAlaGluAspPheHisLysLysIle	19
Db	358	GGGACAGAGGAGAAGAGATAGTGTGTCTCCCAAGAAATAATATCCACCCTCAAAT	417
QY	20	GlyLeuPheCysCysArgGlyCysProAlaGlnHisTyrrLeuLysAlaProCystHrglu	39
Db	418	AATTGCATTGTGTCGTACCAAGTAGGCCACAAGAACCCTACTGTACAAATGACTGTCCAGGC	477
QY	40	ProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluasn	59
Db	478	CCGGGCAGAGATACGAGACTGCAGGAGTGTCAGAGCGCGCTCTCACCGCTTCAGAAAAC	537
QY	60	HisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValala	79
Db	538	CACCTCAGA---CACTGCCCTCAGCTGCTCCAATGCCGAAGAAATGGGTACAGGTGAG	594
QY	80	LeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheVal	99
Db	595	ATCTCTTCTTGCACAGTGGACCCGGACACCCGTGTGTGGCTGCAGGAAGAACAGTACC GG	654
QY	100	GluCys-----GlnValSerGlnCysValSerSerProPheTyrrCysGlnPro	116
Db	655	CATTATTGGAGTGAANAACCTTTTCCAGTGC-----TTCAATTGCAAGCTTC	699
QY	117	CysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThr	136
Db	700	TGCCCTCAAT---GGGACCGTGCAC-----CTCTCCTGCCAGAGAAACAGAAC	744
QY	137	AspCysGlyThrCysLeuProGlyPheTyrrGlnHisGlyAspGlyCysValSerCysPro	156
Db	745	ACCGTGTGCACCTGCCCATGCAGGTTCCTTCTAAGAGAAACGAGTGTGTCTCCTGT---	801
QY	157	ThrSerThrLeuGlySerCysProGlu-----ArgCysAlaAlaValCys-----	171
Db	802	-----AGTAACSTGAAGAAAGCCCTGAGTGCACGAAAGTTGTGCCCTAACCCAG	849
QY	172	-----GlyTrpArgGlnMetPheTrpValGlnValLeu	182
Db	850	ATTGAGAAATGTTAAGGCGACATGACACTCAGGCACACACAGTCTGTGGCCCCGTGCATTT	909
QY	183	LeuAlaGlyLeuValValProLeuLeuLeuGlyAlaThrLeuThrTyrrThrArgHis	202
Db	910	TTCCTTGGTCTTGGCCTTTATTCCTCTCTTCATTTGGTTTAATGTATCGCTACCAACGG	969
QY	203	CysTrpProHisLys-----ProLeuValThrAlaAspGluAla	215

Db	970	--TGGAAAGTCCAAAGCTCTACTCCATGTTTGTGGAAATCGAACACTGA	AAAGAGGGC	1026
QY	216	GLYMETGLAALALEUTHRRPRORPROALATHRRHISLEUSERPROLEUASP	SER-----	233
Db	1027	GAGCTTGAAGGAAGTAATAAGCCC-----CTGGCCCCAAACCAAGCTT	CACT	1077
QY	234	-----ALANISTHRLEULEUALAPROPROASPSERSERGLULYSILE	CYS	248
Db	1078	CCCACTCCAGGCTTCACSSCCACSSCTGGGCTCAGTCCCGTGGCCCA	GTCCACCTTCACC	1137
QY	249	THRVALGINDLEUVALGLYASNSERTTHRRPROGLYTYRPROGLUTHR	GLINDALEU	268
Db	1138	TCC-----AGCTCCACCTATACCCCGGTGAC-----		1164
QY	269	CYSPROGLINVALTHRRTPSERTRPASPGLINLEUPROSERARGALALEU	GLYPRO-----	286
Db	1165	TGTCCCACTTGGC-----GCTCCCCGAGAGGTGGCACCACCTAT		1209
QY	287	-----ALALAALAPROTHRLEUSERPRO---		294
Db	1210	CAGGGGCTGACCCCATCTTGGCAGACGCCCTCGCTCCGACCCCAT	CCCCACCCCTT	1269
QY	295	-----GLUSERPROAGLYSERPROALAMETLEUGLINPROGLYPRO---	GLN	310
Db	1270	CAGAACTGGGAGGACAGCAGCGCCCAACAAGCCACAGAGCCATGAC	ATGACCCCGCAGC	1329
QY	311	LEUTYRASPVALMETASPRALAVALPROALARGATGTRPLYSGLUPHE	VALARGTHRLEU	330
Db	1330	CTGTACGCCCGTGGTGAGAAAGTGC-----CGGTGGCGGTGAAGA	ATTTCGTGCGGCGCTA	1389
QY	331	GLYLEUARGLUALAGLUILEGLUALAVALGLULILEGLYARG---	PHEARGLASP	349
Db	1390	GGCGTGAGCGACACCGAGATCGATCGGCTGGAGCTGCAGAACGGG	CGCTGCGCGAG	1449
QY	350	GLINDINTYRGLUMETLEULYSARGTTPARGGLINGLINPRO-----	ALAGLYLEU	366
Db	1450	GGCGAATACAGCATGCTGGCGGACCTGGAGGCGCGCACGCGCGG	CGCGAGCCACGCTG	1509
QY	367	GLYALAVALTYYRALALALEUGLUARGMETGLYLEUASPGLYCYS	VALGLUASP	386
Db	1510	GAGCTGCTGGGACGCGTGTCCGGACATGGAACCTGCTGGGCTG	CGCTGAGAGCATCGAG	1569
QY	387	SERARGLEU	389	
Db	1570	GAGGCGCTT	1578	

```

RESULT 14
US-09-505-250-3
; Sequence 3, Application US/09505250A
; Patent No. 6329148
; GENERAL INFORMATION:
; APPLICANT: Rosen, Glenn
; APPLICANT: Kao, Peter
; TITLE OF INVENTION: Synergistic Anti-Cancer Therapy with
; TITLE OF INVENTION: Triptolides and Death Domain Ligands
; FILE REFERENCE: SUN-109PRV2
; CURRENT APPLICATION NUMBER: US/09/505,250A
; CURRENT FILING DATE: 2000-02-15
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 2161
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (256)...(1623)
US-09-505-250-3

```

Alignment Scores:	
Pred. No.:	2.2e-21
Score:	369.00
Percent Similarity:	39.05%
	Length: 2161
	Matches: 126
	Conservative: 47

Best Local Similarity: 28.44% Mismatches: 178
Query Match: 16.708 Indels: 92
DB: 4 Gaps: 21

US-09-993-234-6_COPY_25_417 (1-393) x US-09-505-250-3 (1-2161)

```
QY      3 GlyThrArgSerProArg-----CysAspCysAlaGlyAspPheHisLysLysIle 19
      DB      358 GGGGACAGGGAGAGAGAGATAGTGTGTCCCAAGAAATATATCCACCCTCAAAAT 417
QY      20 GlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGlu 39
      DB      418 AATTGATTGTCTGTACCAAGTGCACAAAGAAACCTACTTGTACAATGACTGTCCAGGC 477
QY      40 ProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsn 59
      DB      478 CCGGGCAGGATACGAGCTCAGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAAAC 537
QY      60 HisHisAsnSerGlyCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAla 79
      DB      538 CACCTCACA---CACTGCCCTCAGCTGTCCCAATGCCGAAGAAATGGGTCAGGTGCAG 594
QY      80 LeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheVal 99
      DB      595 ATCTCTTCTTGACACAGTGGACCGGGACCGGTGTGTGTGCTGCAGGAAGAACCAGTACCGG 654
QY      100 GluCys-----GlnValSerGlnCysValSerSerSerProPheTyrCysGlnPro 116
      DB      655 CATTAATTGGAGTGAAAACCTTTTCCAGTGC-----TTCAATTGCAGCCTC 699
QY      117 CysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThr 136
      DB      700 TGGCTCAAT---GGGACCGTGCAC-----CTCTCTGCCAGAGAAACAGAAC 744
QY      137 AspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysPro 156
      DB      745 ACCGTGTGCACCTGCCATGCAGGTTCTTCTTAAGAGAAACGAGTGTCTCTCTGT--- 801
QY      157 ThrSerThrLeuGlySerCysProGlu-----ArgCysAlaAlaValCys----- 171
      DB      802 -----AGTAACGTGAAGAAAGCCCTGGAGTGCACGAACTTGTGCTACCCAG 849
QY      172 -----GlyTrpArgGlnMetPheTrpValGlnValLeu 182
      DB      850 ATTGAGAAATGTTAAGGACAGTACAGACTCAGGCACACAGATGCTGCCCCGTGCAT 909
QY      183 LeuAlaGlyLeuValValProLeuLeuGlyAlaThrLeuThrTyrThrArgHis 202
      DB      910 TTCTTGGTCTTGGCTTTATCCCTCTCTCATTTGTTAATGTATCGCTACCAACGG 969
QY      203 CysTrpProHisLys-----ProLeuValThrAlaAspGluAla 215
      DB      970 ---TGGAAATCCCAAGCTCTACTSCATTTGTTGTGGAAATGCACACCTGAAAAAGAGGGG 1026
QY      216 GlyMetGluAlaLeuThrProProProAlaThrHisLeuSerProLeuAspSer----- 233
      DB      1027 GAGCTTGAAGGAAGTACTACTAAGCCC-----CTGGCCCCAAACCCCAAGCTTCAGT 1077
QY      234 -----AlaHisThrLeuLeuAlaProProAspSerSerGluLysIleCys 248
      DB      1078 CCCACTCCAGGCTTCACCCCGGCTTCAGTCCCGTCCAGGATTCACACCTTCACC 1137
QY      249 ThrValGlnLeuValGlyAsnSerTrpThrProGlyTyrProGluThrGlnGluAlaLeu 268
      DB      1138 TCC-----AGCTCCACCTATACCCCGGTGAC----- 1164
QY      269 CysProGlnValThrTrpSerTrpAspGlnLeuProSerArgAlaLeuGlyPro----- 286
      DB      1165 TGTCCCAACTTTGCG-----GCTCCCGCAGAGAGTGGCACCACCTAT 1209
QY      287 -----AlaAlaAlaProThrLeuSerPro--- 294
      DB      1210 CAGGGGCTGACCCCATCTTGGCAGACGCCCTCGCTCCGACCCCATCCCAACCCCTT 1269
```

```
QY      295 -----GluSerProAlaGlySerProAlaMetMetLeuGlnProGlyPro---Gln 310
      DB      1270 CAGAAGTGGGAGGACAGCGCCCAAGCCACAGAGCCTAGACACTGATGACCCCGCAGC 1329
QY      311 LeuTyrAspValMetAspAlaValProAlaArgArgTrpLysGluPheValArgThrLeu 330
      DB      1330 CTGTACGCCGTGGTGGAGAAGCGTGCCTCCCGCTTGCCTGGAAGGAATTCGTGGCGCCTA 1389
QY      331 GlyLeuArgGluAlaGluIleGluAlaValGluValGluIleGlyArg---PheArgAsp 349
      DB      1390 GGGCTGAGCGCACGACGATCGATCGGCTGAGAGCTGCAGAACGGGCGCTGCTGCGCGAG 1449
QY      350 GlnGlnTyrGluMetLeuLysArgTrpArgGlnGlnPro-----AlaGlyLeu 366
      DB      1450 GCGCAATACAGCATGCTGGCGACCTGGAGGCGGCGCACGCGCGCGGAGCGCAGCTG 1509
QY      367 GlyAlaValTyrAlaAlaLeuGluArgMetGlyLeuAspGlyCysValGluAspLeuArg 386
      DB      1510 GAGCTGTGGGACGCGTGTCTCCGACATGACCTGCTGGGCTGCTGAGGACATCGAG 1569
QY      387 SerArgLeu 389
      DB      1570 GAGGCGCTT 1578
```

RESULT 15

US-08-321-668-1

; Sequence 1, Application US/08321668
; Patent No. 5665859

GENERAL INFORMATION:

APPLICANT: WALLACH, David
APPLICANT: BRAKEBUSCH, Cord
APPLICANT: VARFOLOMEEV, Eugene
APPLICANT: BATKIN, Michael
TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/321,668
FILING DATE: 12-OCT-1994
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: IL 107268
FILING DATE: 12-OCT-1993
ATTORNEY/AGENT INFORMATION:

NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH=13
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 2175 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS

LOCATION: 256..1620
US-08-321-668-1

Alignment Scores:

Pred. No.:	2,22e-21	Length:	2175
Score:	369.00	Matches:	126
Percent Similarity:	39.05%	Conservative:	47
Best Local Similarity:	28.44%	Mismatches:	178
Query Match:	16.70%	Indels:	92
DB:	1	Gaps:	21

US-09-993-234-6_COPY_25_417 (1-393) x US-08-321-668-1 (1-2175)

```
QY 3 GlyThrArgSerProArg-----CysAspCysAlaGlyAspPheHisLysIle 19
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 358 GGGGACAGGAGAGAGATAGTGTGTCCCAAGGAAATATATCCACCCTCAAAAT 417

QY 20 GlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGlu 39
   ||||| ||| ||| ||| ||||| ||| ||| ||| ||| ||| ||| ||| |||
Db 418 AATTCGATTTGCTGTACCAAGTGCACAAAGAACTACTGTACAAATGACTGTCCAGGC 477

QY 40 ProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsn 59
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 478 CCGGGGACGATACGAGCTGCAGGAGTGTAGAGCGGCTCCTCACCGCTTCAGAAAC 537

QY 60 HisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGlnAlaSerGlnValAla 79
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 538 CACCTCAGA---CACTGCCCTCAGCTGCTCCAATGCCGAAGAATGGGTACGTGGAG 594

QY 80 LeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheVal 99
   :::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 595 ATCTCTTCTTGACAGTGGACCGGACCCGTGTGTGGCTGCAGGAAGAACAGTACCGG 654

QY 100 GluCys-----GlnValSerGlnCysValSerSerProPheTyrCysGlnPro 116
   ::||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 655 CATTAITGGAGTGAACCTTTTCCAGTGC-----TTCAATTGCAGCCTC 699

QY 117 CysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgAspThr 136
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 700 TGCCTCAAT---GGGACCGTGCAC-----CTCTCTGCCAGGAGAAACAGAAC 744

QY 137 AspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysPro 156
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 745 ACCGTGTGCACCTGCATGCAGGTTTCTTCTAAGAGAAACGAGTGTCTCTCTGT--- 801

QY 157 ThrSerThrLeuGlySerCysProGlu-----ArgCysAlaAlaValCys----- 171
   ::||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 802 -----AGTAACGTGAAGAAACCTGAGTGCAGAGAGTGTGCTTACCCACAG 849

QY 172 -----GlyTrpArgGlnMetPheTrpValGlnValLeu 182
   ::||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 850 ATTGAGAAATGTTAAGGCACTGAGGACTCAGGACACACAGTGCCTGCTGTCAT 909

QY 183 LeuAlaGlyLeuValValProLeuLeuLeuGlyAlaThrLeuThrTyrThrArgHis 202
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 910 TTCTTTGGTCTTTGCCCTTTATCCCTCTCTCATTTGTTAATGTAATCGCTACCAACGG 969

QY 203 CysTrpProHisLys-----ProLeuValThrAlaAspGluAla 215
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 970 ---TGGAGTCCAAGCTCTACTCTCATTTGTTGTGGAAATCGACACCTGAAAAAGAGGGG 1026

QY 216 GlyMetGluAlaLeuThrProProAlaThrHisLeuSerProLeuAspSer----- 233
   ::||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1027 GAGCTTGAAGAACTACTACTAAGCCC-----CTGGCCCCCAAAACCAAGCTTCAGT 1077

QY 234 -----AlaHisThrLeuLeuAlaProProAspSerSerGluLysIleCys 248
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1078 CCCACTCAGGCTTCACCCCAACCTGGGCTTCAGTCCCGTGCAGTTCACCTTCACC 1137

QY 249 ThrValGlnLeuValGlyAsnSerTrpThrProGlyTyrProGluThrGlnGluAlaLeu 268
   ::||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1138 TCC-----AGCTCCACCTATACCCCGGTGAC----- 1164
```

```
QY 269 CysProGlnValThrTrpSerTrpAspGlnLeuProSerArgAlaLeuGlyPro----- 286
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1165 TGTCCCAACTTTGCG-----GCTCCCCGACAGAGAGGTGGCACCACTAT 1209

QY 287 -----AlaAlaAlaProThrLeuSerPro--- 294
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1210 CAGGGGCTGACCCCATCTTGCAGACAGCCCTGCTCCGACCCCATCCCAACCCCTT 1269

QY 295 -----GluSerProAlaGlySerProAlaMetLeuGlnProGlyPro---Gln 310
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1270 CAGAACTGGAGACAGCGCCACAAAGCCACAGACGCTAGACACTGATGACCCCGCAGC 1329

QY 311 LeuTyrAspValMetAspAlaValProAlaArgTrpLysGluPheValArgThrLeu 330
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1330 CTGTACGCCGTGTGAGAAAGTGCACCCCGTTCGCTGGAAGAAATTCGTGGCGCCCTA 1389

QY 331 GlyLeuArgGluAlaGlnIleGluAlaValGluValGluIleGlyArg---PheArgAsp 349
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1390 GGGCTGAGCGACACGACGATCGATCGGCTGAGCTGCAGAAACGGCGCTGCTGCCGAG 1449

QY 350 GlnGlnTyrGluMetLeuLysArgTrpArgGlnGlnPro-----AlaGlyLeu 366
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1450 GCGCAATACAGCATGCTGCGGACCTGGAAGCGCGCCGACCCCGCGGAGCCACGCTG 1509

QY 367 GlyAlaValTyrAlaAlaLeuGluArgMetGlyLeuAspGlyCysValGluAspLeuArg 386
   ::||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1510 GAGCTGCTGGACGCGTGTCTCGGACATGACCTGTGGGCTGCTGAGAGCATTCGAG 1569

QY 387 SerArgLeu 389
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1570 GAGCGCCTT 1578
```

Search completed: April 6, 2003, 23:29:40
Job time : 87.3429 secs

GenCore version 5.1.4-p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 6, 2003, 15:35:34 ; Search time 4567.25 Seconds
(without alignments)
2504.221 Million cell updates/sec

Title: US-09-993-234-6_COPY_25_417
Perfect score: 2209
Sequence: 1 QGGTRSPRCDCAGDFHKKIG.....ERMGLDGCVEDLRSRLQRCP 393

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPRO_pool/US09993234/runat_27032003_115455_15349/app_query.fasta_1.2346
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09993234 @CGN_1_1_8534 @runat_27032003_115455_15349 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*

29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2209	100.0	1254	6	AR119657	AR119657 Sequence
2	2209	100.0	1254	9	HSU72763	U72763 Human death
3	2209	100.0	1254	9	HSU78029	U78029 Human apopt
4	2209	100.0	1254	9	HSU94501	U94501 Human lymph
5	2209	100.0	1634	9	HSU74611	U74611 Human Apo-3
6	2209	100.0	1662	6	AX055442	AX055442 Sequence
7	2209	100.0	1662	6	AX201344	AX201344 Sequence
8	2209	100.0	1783	6	AR119656	AR119656 Sequence
9	2199	99.5	1528	9	HSU83597	U83597 Human death
10	2199	99.5	1557	9	HSU75380	U75380 Human apopt
11	2198.5	99.5	1257	9	HSU94502	U94502 Human lymph
12	2157.5	97.7	1355	9	HSU94503	U94503 Human lymph
13	2140.5	96.9	1743	6	AX331947	AX331947 Sequence
14	2140.5	96.9	1743	9	HSWSL1	Y09392 H.sapiens m
15	2128	96.3	1669	9	AF026070	AF026070 Homo sapi
16	2114	95.7	1250	6	AX150176	AX150176 Sequence
17	2104.5	95.3	1763	9	AF026071	AF026071 Homo sapi
18	2062.5	93.4	1198	9	HSU94504	U94504 Human lymph
19	1971.5	89.2	1143	9	HSU94510	U94510 Human lymph
20	1902.5	86.1	1119	9	HSU94509	U94509 Human lymph
21	1837	83.2	1087	9	HSU94505	U94505 Human lymph
22	1530.5	69.3	952	9	HSU94506	U94506 Human lymph
23	1517.5	68.7	4811	9	AB051851	AB051851 Homo sapi
24	1498.5	67.8	4825	9	AB051850	AB051850 Homo sapi
25	1498.5	67.8	53982	9	AL158217	AL158217 Human DNA
26	1364	61.7	1665	10	AF329969	AF329969 Mus muscu
27	1290.5	58.4	838	9	HSU94507	U94507 Human lymph
28	1224.5	55.4	1619	10	BC017526	BC017526 Mus muscu
29	1221	55.3	1581	9	AK094463	AK094463 Homo sapi
30	1221	55.3	2053	9	AK094488	AK094488 Homo sapi
31	1036.5	46.9	705	9	HSU94508	U94508 Human lymph
32	957.5	43.3	816	6	AX335086	AX335086 Sequence
33	957.5	43.3	816	9	HSU83598	U83598 Human death
34	952	43.1	808	9	HSU75381	U75381 Human apopt
35	952	43.1	809	9	HSU94512	U94512 Human lymph
36	942.5	42.7	196368	2	AL772240	AL772240 Mus muscu
37	673	30.5	97483	2	AC118359	AC118359 Rattus no
38	636	28.8	18015	10	AF134858	AF134858 Mus muscu
39	609	27.6	651	9	HSU83599	U83599 Human alter
40	409.5	18.5	2004	4	SSU19994	U19994 Sus scrofa
41	393.5	17.8	1956	10	MUSTNR2	M59377 Murine tumo
42	393.5	17.8	2048	10	MUSMTNR1	M60468 Mouse tumor
43	393.5	17.8	2063	10	MMP55R	X59238 Murine mRNA
44	393.5	17.8	2086	10	BC004599	BC004599 Mus muscu
45	393.5	17.8	2115	10	AF329978	AF329978 Rattus no

RESULT 1

ALIGNMENTS

AR119657
LOCUS AR119657 1254 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 3 from patent US 6153402.
ACCESSION AR119657
VERSION AR119657.1 GI:14102356
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1254)
AUTHORS Yu,G.-L., Ni,J., Gentz,R.L. and Dillon,P.J.
TITLE Death domain containing receptors
JOURNAL Patent: US 6153402-A 3 28-NOV-2000;
FEATURES
source 1..1254
/organism="unknown"
BASE COUNT 201 a 420 c 407 g 226 t
ORIGIN

Alignment Scores:

Pred. No.: 7.97e-110 Length: 1254
Score: 2209.00 Matches: 393
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-993-234-6_COPY_25_417 (1-393) x AR119657 (1-1254)

QY 1 GINGLYGLYTHRARGSERPROARGCYSASPCCYSALAAGLYASPRHEHISLISLISLEGLY 20
DB 73 CAGGGCGGCACTCGTAGCCCGCAGGTGTGACTGTGCCGGTGACTTCCACAGAAGATTGGT 132
QY 21 LEUPHECYSARYGLYCYSPROALAGLYHISTYRLEULYSALAPROCYSSTHGLUPRO 40
DB 133 CTGTTTGTGTGACAGAGGCTGCCACGGGGGACACTGTAAGAGCCCTTGCCAGGAGCC 192
QY 41 CYSGLYASNSERTHRCYSLEUVALCYSPROGLINASPTHRLHEUVALATRPGLUASNHIS 60
DB 193 TGGGGCACTCCACCTGCTGTGTGTCCCAAGACACCTTCTTGCGGTGGAGAACCCAC 252
QY 61 HISASNSEGLUCYSALAARGCYSGLINALCYSASPGULGINALASERGLINVALALEU 80
DB 253 CATAATCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCTCCAGGTGGCGCTG 312
QY 81 GLUASNCYSSEIALAVALAALASPTHRARGCYSGLYCYSLYSPROGLYTRPHEVALGLU 100
DB 313 GAGAACTGTTCAGCAGTGGCCGACACCGCTGTGGCTTAAGCCAGGCTGTTGTGGAG 372
QY 101 CYSGLINVALSERGLNCYSVALSERSESRPROPHETRYCYSGLINPROCYSLEUASPCYS 120
DB 373 TGCAGGTTCAGCCATGTGTCCAGAGTTACCTTCTACTGCCAACCATGCTAGACTGC 432
QY 121 GLYALALEUHHISARGHISTHRARGLEUUCYSSERARGARGASPTHASPCYSGLYTHR 140
DB 433 GGGGCCCTGCACGCCACACACGGCTACTCTGTTCGCCGACAGATACTGATGGGACC 492
QY 141 CYSLEUPROGLYRHETYRGLUNHISGLYASPCLYCYSVALSERCYSPTOTHRSETRHLEU 160
DB 493 TGCCTGCTGGCTTCTATGAACATGGCGATGGCTGCTGCTGCCCCACGAGCACCCCTG 552
QY 161 GLYSERCYSPROGLUARGCYSALAALVALCYSGLYTRPARGLMETPHETRVALGLN 180
DB 553 GGGAGCTGTCCAGAGCGCTGTGCCGCTGTGTGGCTGGAGGACAGATGTCTGGGTCCAG 612
QY 181 VALLEULEUALAGLYLEUVALVALPROLEULEULEUGLYALATHRLHEUTHRYTRTYR 200
DB 613 GTGCTCTGTGGCTGTGGTGTGCCCTCTGCTTGCGGACACCTGACCTACACATAC 672
QY 201 ARGHISCYSTPRPROHISLYSPROLEUVALTHRALASPGUALAGLYMETGLUALALEU 220
DB 673 CGCCACTGTGGCTTCACAAAGCCCGGTACTGACATGAAAGCTGGATGGAGGCTCTG 732

QY 221 THRPROPROALATHRHISLEUSERPROLEUASPSERALAHHISTHRLHEUVALPRO 240
DB 733 ACCCCACACCGGCCACCACTGTCAACCCCTTGACACAGCCGCCACACCCCTTCTAGCACT 792
QY 241 PROASPSESRERGLULYSILECYSTHRVALGLINLEUVALGLYASNSETRTPHTRPROGLY 260
DB 793 CCTGACAGCAGTAGAGAAGATCTGCACCCGTCCAGTGTGGGTAAACAGCTGGACCCCTGCC 852
QY 261 TYRPROGLUTHRGLINGLUALALEUCYSPROGLINVALTHRTTPSETRTPASPGINLEUPRO 280
DB 853 TACCCCGAGACCCACAGAGCGCTCTGCCCGCAGGTGACATGCTCTGGACCACTGGCCC 912
QY 281 SERARGALALEUGLYPROALAALALAPROTHRLSEUSERPROGLUSERPROALAGLYSER 300
DB 913 AGCAGAGCTCTGGCCCCCTGCTGCGCCACACTCTCCAGAGTCCCCACCGCGCTCG 972
QY 301 PROALAMETLEUGLINPROGLYPROGLINLEUTYRASPVALMETASPALAVALPROALA 320
DB 973 CCAGCCATGATGTGCAGCGCGCGCCCGCAGCTCTACGACGTGATGACGCGGCTCCACGCG 1032
QY 321 ARGARGTRPLYSGLUPHEVALARGTHRLEUGLYLEUARGGLUALAGLUILEGLUALAVAL 340
DB 1033 CGGCGCTGGAAGAGTTCGTGCGCACGCTGGGCTGGCGGACAGAGATTCAGACCCGTG 1092
QY 341 GLUVALGLULIEGLYARGPHEARGASPGINGLINTRYGLUMETLEULYSARGTRPARGLN 360
DB 1093 GAGGTGAGATCGCGCGCTTCCGAGACACGACGACGATGCTCAAGCCCTGGCGCCAG 1152

QY 361 GINGLINPROALAGLYLEUGLYALALVALTYRRLAALALEUGLUARGMETGLYLEUASPGLY 380
DB 1153 CAGCAGCCCGCGGCTCGGAGCCGTTTACCGCGCCCTGAGCGCATGGGCTGGACGGC 1212
QY 381 CYSVALGLUASPLEUARGSERARGLEUGLINARGGLYPRO 393
DB 1213 TGCCTGGAAGACTTGCAGCAGCCGCTGCAGCGCGGCCCG 1251

RESULT 2

HSU72763 1254 bp mRNA linear PRI 15-NOV-1996
LOCUS Human death receptor 3 (DR3) mRNA, complete cds.
DEFINITION U72763
ACCESSION U72763
VERSION U72763.1 GI:1669511

KEYWORDS

ORGANISM

REFERENCE 1 (bases 1 to 1254)
AUTHORS Chinnaiyan,A.M., O'Rourke,K., Yu,G.L., Lyons,R.H., Garg,M.,
Duan,D.R., Xing,L., Gentz,R., Ni,J. and Dixit,V.M.
TITLE Signal transduction by DR3, a death domain-containing receptor
related to TNFR-1 and CD95
JOURNAL Science 274 (5289), 990-992 (1996)

TITLE

JOURNAL MEDLINE 97081063
PUBMED 8875942
REFERENCE 2 (bases 1 to 1254)

AUTHORS

Chinnaiyan,A.M., O'Rourke,K., Yu,G.-L., Lyons,R.H., Garg,M.,
Duan,R., Xing,L., Gentz,R., Ni,J. and Dixit,V.M.
TITLE Direct Submission
JOURNAL Submitted (29-SEP-1996) Pathology, University of Michigan Medical
School, 1301 Catherine St., Box 0602, Ann Arbor, MI 48109, USA

FEATURES

source 1..1254
/organism="Homo sapiens"
/db_xref="taxon:9606"
1..1254
/gene="DR3"
1..1254
/gene="DR3"
/gene="DR3"
/codon_start=1
/product="death receptor 3"
/protein_id="AAC50819.1"
/db_xref="GI:1669512"

/translation="MEQRPRGCAVAALLVLGARAQGGTRSPRCDCAGDFHKKIG
LFCCRGPAGHYLKAPCTEPCGNSTCLVCPQDFTLAWENHNHNSCARCQACDEQASQY
ALENCASAVADTRCGCKPGWFEVSCQVSSSPFYCQPCLDGALHNRTRLCSRDY
DCGTCLPGFEYEHGDCVSCPTSLGSCPERCAAVCGWROMFWOVLLAGLVVPLLIGA
TLTYTYRHWCWPHKPLVTADAGMEALTPPPATHLSPLDSAHTLAPDSEKICTYQL
VGNSWTPGYPETQALCPQVYWSMDQLPSRALGPAAPTLSPESPAGSPAMLOPQ
LYDVMADVAPARRWKEFVRTIGLREAEIEAVEVEIGRFRDQOYEMLKRRWQOQPAIGLGA
VYVALERMGLDGCVEDLRSLQRG"

BASE COUNT 201 a 420 c 407 g 226 t
ORIGIN

Alignment Scores:
Pred. No.: 7.97e-110 Length: 1254
Score: 2209.00 Matches: 393
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-993-234-6_COPY_25_417 (1-393) x HSU72763 (1-1254)

QY 1 GlnGlyIyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGly 20
Db 73 CAGGGCGCAGCTCGTAGCCCCAGGTGACTGTGCCGGTAGCTTCACAGAAGATTGGT 132
QY 21 LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
Db 133 CTGTTTGTGTGCAGAGGCTGCCACAGCGGGGCACTACCTGAAGGCCCTTGCACAGGAGCCC 192
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db 193 TGGCGCACTCCACCTGCTGTGTGTCCCAAGACACCTTCTTGCCCTGGGAGAACCCAC 252
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db 253 CATAAATCTGAATGTGCCCGCTGCCAGCTGTGATGAGCAGGCCCTCCACAGGTGGCGCTG 312
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
Db 313 GAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGGCTGTAAAGCCAGGCTTGTGTGAG 372
QY 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120
Db 373 TGCCAGGTACGCCAATGTGTACAGAGTACACCTTCTACTGCCAACCATGCCCTAGACTGC 432
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 433 GGGGCCCCGTGCACCCGACACACGGCTACTGTTCGCCGAGAGATGACTGTGGGACC 492
QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db 493 TGCCTGCTGGCTTCTATGACATGGCGATGGCTGCTGCTGCCACGAGCACCCCTG 552
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArgGlnMetPheTrpValGln 180
Db 553 GGGAGCTGTCCAGAGCGCTGTGCCGTGTGGCTGGAGGACAGATCTTGTGGTCCAG 612
QY 181 ValLeuLeuAlaGlyLeuValValProLeuLeuGlyAlaThrLeuThrTyrThrTyr 200
Db 613 GTGCTCCTGGCTGGCCTGTGTGTCCTCCCTGCTTGGGGCCACCCCTGACCTACACATAC 672
QY 201 ArgHisCysTrpProHisLysProLeuValThrAlaAspGluAlaGlyMetGluAlaLeu 220
Db 673 CGCCACTGCTGGCCTCACAAGACCCCTGGTTACTGCAGATGAAGCTGGGATGGAGGCTCTG 732
QY 221 ThrProProAlaThrHisLeuSerProLeuAspSerAlaHisThrLeuLeuAlaPro 240
Db 733 ACCCCACACCGGCCACCCATCTGTACCTTGGACAGCGGCCACACCCCTTCTAGCACCT 792
QY 241 ProAspSerSerGluLysIleCysThrValGlnLeuValGlyAsnSerTrpThrProGly 260
Db 793 CCTGACAGCAGTGAAGAATCTGACCGCTCCAGTTGGTGAACAGCTGGAACCCCTGGC 852
ORIGIN

QY 261 TyrProGluThrGlnGluAlaLeuCysProGlnValThrTrpSerTrpAspGlnLeuPro 280
Db 853 TACCCCGAGACCCAGGAGCGGCTCTGCCCGCAGGTGACATGTCTCTGGACCAGTTGCC 912
QY 281 SerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSerProAlaGlySer 300
Db 913 AGCAGAGCTTGTGGCCCGCTGTGCGCCACACTCTGCCAGAGAGTCCCGACCGGCTCG 972
QY 301 ProAlaMetLeuGlnProGlyProGlnLeuTyrAspValMetAspAlaValProAla 320
Db 973 CCAGCATGATGTTCAGACCGCGGCGCCAGCTTACGACGTGATGAGACGCGCTGCCAGCG 1032
QY 321 ArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGluAlaGluIleGluAlaVal 340
Db 1033 CGCGCTGGAAGGAGTTCGTGCGCACGCTGGGGCTGCGGAGGACAGATCGAACCGCTG 1092
QY 341 GluValGluIleGlyArgPheArgAspGlnGlnTyrGluMetLeuLysArgTrpArgGln 360
Db 1093 GAGGTGAGATCGGCGGCTTCGAGACCAAGCAGTACGAGATGCTCAAGCGCTGGCCAG 1152
QY 361 GlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMetGlyLeuAspGly 380
Db 1153 CAGCAGCCCGCGGCTCGGAGCCGTTTACGGCGGCTTGAGCGCATGGGCTGAGCGGC 1212
QY 381 CysValGluAspLeuArgSerArgLeuGlnArgGlyPro 393
Db 1213 TGGGTGAAGACTTGCAGACCGGCTGACAGCGGCGCCG 1251

RESULT 3
HSU78029
LOCUS HSU78029 1254 bp mRNA linear PRI 15-JAN-1997
DEFINITION Human apoptosis inducing receptor AIR mRNA, complete cds.
ACCESSION U78029
VERSION U78029.1 GI:1778763
KEYWORDS
SOURCE
ORGANISM Homo sapiens.
Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1254)
Degli-Esposti,M.A., Din,W.S., Cosman,D., Smith,C.A. and
Goodwin,R.G.
AIR, A Novel Member of the TNF Receptor Family, Is a Strong Inducer
of Apoptosis
Unpublished
2 (bases 1 to 1254)
Degli-Esposti,M.A. and Goodwin,R.G.
Direct Submission
Submitted (12-NOV-1996) Biochemistry, Immunex Corporation, 51
University St., Seattle, WA 98101, USA
location/Qualifiers
1. 1254
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/map="1pter"
/cell_type="peripheral blood T-cells"
1. 1254
/codon_start=1
/product="apoptosis inducing receptor AIR"
/protein_id="AAB40918.1"
/db_xref="GI:1778764"

/translation="MEQRPRGCAVAALLVLGARAQGGTRSPRCDCAGDFHKKIG
LFCCRGPAGHYLKAPCTEPCGNSTCLVCPQDFTLAWENHNHNSCARCQACDEQASQY
ALENCASAVADTRCGCKPGWFEVSCQVSSSPFYCQPCLDGALHNRTRLCSRDY
DCGTCLPGFEYEHGDCVSCPTSLGSCPERCAAVCGWROMFWOVLLAGLVVPLLIGA
TLTYTYRHWCWPHKPLVTADAGMEALTPPPATHLSPLDSAHTLAPDSEKICTYQL
VGNSWTPGYPETQALCPQVYWSMDQLPSRALGPAAPTLSPESPAGSPAMLOPQ
LYDVMADVAPARRWKEFVRTIGLREAEIEAVEVEIGRFRDQOYEMLKRRWQOQPAIGLGA
VYVALERMGLDGCVEDLRSLQRG"

BASE COUNT 201 a 420 c 407 g 226 t
ORIGIN

Alignment Scores:

Pred. No.: 7.97e-110
Score: 2209.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 9
Length: 1254
Matches: 393
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-09-993-234-6_COPY_25_417 (1-393) x HSU78029 (1-1254)

QY	1	GINGLYGLYTHRARGSERPROARGCYSASPCYSALAGLYASPRHEHISLYSLYSILEGLY	20
DB	73	CAGGGCGGCACTCGTAGCCCCAGGTGTGACTGTGCCGGTACTCCACAAGAAGATTGTT	132
QY	21	LEUPHECYSYSARGGLYCYSPROALAGLYHISTYRLEULYSALAPROCYSYTHRGU	40
DB	133	CTGTTTGTGTGACAGGCTGCCCCAGGGGGGCACTACTGAAGGCCCTTGACAGGAGCC	192
QY	41	CYSGLYASNSERTHRCYSLEUVALCYSPROGLNASPTHRPHEUVALATRPGLUASN	60
DB	193	TGCGGCACTCCACCTGCTGTGTGTCCCAAGACACCTCTTGCGCTGGAGAACAC	252
QY	61	HISASNSEGLUCYSALAAARGCYSGLINALACYSASPGUINALASERGLNVALALEU	80
DB	253	CATAATTCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCCCTCCAGGTGGCG	312
QY	81	GLUASNCSYSERALAVALLAASPTHRARGCYSGLYCYSLSPROGLYTRPHEVALGLU	100
DB	313	GAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGCTGTAAAGCCAGGCTGTTGTGAG	372
QY	101	CYSGLNVALSERGLNCYSVALSERSERPROPHETRYCYSGLNPROCYSLEUASPCYS	120
DB	373	TGCCAGGTCAAGCAATGTGTGACAGATTACCCCTTCTACTGCCAACCATGCTAGACTGC	432
QY	121	GLYALALEUHHISARGHISHTHARGLEULCYSSEARGARGASPTHRASPCYSGLYTHR	140
DB	433	GGGGCCCTGCACCGCCACACAGGGCTACTCTGTGCCGACAGAGATACTGACTGTGGGACC	492
QY	141	CYSLEUPROGLYPHETRYGLUHHISGLYASPGLYCYSVALSERCYSPROTHRSE	160
DB	493	TGCCTGCTGCTGTATGACATGCGATGCGTGTCTGCTGCCACAGACACCTG	552
QY	161	GLYSERCYSPROGLIARGCYSALAAVALCYSGLYTRPARGLMETPHETRYVALGLN	180
DB	553	GGGAGCTGTCCAGAGCGCTGTGCCGCTGTCTGTGCTGGAGGACAGATGTTCTGGGCTCCAG	612
QY	181	VALLEULAUAGLYLEUVALVALPROLEULEULEUGLYALATHRLEUTHRYRTHRYT	200
DB	613	GTGCTCCTGCTGCGCTGTGTGCTGCCCTCTGCTGGGGCCACCCCTGACCTACACATAC	672
QY	201	ARGHISCYSTPRPROHISLYSPROLEUVALTHRALAASPGUVALAGLYMETGLUALALEU	220
DB	673	CGCCACTGCTGGCCCTACACAAGCCCTGTTACTGCAGATGAAGCTGGATGGAGCTCTG	732
QY	221	THRPROPROALATHRHHISLEUSERPROLEUASPSERALAHISTHRLLEUVALAPRO	240
DB	733	ACCCACACACCGGCCACCATCTGTACACCTTGAGACAGCCACACACCTTCTAGCACCT	792
QY	241	PROASPSERSEGLULYSILECYSYTHRVALGLNLEUVALGLYASNSE	260
DB	793	CCTGACAGCAGTGAAGATCTGCACCGCTCCAGTTGGTGGTAACAGCTGGACCCCTGGC	852
QY	261	TYRPROGLUTHRINGLUALALEUCYSPROGLNVALTHRTTRPSE	280
DB	853	TACCCCGAGAGCCAGGAGCGCTGTGCCGAGGTGACATGTTCTGGGACACAGTTGCC	912
QY	281	SERARGALALEUGLYPROALAAALAPROTHRLEUSERPROGLUSERPROALAGLYSER	300
DB	913	AGCAGAGCTCTTGCCCCGCTGTGCCGCCACACTCTGCCAGAGTCCCAAGCCGGCTCG	972
QY	301	PROALAMETLEUGLNPROGLYPROGLNLEUTYRSPVALMETASPALAVAI	320
DB	973	CCAGCCATGATGCTGCAGCGCGGGCCGACGCTTACGACGTGATGAGCGCGGTCCACGCG	1032

QY	321	ARGARGTRPLYSGLUPHEVALARGTHRLEUGLYLEUARGGLUALAGLUILEGLUALAVAI	340
DB	1033	CGGGCTGGAGAGAGTCTGTGCCACCGCTGGGCTGCGCGAGGACAGATCGAAGCCGTG	1092
QY	341	GLUVALGLUILEGLYARGPHARGASPGINGLNTYRGLUMETLEULYSARGTRPARGLN	360
DB	1093	GAGGTGAGATCGGGCGCTTCGAGACACAGCAGTACGAGATGCTCAAGCGCTGGCCAG	1152
QY	361	GLINGNPROALAGLYLEUGLYALAVAITYRVALALEUGLUARGMETGLYLEUASPGLY	380
DB	1153	CAGCAGCCCGCGGCTCGAGCCGTTTACGCGCGCTGAGCGCATGGGCTGACGCG	1212
QY	381	CYSVALGLUASPLEUARGSERARGLEUGLNARGGLYPRO	393
DB	1213	TGCGTGGAAAGACTTGCGCAGCGCCCTGCAGCGCGGCCG	1251

RESULT 4

HSU94501 1254 bp mRNA linear PRI 15-MAY-1997
LOCUS Human lymphocyte associated receptor of death 1a mRNA, complete

DEFINITION

ACCESSION U94501
VERSION U94501.1
KEYWORDS GI:2071948

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

CDS

BASE COUNT

ORIGIN

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

Location/Qualifiers

1..1254

/organism="Homo sapiens"

/db_xref="taxon:9606"

/cell_line="Hela"

/cell_type="lymphocyte"

1..1254

/function="mediates apoptosis"

/note="LARD-1a; membrane protein; similar to Fas and

TNF-R1; contains a death domain"

/codon_start=1

/product="lymphocyte associated receptor of death 1a"

/protein_id="AAC51306.1"

/db_xref="GI:2071949"

/translation="MEQRPRGCAAVAAALLVILGARAOGGTRSPRCDCAGDFHKKIG

LFCCRGPAGHYLAKAPCTEPCGNSCLVCPQDTFLAMENHNSCARCQACDEQASQV

ALENCASAVADTRCGCKPGWFEQVQSQVSSPFYQPCPLDCGALHRTLLCSRRDT

DCGTCLPGFEYHGDGCVSCPSTLGSCEPCERCAVCGWFMVQVLLAGLVVLLGA

TLTYTYRHCHWPHKPLVTADEAGMALTPPATHTSLPDSAHHTLAPPDSEETVQL

VGNSWTPGYPETQELCPQVNTWSMDLPRLALGPAAPTLSPESPAGSPAMNQPQP

LYDVMADVPRRMKEFRTILGLREAFIEAVEVEIGRFRDQYEMLKRWROQPAFLGA

VYALERMGLDGCVEEDRLRSRLQRG"

BASE COUNT 201 a 420 c 407 g 226 t


```

Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-09-993-234-6_COPY_25_417 (1-393) x HS094501 (1-1254)

```

QY	1	GI	NG	L	Y	G	L	I	G	L	Y	G	L	Y	T	H	R	A	R	G	S	E	R	P	R	O	A	R	G	C	S	A	S	P	C	S	A	L	A	G	L	A	S	P	H	E	N	I	S	L	Y	S	I	L	E	G	L	Y	20
Db	73	C	A	G	G	G	G	G	C	A	C	T	G	T	A	G	C	C	C	C	C	A	G	G	T	G	T	G	A	C	T	G	T	G	C	C	G	T	G	A	C	T	T	C	C	A	C	A	G	A	G	A	T	T	G	T	132		
QY	21	L	E	U	P	H	E	C	Y	S	C	S	A	R	G	L	I	C	Y	S	P	R	O	A	L	A	G	L	I	H	I	S	T	Y	L	E	U	L	Y	S	A	L	A	P	R	O	C	S	T	H	R	G	L	I	P	R	O	40	
Db	133	C	T	G	T	T	T	T	G	T	G	C	A	G	A	G	C	T	G	C	C	A	G	C	C	T	T	G	C	C	A	A	G	A	C	T	T	T	G	C	C	T	T	G	C	C	A	G	A	C	C	T	T	G	C	A	C	C	192
QY	41	C	Y	S	G	L	Y	A	S	N	S	E	R	T	H	C	Y	S	L	E	U	V	A	L	C	Y	S	P	R	O	G	L	N	A	S	P	T	H	R	P	H	E	U	A	L	A	T	R	P	L	A	S	N	H	I	S	60		
Db	193	T	G	C	G	C	A	C	T	C	C	A	C	T	G	C	C	T	T	G	T	G	T	C	C	C	A	A	G	A	C	C	T	T	T	G	C	C	T	G	G	A	G	A	C	C	A	C	252										
QY	61	H	I	S	A	S	N	S	E	R	L	U	C	S	A	I	A	R	G	C	Y	S	G	L	N	A	L	C	Y	S	A	S	P	L	I	G	N	A	L	A	S	E	R	G	L	N	V	A	L	A	L	E	U	80					
Db	253	C	A	T	A	T	T	C	T	G	A	A	T	G	C	C	C	C	C	T	G	C	C	A	G	C	C	T	G	T	G	A	T	A	G	A	C	A	G	C	C	T	C	C	A	G	T	G	C	C	T	G	312						
QY	81	G	L	U	A	S	N	C	S	S	E	R	A	V	A	L	A	A	S	P	T	H	R	A	R	G	C	Y	S	G	L	Y	C	S	L	Y	S	P	R	O	G	L	Y	T	R	P	H	E	V	A	L	I	U	100					
Db	313	G	A	G	A	C	T	G	T	T	C	A	G	A	C	T	G	G	C	C	G	C	A	C	A	C	C	C	G	C	T	G	T	G	G	C	T	G	T	A	A	C	C	A	G	C	T	G	T	T	G	T	G	A	G	372			
QY	101	C	Y	S	G	L	N	V	A	S	E	R	G	L	N	C	Y	S	V	A	L	S	E	R	S	E	R	S	E	R	P	R	O	T	H	E	T	Y	C	Y	S	G	L	N	P	R	O	C	Y	S	L	E	A	S	P	C	Y	S	120
Db	373	T	G	C	C	A	G	T	C	A	C	C	A	T	G	T	C	A	G	A	G	T	C	A	C	C	C	T	T	A	C	T	T	A	C	T	T	A	C	T	G	C	C	A	A	C	A	T	G	C	C	T	A	G	A	C	T	G	432
QY	121	G	L	Y	A	L	A	L	E	U	H	I	S	A	R	G	H	I	S	T	H	R	A	R	G	L	E	U	E	U	C	Y	S	S	E	R	A	R	G	A	S	P	T	H	R	A	S	P	C	Y	S	G	L	Y	T	H	R	140	
Db	433	G	G	G	G	C	C	T	G	C	A	C	C	C	C	A	C	A	C	A	C	G	G	C	T	A	C	T	C	T	G	T	T	C	C	G																							

QY	341	GIUValGIUIleGIlyArgPheArgAspGlnGlnTyrgLumetleuLysArgTTrparGln	360
Db	1093	GAGGTGAGATCGCGCGCTTCGAGACCAGCAGTACGAGATGCTCAAGCGCTGGCGCCAG	1152
QY	361	GIcInProAlaGIlyLeuGIyAlaValTyrrAlaAlaLeuGIuArgMetGIlyLeuAspGIy	380
Db	1153	CAGCAGCCCGCGGGCCTCGAGCGCTTTACGCGGCCCTGAGCGCATGGGGCTGTGACGGC	1212
QY	381	CysValGIuAspLeuArgSerArgLeuGlnArgGIyPro	393
Db	1213	TGCGTGGAAGACTTGCGCAGCCGCTGCAGCGCGGCGCG	1251

RESULT 5			
HSU74611			
LOCUS	HSU74611	1634 bp	mRNA
DEFINITION	Human Apo-3 mRNA, complete cds.	linear	PRI 02-JAN-1997
ACCESSION	U74611		
VERSION	U74611.1		
KEYWORDS			
SOURCE	Homo sapiens.		
ORGANISM	Homo sapiens		

REFERENCE AUTHORS	TITLE	JOURNAL REFERENCE AUTHORS
1 (bases 1 to 1634) Marsters,S.A., Sheridan,J.P., Donahue,C.J., Pitti,R.M., Gray,C.L., Goddard,A.D., Bauer,K.D. and Ashkenazi,A.	Apo-3, a new member of the tumor necrosis factor receptor family, contains a death domain and activates apoptosis and NF- κ B	2 (bases 1 to 1634) Marsters,S.A., Sheridan,J.P., Donahue,C.J., Pitti,R.M., Gray,C.L., Goddard,A.D., Bauer,K.D. and Ashkenazi,A.

JOURNAL Submitted (15-OCT-1996) Molecular Oncology, Genentech, 460 Pt. San Bruno Blvd., South San Francisco, CA 94080, USA

FEATURES Location/Qualifiers

```

source
1. .1634
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/map="1p36.3"
/tissue_type="heart"
/dev_stage="fetal"
89. .1342
/notes="contains death domain, activates apoptosis and
NF-kB; TNF receptor family member"
CDS

```

```

/product="Apo-3"
/protein_id="AAB39714.1"
/db_xref="GI:1763293"
/translation="MEQRPRGCAVAANAALLVLLGARAQGGTRSPRCDCAGDFHKKIG
LFCCRGCPAGHYLKAPCTEPCGNSSTLCPEQDTFLAMENHHNSECARQACDEQASOV
ALENCSAVADTRCGCKPGWFVECVSQCVSSPFYCQPCLDGALHRTLRLLCSRDT
DCGICLPGEYEHGDGCVSCTSTLGSCEPERCAAVCGMROMFWVOVLLGLVPLLGA
TLTYTYRHCMPHKPLVTADAGMEALTTPRATHLSPLDSANTLLARPDSSEKICTVQ
VGNSWTPGYPETQELCPQVTDAGMELTPSLRPAAPLSPESPAGSPAMMLQPGPO
LYDVMDAVPARRMKEFVRTLGLREAEIEAVEVEIGRFRDQYEMLKRMKQQQPAGLGA
VYAALERMGDGCVEDLRSLQGRP"

```

Alignment Scores:	1.06e-109	Length:	1634
Score:	2209.00	Matches:	393
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-993-234-6_COPY_25_417 (1-393) x HSU74611 (1-1634)

QY 1 G I N G I L G L Y T H r a r S e r P r o A r G C y s a s P C y s a l a c l y a s p h e n i s l s l s l e c t y 20
|||||

Db 161 CAGGGCGCACTCGTAGCCCCAGGTTGTACTGTGCCGGTGACTTCCACAAGAAGATTGGT 220
QY 21 LeuphEcysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
Db 221 CTGTTTGTGTGACAGAGCTGCCCCAGGGGGGACTACTGTAAGGCCCTTGACAGGAGCC 280
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db 281 TGGGGCAACTCCACCTGCGTTGTGTCTCCCAAGACACCTTCTTGCGCTGGAGAACAC 340
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGlnAlaSerGlnValAlaLeu 80
Db 341 CATTAATTCTGAATGTGCCCGCTGCCAGGCCCTGTGATGAGCAGGCCCTCCAGGTGGCTG 400
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
Db 401 GAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGGCTGTAGCCAGGCTGTTGTGGAG 460
QY 101 CysGlnValSerGlnCysValSerSerSerProPheTyrCysGlnProCysLeuAspCys 120
Db 461 TGGCAGGTTCAGCCAATGTGTACAGCAAGTTACACCTTCTACTGCCAACCATGCGCTAGACTGC 520
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 521 GGGGCCCTGCACCGCCACACAGGGCTACTCTGTTCGCCAGAGATACTGACTGTGGAGCC 580
QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db 581 TGGCTGGCTGGCTCTTAATGAACATGGCGATGGCTGGCTGTCTGCCACAGACACCTTG 640
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArgGlnMetPheTrpValGln 180
Db 641 GGGAGCTGTCCAGAGCGGTGTGCCGCTGTCTGTGGCTGGAGGACAGATGTTCTGGGTCCAG 700
QY 181 ValLeuLeuAlaGlyLeuValValProLeuLeuLeuGlyAlaThrLeuTyrThrTyr 200
Db 701 GTGCTCTGTGGCTGGCTTTGTGTCTCCCTCTCTGTGGGGCCACCTGACCTACACATAC 760
QY 201 ArgHisCysTrpProHisLysProLeuValThrAlaAspGluAlaGlyMetGluAlaLeu 220
Db 761 CGCCACTGTGGCTGCACAAAGCCCTGTGTACTGACAGATGAAGCTGGATGGAGGCTCTG 820
QY 221 ThrProProProAlaThrHisLeuSerProLeuAspSerAlaHisThrLeuAlaPro 240
Db 821 ACCCCACACCGGCGACCATCTGTACACCTTGGACAGCGCCACACACCTTCTAGCACT 880
QY 241 ProAspSerSerGluLysIleCysThrValGlnLeuValGlyAsnSerTrpThrProGly 260
Db 881 CCTGACAGCAGTGAAGAATCTGCACCGCTTCAGTTGGTGGTAACACAGCTGACCCCTGGC 940
QY 261 TyrProGluThrGlnGluAlaLeuCysProGlnValThrTrpSerTrpAspGlnLeuPro 280
Db 941 TACCCCGAGACCCAGAGAGCGGCTGTGCCCGAGGTGACATGTGCTGGGACCAAGTTGCC 1000
QY 281 SerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSerProAlaGlySer 300
Db 1001 AGCAGAGCTCTTGCGCCCGCTGTGCGCCACACTCTGCGCAGAGTCCCAAGCCGCGCTCG 1060
QY 301 ProAlaMetLeuLeuGlnProGlyProGlnLeuTyrAspValMetAspAlaValProAla 320
Db 1061 CCAGCCATGATGTGCAGCGCGGCGCGCACTCTACGACGTGATGAGCGGCTCCACAGCG 1120
QY 321 ArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGluAlaGluIleGluAlaVal 340
Db 1121 CGGCGCTGAGAGAGTTCGTGCGCAGCGTGGGGCTGCGGAGGACAGATCGAAGCCGTG 1180
QY 341 GluValGluIleGlyArgPheArgAspGlnGlnTyrGluMetLeuLysArgTrpArgGln 360
Db 1181 GAGGTGAGATCGGCCGCTTCGAGACAGCAGTACGAGATGCTCAAGCGCTGGCGCCAG 1240
QY 361 GlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMetGlyLeuAspGly 380
Db 1241 CAGCAGCCCGGGGCTCGAGGCCGTTTACGCGGCGCTGAGCGCATGGGGCTGAGCGCG 1300

QY 381 CysValGluAspLeuArgSerArgLeuGlnArgGlyPro 393
Db 1301 TGGGTGAAGACTTGGCGACGCCGCTTGACAGCGGCGCCG 1339
RESULT 6
AX055442
LOCUS AX055442 1662 bp DNA linear PAT 13-JAN-2001
DEFINITION Sequence 72 from Patent WO0073452.
ACCESSION AX055442
VERSION AX055442.1 GI:12228713
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1662)
AUTHORS Ashkenazi,A.J., Baker,K.P., Chan,B., Goddard,A., Godowski,P.J.,
Gurney,A.L., Hebert,C., Henzel,W., Kabakoff,R.C., Shelton,D.L.,
Tumas,D., Watanabe,C.K. and Wood,W.I.
TITLES Compositions and methods for the treatment of immune related
diseases
JOURNAL Patent: WO 0073452-A 72 07-DEC-2000;
Genentech, Inc. (US)
FEATURES
source 1. 1662
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 302 a 540 c 531 g 289 t
ORIGIN
Alignment Scores: 1.08e-109 Length: 1662
Pred. No.: 2209.00 Matches: 393
Score: 2209.00 Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
US-09-993-234-6_COPY_25_417 (1-393) x AX055442 (1-1662)
QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGly 20
Db 175 CAGGGCGGCACTCGTAGCCCCAGGTGTGACTGTGCCGGTGTGACTTCCACAAGAAGATTGGT 234
QY 21 LeuphEcysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
Db 235 CTGTTTGTGTGACAGAGCTGCCCCAGGGGGGACTACTGTAAGGCCCTTGACAGGAGCC 294
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db 295 TGGGGCAACTCCACCTGCTGTGTGTCTCCCAAGACACCTTCTTGCGCTGGAGAACAC 354
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGlnAlaSerGlnValAlaLeu 80
Db 355 CATTAATTCTGAATGTGCCCGCTGCGCAGGCTGTGATGAGCAGGCTCCCAAGTGGAG 414
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
Db 415 GAGAACTGTTCAGCAGTGGCCGACACCGGCTGTGGCTGTAGCCAGGCTGTTGTGGAG 474
QY 101 CysGlnValSerGlnCysValSerSerSerProPheTyrCysGlnProCysLeuAspCys 120
Db 475 TGGCAGGTTCAGCCAATGTGTACAGCAAGTTCACCTTCTACTGCCAACCATGCGTACTG 534
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 535 GGGGCCCTGCACCGCCACACAGGGCTACTCTGTTCGCCAGAGATACGACTGTGGACC 594
QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db 595 TGGCTGGCTGGCTCTTAATGAACATGGCGATGGCTGGCTGTCTGCCACAGACACCTTG 654

QY 161 GlyserycProgluArgCysAlaAlaValCysGlyTrparglMetPheTrpValGln 180
Db 655 GGGAGCTGTCCAGAGCGGTGGCGCTGTCTGTGGCTGGAGGAGATGTCTGGGTCCAG 714
QY 181 ValLeuLeuAlaGlyLeuValValProLeuLeuLeuGlyAlaThrLeuThrTyrThrTyr 200
Db 715 GTGCTCTGGCTGGCTGTGTGTGCTCCCTCTGCTTGGGGCCACCCCTGACCTACACATAC 774
QY 201 ArgHisCysTrpProHisLysProLeuValThrAlaAspGluAlaGlyMetGluAlaLeu 220
Db 775 CGCCACTGTGGCTCACAAGCCCTGGTTACTGACAGATGAAGCTGGAGTGGAGGCTCTG 834
QY 221 ThrProProProAlaThrHisLeuSerProLeuAspSerAlaHisThrLeuAlaPro 240
Db 835 ACCCCACACCGGCCACCCATCTGTACACCTTGGACAGCGCCACACACCTTCTAGCACCT 894
QY 241 ProAspSerSerGluLysIleCysThrValGlnLeuValGlyAsnSerTrpThrProGly 260
Db 895 CCTGACAGCAGTGAGAAGATCTGCACCGTCCAGTGGTGGTAACAGCTGGACCCCTGGC 954
QY 261 TyrProGluThrGlnGluAlaLeuCysProGlnValThrTrpSerTrpAspGlnLeuPro 280
Db 955 TACCCCGAGACCCAGAGGGCGCTCTGCCCGCAGGTGACATGGTCTTGAGCACGTTGCC 1014
QY 281 SerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSerProAlaGlySer 300
Db 1015 AGCAGAGCTCTGGCCCCGCTGTGCGCCACACTCTGCCAGAGTCCCGCAGCGGCTCG 1074
QY 301 ProAlaMetMetLeuGlnProGlyProGlnLeuTyrAspValMetAspAlaValProAla 320
Db 1075 CCAGCATGATGCTGCAGCCGGGCGCCAGCTCTACGACGTGATGGACGGCTCCACGG 1134
QY 321 ArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGluAlaGluIleGluAlaVal 340
Db 1135 CGGCGCTGGAAGAGTTCGTGGCGACGCTGGGGCTGCGCGAGCAGAGATCGAAGCCGTG 1194
QY 341 GluValGluIleGlyArgPheArgAspGlnGlnTyrGluMetLeuLysArgTrpargln 360
Db 1195 GAGTGGAGATCGCGGCTCCGAGACCAAGCAGTACGAGATGCTCAAGCGCTGGCGCCAG 1254
QY 361 GlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMetGlyLeuAspGly 380
Db 1255 CAGCAGCCCGCGGCGCTCGGAGCCGTTTACGGCGCCCTGGAGCGCATGGGGCTGGACGGC 1314
QY 381 CysValGluAspLeuArgSerArgLeuGlnArgGlyPro 393
Db 1315 TGGGTGGAAGACTTGGCGCAGCCGCTGCAGCGCGGCGCG 1353

RESULT 7
AX201344

LOCUS AX201344 1662 bp DNA linear PAT 30-AUG-2001
DEFINITION Sequence 23 from Patent WO0153486.
ACCESSION AX201344
VERSION AX201344.1 GI:15391165

KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Ashkenazi,A.J., Goddard,A., Godowski,P.J., Gurney,A.L.,
Hillan,K.J., Marsters,S.A., Pan,J., Pittl,R.M., Roy,M.A., Smith,V.,
Stone,D.M., Watanabe,C.K. and Wood,W.I.
TITLE Compositions and methods for the treatment of tumour
JOURNAL Patent: WO 0153486-A 23 26-JUL-2001;
Genentech, Inc. (US)

FEATURES
Source location/Qualifiers
1..1662
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 302 a 540 c 531 g 289 t

Alignment Scores:
Pred. No.: 1.08e-109 Length: 1662
Score: 2209.00 Matches: 393
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-993-234-6_copy_25_417 (1-393) x AX201344 (1-1662)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
Db 175 CAGGGCGGCACTCGTAGCCCGAGGTGTGACTGTGCCGGTGACTTCCACAGAAGATTGGT 234
QY 21 LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
Db 235 CTGTTTGTGTCAGAGGCTGCCACGGGGGCACTACCTGAAGGCCCTTGCACGGAGCCC 294
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db 295 TGGGGCACTCCACCTGCTGTTGTGTCCCAAGACACCTTCTTGGCTTGGAGAACCCAC 354
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db 355 CATAATTCTGAATGTGCCCCGCTGCCAGCGCTGTGATGAGCAGCGCTCCACAGTGGCGCTG 414
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
Db 415 GAGAACTGTTCAGACAGTGGCGCCAGACCCGCTGTGGCTGTAAGCCAGGCTGTGTGAG 474
QY 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120
Db 475 TGCCAGGTACGCCAATGTGTACAGAGTTCACCCCTTCTACTGCCAACCATGCTAGACTGC 534
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 535 GGGGGCTGCACCCGCCACACACCGGCTACTCTGTTCCCGCAGAGATGCTACTGTGGAGCC 594
QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db 595 TGGCTGCTGGCTTCTATGAACATGGCGATGGCTGCTGTCTGCTGCCCCACGAGCACCCCTG 654
QY 161 GlyserycProGluArgCysAlaAlaValCysGlyTrparglMetPheTrpValGln 180
Db 655 GGGAGCTGTCCAGAGCGCTGTGCGCTGTCTGTGGCTGGAGGCAATGTCTGGGTCCAG 714
QY 181 ValLeuLeuAlaGlyLeuValValProLeuLeuLeuGlyAlaThrLeuThrTyrThrTyr 200
Db 715 GTGCTCTGGCTGGCTGTGTGTGCTCCCTCTGCTTGGGGCCACCCCTGACCTACACATAC 774
QY 201 ArgHisCysTrpProHisLysProLeuValThrAlaAspGluAlaGlyMetGluAlaLeu 220
Db 775 CGCCACTGTGGCTCACAAGCCCTGGTTACTGACAGATGAAGCTGGAGTGGAGGCTCTG 834
QY 221 ThrProProProAlaThrHisLeuSerProLeuAspSerAlaHisThrLeuAlaPro 240
Db 835 ACCCCACACCGGCCACCCATCTGTCAACCTTGGACAGCGCCACACACCTTCTAGCACCT 894
QY 241 ProAspSerSerGluLysIleCysThrValGlnLeuValGlyAsnSerTrpThrProGly 260
Db 895 CCTGACAGCAGTGAGAAGATCTGCACCGCTCCAGTTGGTGGGTAAACAGCTGGACCCCTGGC 954
QY 261 TyrProGluThrGlnGluAlaLeuCysProGlnValThrTrpSerTrpAspGlnLeuPro 280
Db 955 TACCCCGAGACCCAGAGGGCGCTTGGCCGCAAGTGACATGGTCTGGGACACAGTTGCC 1014
QY 281 SerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSerProAlaGlySer 300
Db 1015 AGCAGAGCTCTGGCCCCGCTGTGCGCCACACTCTGCCAGAGTCCCGCAGCGGCTCG 1074
QY 301 ProAlaMetMetLeuGlnProGlyProGlnLeuTyrAspValMetAspAlaValProAla 320
Db 1075 CCAGCATGATGCTGCAGCGCGGCGCCGACGCTTACGACGTGATGACGCGGTCCACGGC 1134

QY 321 ArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGluAlaGluIleGluAlaVal 340
Db 1135 CGCGCTGGAAGAGATTGTCGCGACAGCTGGGGCTGCGCGAGCAGAGATCGAAGCCGTG 1194
QY 341 GluValGluIleGlyArgPheArgAspGlnGlnTyrGluMetLeuLysArgTrpArgGln 360
Db 1195 GAGGTGAGATCGCGCTTCGAGACAGCAGATAGATGCTCAAGCGCTGGCGCCAG 1254
QY 361 GlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMetGlyLeuAspGly 380
Db 1255 CAGCAGCCCGCGGCTCGAGCCGTTTACGCGGCCCTGGAGCGCATGGGGCTGAGCGGC 1314
QY 381 CysValGluAspLeuArgSerArgLeuGlnArgGlyPro 393
Db 1315 TCGGTGGAAGACTTGGCGACCGCCCTGCAGCCGCGCCG 1353
RESULT 8
ARL19656
LOCUS ARL19656 1783 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 1 from patent US 6153402.
ACCESSION ARL19656
VERSION ARL19656.1 GI:14102355
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1783)
AUTHORS Yu, G.-L., Ni, J., Gentz, R.L. and Dillon, P.J.
TITLE Death domain containing receptors
JOURNAL Patent: US 6153402-A 1 28-NOV-2000;
FEATURES
source 1.1783
location/Qualifiers
BASE COUNT 330 a 562 c 564 g 327 t
ORIGIN
Alignment Scores:
Pred. No.: 1.16e-109 Length: 1783
Score: 2209.00 Matches: 393
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 gaps: 0
US-09-993-234-6_COPY_25_417 (1-393) x ARL19656 (1-1783)
QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGly 20
Db 303 CAGGGCGGACATCGTAGCCAGGTGTGACTGTGCCGGTGACTTCCACAAGAATTGTT 362
QY 21 LeupheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
Db 363 CTGTTTGTTCAGAGAGCTGCCAGCGGGCACTACCTGAAGGCCCTTGACAGAGCCC 422
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db 423 TGGCGCAACTCCACCTGCTGTGTGCCCAAGACACCTTCTTGCGCTGGAGAACCAC 482
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db 483 CATTAATTCGAATGTGCCCGCTGCCAGCGCTGTATGAGCAGAGCGCTTCCAGGTGGCGCTG 542
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
Db 543 GAGAACTGTTCAAGAGTGGCGCACCGCTGTGCTGTAAGCCAGCGCTGTTGTGAG 602
QY 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120
Db 603 TGCCAGGTCAAGCAATGTGTACAGAGTTCAACCTTCTACTGCCAACCATGCTAGACTGC 662
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
|||||

Db 663 GGGGCCCTGCACCGCCACACAGCGCTACTCTGTTCGCCGACAGATACTGACTGGGACC 722
QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db 723 TGCCTGCTGCTTCTTAAGACATGGCGATGGCTGGCTGTCTGCCCCACAGACACCTTG 782
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArgGlnMetPheTrpValGln 180
Db 783 GCGAGCTGTCCAGAGCGCTGTGCCGCTGTCTGTGGCTGAGGACAGATGTTCTGGGTTCCAG 842
QY 181 ValLeuLeuAlaGlyLeuValValProLeuLeuGlyAlaThrLeuThrTyrThrTyr 200
Db 843 GTGCTCTGGCTGGCTTGTGTGTTCCCTCTGCTTGGGGCCACCCTGACTACACATAC 902
QY 201 ArgHisCysTrpProHisLysProLeuValThrAlaAspGluAlaGlyMetGluAlaLeu 220
Db 903 CGCCACTGTGGCTTCACAGCCCTGTGTTACTGCAGATGAAGCTGGATGAGGCTCTG 962
QY 221 ThrProProAlaThrHisLeuSerProLeuAspSerAlaHisThrLeuLeuAlaPro 240
Db 963 ACCCCACACCGCGCCACCATCTGTACACCTTGAGACAGCCGCCACACCTTCTAGACACT 1022
QY 241 ProAspSerSerGluLysIleCysThrValGlnLeuValGlyAsnSerTrpThrProGly 260
Db 1023 CCTGACAGCAGTGAAGAATCTGCACCGCTCAAGTTGGTGAACAGCTGGAGACCCCTGGC 1082
QY 261 TyrProGluThrGlnGluAlaLeuCysProGlnValThrTrpSerTrpAspGlnLeuPro 280
Db 1083 TACCCCGAGACCCAGAGCGCTGTGCCGAGGATGACATGCTCTGGAGACCAAGTTGCC 1142
QY 281 SerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSerProAlaGlySer 300
Db 1143 AGCAGAGCTCTGGCCCCCGCTGCTGCCGCCACACTCTGCCAGAGTCCACGCCGCTCG 1202
QY 301 ProAlaMetLeuGlnProGlyProGlnLeuTyrAspValMetAspAlaValProAla 320
Db 1203 CCAGCCATGATGCTGCAGCCGGGCCCGCACTTACGACGTGATGAGCGCGTCCAGCG 1262
QY 321 ArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGluAlaGluIleGluAlaVal 340
Db 1263 CGGCGTGAAGGAGTTGTCGCGCACGCTGGGGCTGGCGAGGACAGATCGAAGCCGTG 1322
QY 341 GluValGluIleGlyArgPheArgAspGlnGlnTyrGluMetLeuLysArgTrpArgGln 360
Db 1323 GAGGTGAGATCGCGCGCTTCCGAGACAGCAGATGATGATGAGCGCTGGCGCCAG 1382
QY 361 GlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMetGlyLeuAspGly 380
Db 1383 CAGCAGCCCGCGGCTCGAGCGCTTACGCGGCCCTGAGAGCGCATGGGGCTGAGCGGC 1442
QY 381 CysValGluAspLeuArgSerArgLeuGlnArgGlyPro 393
Db 1443 TGGGTGGAAGACTTGGCGACCGCCCTGCAGCGCGGCCG 1481
RESULT 9
LOCUS HSU83597 1528 bp mRNA linear PRI 27-JAN-1997
DEFINITION Human death domain receptor 3 (DDR3) mRNA, partial cds.
ACCESSION U83597
VERSION U83597.1 GI:1800292
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1528)
AUTHORS Chaudhary, P.M. and Hood, L.E.
TITLE Direct Submission
JOURNAL Submitted (03-JAN-1997) Molecular Biotechnology, University of
Washington, 1705 NE Pacific Street, HSB-K360, Seattle, WA 98195,
USA
FEATURES
source location/Qualifiers
1..1528


```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/map="1p36"
1..1528
/gene="DDR3"
<1..1238
CDS

```

```

/function="mediates apoptosis when cross-linked"
/note="A TNFR1-related death-domain containing receptor;
DR3, WSL-LR, Apo-3, TRAMP; transmembrane form; similar to
human EST clone 298913, GenBank Accession Number N71143"
/codon_start=3
/product="death domain receptor 3"
/product_id="AAB41432.1"
/db_xref="GI:1800293"

```

```

/translation="GCAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKIKGLFCRRG
CPAGHTLAKPCTGEENSTCLVCPDPEFLAMENHNHNSCARQACQASQVAOLEGCS
AVADTRCGCKPGWFVEVCQSQVCSDFYCPCLDCGALHRTILCLCSRDYDGTCLL
LGFEHGDGCVSCTPTSGSCPCECAVCGWROMFVQVLLAGLVPLLGATILTYTY
RHCMPHKPLVTADDEAGMEALTPPPATHSLPDSAHTLAPPDSEKCTVOLVGNSTW
PGYPEPEQELCPQVWTSMDEQLPSRLGPAAPLTLSPSPAGSPAMMLQPGPOLYDMD
AVPARRRKEFVTRLGLRWELEAVEVEIGRFDDQYEMLKRRWRQDPAGLGAVYAALE
RMGLDGCVEDLRSRLQGP"

```

BASE COUNT	280 a	496 c	470 g	282 t
ORIGIN				

Alignment Scores:

Pred. No.:	3,37e-109	Length:	1528
Score:	2199.00	Matches:	392
Percent Similarity:	99.75%	Conservative:	0
Best Local Similarity:	99.75%	Mismatches:	1
Query Match:	99.55%	Indels:	0
DB:	9	Gaps:	0

US-09-993-234-6_COPY_25_417 (1-393) x HSU83597 (1-1528)

Oy 1 GINGLGLYTHrargSerProarGcysasrcysAlaGLyAsrphenIsLysLysIleGLy 20
 |||||
 Db 57 CAGGGCGGCACTGTAGCCCCAGGTGTACTGTGCCGGTGACTTCCACAAGAAGATTGGT 116

QY 21 LeuphEcysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
|||||
Db 117 CTGTTTGTTCAGAGGCTGCCAGCGGGGCACTACCTGAAGGCCCTTGCACGAGGCC 176

QY 41 CysgIyAsnSerThrCysLeuValcysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
 |||||
 Db 177 TGGGGCACTCCACCTGGCTTGTGTGTCCCAAGACACCTTCTGGCTGGGAGAACCC 236

QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
 |||
 Db 237 CATAAATTCGATGTGCCCGCTGCCGCTGTGATGAGCAGGCTCCAGGTGGCGTG 296

QY 81 GLuAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTyrPheValGlu 100
 |||||
 Db 297 GAGAACTGTTACAGCAGTGGCCGACACCGCTGTGGCTGTAAAGCAGGCTGGTTTCTGAG 356

QY 101 CysGlnValSerGlnCysValSerSerSerProPhenylTyrCysGlnProCysLeuAspCys 120
 |||||
 Db 357 TGCCAGGTCAGCCAAATGTGTGACGACAGTTCACCCCTTCTACCTGCACCAACCAATGCGCTACGACATCC 416

QY 121 G I Y A L A L E U H I S A R G H I S T H r A r g L e u L e u C y s S e r A r g A r g A s p T h r A s p C y s G l y T h r 1400

Dh 417 G G G G C C C T G A A C C G C C A C A C A G G G T A C T C T G T T C C C G A A A G A T A A C T G A T C T G C C A A 476

Dh 477 TGGCTGCTTGAGATTATGAACATGCGCATGGCTGCCTGTCTCCCTCCCCAACCAAGGCC 536

OY 141 CysLeuProCl^ypheTyrGl^uHisGlyAspGlyCysValSerCysProThrSerThreⁿ 1600

QY 161 GlySerCysProGluArgCysAlaIaIaValCysGlyTrpArgGlnMetPheTrpValGln 1800

[illegible][illegible]

QY 241 ProaspserserGlutylsilecysthrvalglnleuValglyasnsertTrpThrProgly 260
 |||||
 Db 777 CCTGACAGCAGTGAGAGACTCTGCACCGTCCAGTGTGGGTAAACAGCTGCACCCCTGGC 836

QY 261 TyrProGluThrGlnAlaLeuGlyProGlnValThrTrpSerTrpAspGlnLeuPro 280
 |||||
 Db 837 TACCCGAGACCCAGAGAGCGCTCTGCCCGCAGGTGACATGCTCCTGGGACAGTTGCC 896

QY 281 SerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSerProAlaGlySer 300
 |||||
 Db 897 AGCAGAGCTCTTGCGCCGCTGCTGCGCCACACACTCTGCGCAGAGTCCCCAGCGCGCTCG 956

QY 301 ProIaMetMetLeuGlnProGlyProGlnLeuTyrAspValMetAspAlaValProAla 320
 |||||
 Db 957 CCAGCCATGATGCTGCAGCCGGCCCGCAGCTCTPACGAGCTGATGGACGGCGGCCCCAGCG 1016

QY 321 ArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGluAlaGluIleGluAlaVal 340
 |||||
 Db 1017 CAGCGCTGGAGAGACTTCGCGCACGCTGGGGCGCGGAGGAGAGATCGAGCCGTG 1076
 |||||

QY 341 GIUValGIUIleGlyArgPheArgAspGlnGlnI TyrGluMetLeuLysArgTTPArgGln 360
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1077 GAGGTGGAGATCGGCCGCTCCAGACCAAGCAGTCAGAGATGCTCAAGCGCGTGGCCAG 1136

QY 361 GlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGlnIargMetGlyLeuaspGly 380
 |||||
 Db 1137 CAGCAACCCGGGGCCCTGGAGCCGCTTACGGCGGCCCTGGAGCCGATGGGAGTCGACCGG 1196

QY 381 CysValGluAspLeuArgSerArgLeuGlnArgGlyPro 393
 |||||
 Db 1197 TGCGTGAAGACTTGCGGAGCCGCTGCAGCGCGCGCG 1235

RESULT 10	
HSU75380	
LOCUS	1557 bp
MSU75380	mpna
	1400000
	DBT_05-MDB-1007

DEFINITION	Human apoptosis-mediating receptor TRAMP mRNA, partial cds.
ACCESSION	U75380
VERSION	U75380.1
KEYWORDS	GI:1695924

SOURCE	ORGANISM
Homo sapiens.	Homo sapiens
Eukaryota; Metazoa;	Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria;	Carnivora; Canidae; Mustelidae;
Nasutidae	

REFERENCE

AUTHORS

1 (bases 1 to 1557)

Bodmer, J.L., Burns, K., Schnelder, P., Hofmann, K., Steiner, V.,
Thome, M., Bornand, T., Hahne, M., Schroter, M., Becker, K., Wilson, A.,
Rochet, J.C., Baudouin, C.

TITLE	TRAMP, a novel apoptosis-mediating receptor with sequence homology to tumor necrosis factor receptor 1 and Fas(Apo-1/CD95)
JOURNAL	Immunity 6 (1), 79-88 (1997)
VOLUME	
ISSUE	
PAGES	
DOI	
URL	

PUBMED	9052839
REFERENCE	2 (bases 1 to 1557)
AUTHORS	Bödmer, J.L., Burns, K., Schneider, P., Hofmann, K., Steiner, V.,

TITLE French, L.E., Browning, J.L., Macdonald, R. and Tschopp, J.
Direct Submission
JOURNAL Submitted (18-OCT-1996) Institute of Biochemistry, University of

FEATURES

Lausanne, 155 Chemin des Boveresses, Epalinges, CH 1066, Switzerland

Location/Qualifiers

FEATURES

Location/Qualifiers

```
source
1. .1557
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/map="1p36.2"
/tissue_type="fetal lung"
<1. .1245
/function="activates NF-kB"
/function="mediates apoptosis"
/notes="contains a death domain; similar to TNF receptor"
/codon_start=1
/product="apoptosis-mediating receptor TRAMP"
/protein_id="AAC51192.1"
/db_xref="GI:1695925"
/translation="AAAGCAVAAALLVLGARAQGTSPRCDCAGDFHKKIGLFC
CRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAMENHNHNSCARCQASQVALE
NCSAVADTRCGCKPGWFEVCQVSSPFCQPCIDGALHRTILCSRDTCG
TCLLGFVEHGDGCVSCPSTLIGSCPERCAVCGWRQFWQVLLAGLVPLLGLATLT
YTYRHQWPHKPLVTADDEAGMEALTPPATHLSPIDSAHTLLAPPDSEKICTVQLVN
SWTPGYPETQALCPQVYTWSDQLPSRALGPAAPLSPESPAGSPAMLIQGPQLYD
VMDAVPARRMKEFVETLGLREAEIEAVEVEIGRFRDQYEMLKRWQQPAGLGAVYA
ALERMGIDGCEVDIRSLQRP"

BASE COUNT      286 a      508 c      477 g      286 t
ORIGIN

Alignment Scores:
Pred. No.:      3.43e-109      Length:      1557
Score:          2199.00      Matches:      392
Percent Similarity: 99.75%      Conservative: 0
Best Local Similarity: 99.75%      Mismatches: 1
Query Match:    99.55%      Indels:      0
DB:             9      Gaps:         0

US-09-993-234-6_COPY_25_417 (1-393) x HSU75380 (1-1557)

QY      1  GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
Db      64  CAGGGCGGCACTCGTAGCCCGCAGGTGTGACTGTGCCGGTGACTTCCACAGAAGATTGGT 123
QY      21  LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
Db      124 CTGTTTGTGTGACAGAGGCTGCCCGCAGCGGGGACACTACTGGAAGGCCCTTGACGCGGCC 183
QY      41  CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db      184 TGCAGCACTCCACCTGCTGTGTGTCCCAAGACACTTCTTGCCCTGGAGAACCCAC 243
QY      61  HisAsnSerGluCysAlaArgCysGlnAlaCysAspGlnAlaSerGlnValAlaLeu 80
Db      244 CATATCTGATGTGCCGCTGCCAGGCTGTGATGACAGCGCTCCCGCAGGTGCGCTG 303
QY      81  GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
Db      304 GAGAACTGTTCAAGCAGTGGCCGACACCGCTGTGCTGTAAGCCAGCGCTGTTGTGGAG 363
QY      101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLysAspCys 120
Db      364 TGCAGGTCAAGCAATGTGTCAAGCATCACCTTCTACTGCCAACCATGCGCTAGACTGC 423
QY      121 GlnAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db      424 GGGGCCCTGCACCGCACACAGGCTACTCTGTTCCTCCGACAGATACTGACTGTGGAGCC 483
QY      141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db      484 TGCCTGCTGGCTTATGAAACATGGCGATGCTGCTGCTGCTGCCACAGACACCCCTG 543
QY      161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArgGlnMetPheTrpValGln 180
Db      544 GGGAGCTGTCCAGAGCGCTGTGCCGTGTGTGTGGCTGGAGGAGATGTCTGGGTCCAG 603
QY      181 ValLeuLeuAlaGlyLeuValValProLeuLeuLeuGlyAlaThrLeuThrTyrThrTyr 200
|||||
```

```
Db      604 GTGCTCTGGCTGGCCCTTGTGTGTTCCCTCTGCTTGGGGCCACCTGACCTACACATAC 663
QY      201 ArgHisCysTrpProHisLysProLeuValThrAlaAspGluAlaGlyMetGluAlaLeu 220
Db      664 CGCAGCTGTGGCTTACAAAGCCCTGTGTTACTGACAGATGAAGCTGGATGAGAGCTCTG 723
QY      221 ThrProProAlaThrHisLeuSerProLeuAspSerAlaHisThrLeuLeuAlaPro 240
Db      724 ACCCCACACCGGCCACCATCTGTACACCTTGACAGCGGCCACACCTTCTAGACACT 783
QY      241 ProAspSerSerGluLysIleCysThrValGlnLeuValGlyAsnSerTrpThrProGly 260
Db      784 CCTGACAGCAGTAGAGAGATCTGCACCGTCCAGTTGGTGGTAACAGCTGACCCCTGGC 843
QY      261 TyrProGluThrGlnGluAlaLeuCysProGlnValThrTrpSerTrpAspGlnLeuPro 280
Db      844 TACCCCGAGACCCAGAGAGCGCTCTGCCCGCAGGTGACATGCTCTGGAGACAGTTGCC 903
QY      281 SerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSerProAlaGlySer 300
Db      904 AGCAGAGCTCTTGGCCCGCTGCTGCGCCACACTCTGCCACAGATGCCACAGCGGCTCG 963
QY      301 ProAlaMetLeuGlnProGlyProGlnLeuTyrAspValMetAspAlaValProAla 320
Db      964 CCAGCATGATGCTGCAGCGCGGCCCGCCGACGCTCTAGACGTGATGAGCGCGTCCACGG 1023
QY      321 ArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGluAlaGluIleGluAlaVal 340
Db      1024 CGGCGCTGGAAGAGATTCTGCGCACGCTGGGGCTGGCGGAGCAGAGATCGAACCCGTG 1083
QY      341 GluValGluIleGlyArgPheArgAspGlnGlnIleTyrGluMetLeuLysArgTrpArgGln 360
Db      1084 GAGGTGAGAGATCGCGGCTTCCGAGACACAGACAGATGATGCTCAAGCGCTGGCGCCAG 1143
QY      361 GlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMetGlyLeuAspGly 380
Db      1144 CAGCAGCGCGCGGCTTCGAGAGCGCTTACCGCGGCTGGAAGCGCATGGGCTGGACGGC 1203
QY      381 CysValGluAspLeuArgSerArgLeuGlnArgGlyPro 393
Db      1204 TGCGTGGAAGACTTGCACAGCGGCTGACGAGGCGCCG 1242

RESULT 11
HSU94502      1257 bp      mRNA      linear      PRI 15-MAY-1997
LOCUS
DEFINITION
Human lymphocyte associated receptor of death 1b mRNA,
alternatively spliced, complete cds.
ACCESSION
U94502
VERSION
U94502.1
KEYWORDS
GI:2071950
SOURCE
Homo sapiens.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 1257)
Screation,G.R., Xu,X.N., Olsen,A.L., Cowper,A.E., Tan,R.,
McMichael,A.J. and Bell,J.I.
LARD: a new lymphoid-specific death domain containing receptor
regulated by alternative pre-mRNA splicing
Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)
MEDLINE
97272273
PUBMED
9114039
REFERENCE
2 (bases 1 to 1257)
Screation,G.R.
Direct Submission
Submitted (19-MAR-1997) Molecular Immunology Group, Institute of
Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3
9DU, UK
FEATURES
source
location/Qualifiers
1. .1257
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Hela"
```

```

CDS
    /cell_type="lymphocyte"
    1..1257
    /function="mediates apoptosis"
    /note="LARD-1b; membrane protein; similar to Fas and
    TNF-R1; contains a death domain"
    /codon_start=1
    /product="lymphocyte associated receptor of death 1b"
    /protein_id="AAC51307.1"
    /db_xref="GI:2071951"
    /translation="MEORRRCAGAAVAALLLVLLGARAGGTRSPRCDAGDFHKIG
    LFCCRCPAGHYLKAPCTEPCGNSTCLVCPDITFLAMENHNHNSCARCQACDEQASQY
    ALENCASAVADTRCGCKPGMEVECCQVSQSSSPFYCQPCLDGALHRTRLCSRDY
    DCGTCLPGFEYEHGDGVCSCPTSLGSCPERCAAVCGWRQMFVQVLLAGLVVPLIGA
    TLTYTRHCWPHKPLVTADEAGMEALTTPPATHLSPIDSAHTLLAPDSSEKICTVO
    LVGNSWTPGYPETQALCPQVWMSDQLPSRALGPAAPTLSPESPAGSPAMMQBGP
    QLYDVMADVAPARRWKEFVRTLGLREAEI EAVEVEIGRFRDQOYEMLKRWRRQQPAGLG
    AVYALERMGLDGCVEDLRSLRQRP"
misc_feature
    708..711
    /note="insertion compared to LARD-1a, deposited in GenBank
    Accession Number U94501, probably represents alternative
    3' splice site"
BASE COUNT      202 a      421 c      408 g      226 t
ORIGIN
Alignment Scores:
Pred. No.:      2,91e-109      Length:      1257
Score:          2198.50         Matches:      393
Percent Similarity: 99.75%      Conservative: 0
Best Local Similarity: 99.75%      Mismatches: 0
Query Match:      99.52%         Indels:      1
DB:               9             Gaps:        1
US-09-993-234-6_COPY_25_417 (1-393) x HSU94502 (1-1257)
QY      1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
Db      73 CAGGGCGGCGACTCGTAGCCCCAGGTGTGACTGTGCCGGTACTCCACAGAAGATTGGT 132
QY      21 LeuPheCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
Db      133 CTGTTTGTGTCAGAGGCTGCCACGGGGGCACTACCTGAAGGCCCTTTGCACAGGAGCCC 192
QY      41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db      193 TGGCGCACTCCACCTGCCTGTGTGTCTCCCAAGACACCTTCTTGCCCTGGGAGAACCCAC 252
QY      61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db      253 CATAATTCTGAATGTGCCCGCTGCAGGCTGTGATGAGCAGGCGCTCCACAGGTGGCGCTG 312
QY      81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
Db      313 GAGAACTGTTCAGCAGTGGCGGACACCCGCTGTGGCTGTAAAGCCAGGCTGTTGTGAGAG 372
QY      101 CysGlnValSerGlnCysValSerSerSerProPheTyrCysGlnProCysLeuAspCys 120
Db      373 TGGCAGGTCAAGCAATGTGTACAGCAGTTTACCCCTTCTACTGCCAACCATGCCCTAGACTGC 432
QY      121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db      433 GGGGCCCTGCACCGCCACACACAGGCTACTTGTCCCGCAGAGATGACTGTGGGACC 492
QY      141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db      493 TGCCTGCCTGGCTTCTATGAACATGGCGATGGCTGCCTGCTGCCACAGACACCCCTG 552
QY      161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArgGlnMetPheTrpValGln 180
Db      553 GGGAGCTGTCCAGAGCGCTGTGCCGCTGTGTGGCTGAGGACAGATTTCTGGGCTCCAG 612
QY      181 ValLeuLeuAlaGlyLeuValValProLeuLeuLeuGlyAlaThrLeuThrTyrThrTyr 200
Db      613 GTGCTCCTGGCTGGCTGTGTGTCCTCCCTCTGCTTGGGGCCACCCCTGACCTACACATAC 672
```

```

QY      201 ArgHisCysTrpProHisLysProLeuValThr---AlaAspGluAlaGlyMetGluAla 219
Db      673 CGCCACTGTGGCTTCACAAGCCCCCTGGTACTGTACAGCAGATGAAGCTGGATGGAGGCT 732
QY      220 LeuThrProProAlaThrHisLeuSerProLeuAspSerAlaHisThrLeuLeuAla 239
Db      733 CTGACCCACACCGGGCCACCCCATCTGTACCTTGGACAGCGCCACACCTTCTAGCA 792
QY      240 ProProAspSerSerGluLysIleCysThrValGlnLeuValGlyAsnSerTrpThrPro 259
Db      793 CCTCCTGACAGCAGATGAGAAGATCTGCACCCGTCCAGTTGGTGGTAACAGCTGAACCCCT 852
QY      260 GlyTyrProGluThrGlnGluAlaLeuCysProGlnValThrTrpSerTrpAspGlnLeu 279
Db      853 GGCTACCCCGAGACCCAGAGGCGCTCTGCCCGCAGGTGACATGGTCTCGGAGCACAGTTG 912
QY      280 ProSerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSerProAlaGly 299
Db      913 CCCAGCAGAGCTCTTGGCCCCCGCTGCTGCCGCCACACTCTGCCACAGATCCACAGCCGCG 972
QY      300 SerProAlaMetMetLeuGlnProGlyProGlnLeuTyrAspValMetAspAlaValPro 319
Db      973 TCGCAGCAGCAATGATGCTGCAGCCGCGGCCGAGCTTACGACGTGATGAGCGCGTCCCA 1032
QY      320 AlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGluAlaGluIleGluAla 339
Db      1033 GCGCGGCGCTGGAAGAGAGTTCTGTCGCCACGCTGGGGCTGCCGCGAGGACAGATCCGAAGCC 1092
QY      340 ValGluValGluIleGlyArgPheArgAspGlnGlnTyrGluMetLeuLysArgTrpArg 359
Db      1093 GTGAGGTGAGATCGGCCCTCTCCGAGACCAAGATGATGCTCAAGCGCTGGCGC 1152
QY      360 GlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMetGlyLeuAsp 379
Db      1153 CAGCAGCAGCCGCGGGCGCTCGGAGCGCTTACCGCGGCGCTGGAGCGCATGGGGCTGGAC 1212
QY      380 GlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 393
Db      1213 GGCTGCGTGAAGACTTGGCGCAGCCGCTGCAGCGCGGCGCG 1254
FEATURES
    LOCUS      HSU94503              1355 bp      mRNA      linear      PRI 15-MAY-1997
    DEFINITION Human lymphocyte associated receptor of death 2 mRNA, alternatively
    spliced, complete cds.
    ACCESSION   U94503
    VERSION     U94503.1
    KEYWORDS    GI:2071952
    SOURCE      Homo sapiens.
    ORGANISM    Homo sapiens.
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
    REFERENCE   1 (bases 1 to 1355)
    AUTHORS    Sreaton,G.R., Xu,X.N., Olsen,A.L., Cowper,A.E., Tan,R.,
    McMichael,A.J. and Bell,J.I.
    TITLE      LARD: a new lymphoid-specific pre-mRNA splicing
    regulated by alternative pre-mRNA splicing
    JOURNAL    Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)
    MEDLINE    97272273
    PUBMED     9114039
    REFERENCE   2 (bases 1 to 1355)
    AUTHORS    Sreaton,G.R.
    TITLE      Direct Submission
    JOURNAL    Submitted (19-MAR-1997) Molecular Immunology Group, Institute of
    Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3
    9DU, UK
FEATURES
    source      Location/Qualifiers
    1..1355
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /cell_line="Hela"
    /cell_type="lymphocyte"
```


CDS

1..762

/function="mediates apoptosis"

/note="LARD-2; similar to Fas and TNF-R1; possibly soluble; truncated before the transmembrane domain"

/codon_start=1

/product="lymphocyte associated receptor of death 2"

/protein_id="AAC51308.1"

/db_xref="GI:2071953"

/translation="MEQRPRGCAVAALLLVLLGARAQGGTRSPRCDAGDFHKKIG LFCCRGCPAGHYLAKPCTEPCGNSTLYCPDTEFLAWENHNSECAQCQADEQASQV ALENCASAVADTRCGCKPGWFVECOVSCVSSSPFYCQPLDCGALHNRHLCSRDY DCGTLPGEYEHGDGCVSCPSTSLGSCBERCAAVCGWRSRWCAGNNSGRTGMDRGEA GEEGNNPTPTSCFQCSGRCSWLALMSPSCLGP"

misc_feature

599..700

/note="insertion compared to LARD 1a, deposited in GenBank Accession Number U94501, probable retained intron leading to premature transcriptional termination"

BASE COUNT 223 a 441 c 451 g 240 t

ORIGIN

Alignment Scores:

Pred. No.: 4.87e-107 Length: 1355

Score: 2157.50 Matches: 392

Percent Similarity: 91.80% Conservative: 0

Best Local Similarity: 91.80% Mismatches: 1

Query Match: 97.67% Indels: 35

DB: 9 Gaps: 1

US-09-993-234-6_COPY_25_417 (1-393) x HSU94503 (1-1355)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20

Db 73 CAGGGCGGCACTCGTACCCCCAGGTGTGACTGTGCGGTGACTTCCACAAAGATTGGT 132

QY 21 LeuphCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40

Db 133 CTGTTTGTGTGACAGAGCTGCCAGCGGGGCACTGAAAGGCCCTTGACGGAGACC 192

QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60

Db 193 TGGCGCACTCCACTGCTGCTGTGTCCCAAGACACCTTCTTGCGCTGGGGAACCCAC 252

QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGlnAlaSerGlnValAlaLeu 80

Db 253 CATATTCTGAATGTGCCCGCTGCCAGCGCTGTGATGAGCAGGCTCCAGGTGGCGCTG 312

QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100

Db 313 GAGAACTGTTCAGAGTGGCCGACACCGGCTGGGCTGTAAGCCAGGCTGGTTGTGGAG 372

QY 101 CysGlnValSerGlnCysValSerSerSerProPheTyrCysGlnProCysLeuAspCys 120

Db 373 TGGCAGGTACGCCAATGTGTACAGCATTCACCTTCTACTGCCAACCATGCTTAGACTGC 432

QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140

Db 433 GGGGCCCTGCACGCCACACACAGGCTACTGTGTCCGACAGATACTGACTGTGGGACC 492

QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160

Db 493 TGCTTGCTGCTGTATGACATGGCGATGGCTGCTGCTGCGCCACGACGACCCCTG 552

QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArg----- 174

Db 553 GGGAGCTGTTCAGAGCGCTGTGCCGCTGTGTGCTGAGAGCAGATAGGTGTGTGCT 612

QY 174 ----- 174

Db 613 GGAATGCGAGTGGGAGAACTGGATGACCGAGGGGCGGTGACGAGGGGGCAAC 672

QY 175 -----GlnMetPheTrpValGlnValLeuLeuAlaGlyLeu 186

Db 673 CACCAACACCAACCAAGCTGCTTTCAGTGTG- TTCTGGGTCCAGGTGCTGCTGCGCTT 731

QY 187 ValValProLeuLeuGlyAlaThrLeuThrTyrThrTyrArgHisCysTrpProHis 206

Db 732 GTGGTCCCCCTCCTGCTGGGGGCCACCCCTGACCTACACATACCGCCACTGCTGCTCAC 791

QY 207 LysProLeuValThrAlaAspGluAlaGlyMetGluAlaLeuThrProProProAlaThr 226

Db 792 AAGCCCCGTGTACTGCAGATGAAGCTGGATGAGGCTCTGACCCACACCGGCCACC 851

QY 227 HisLeuSerProLeuAspSerAlaHisThrLeuLeuAlaProProAspSerSerGlyLys 246

Db 852 CATCTGTACCCCTTGACAGCGCCACACACCCCTTACACACCTCTGACAGCAGTGAAGAAG 911

QY 247 IleCysThrValGlnLeuValGlyAsnSerTrpThrProGlyTyrProGluThrGlnGlu 266

Db 912 ATCTGCACCGTCCAGTTGTGGGTAAACAGCTGACCCCTGCTACCCCGACAGCCAGAG 971

QY 267 AlaLeuCysProGlnValThrTrpSerTrpAspGlnLeuProSerArgAlaLeuGlyPro 286

Db 972 GCGCTCTGCCCGCAGGTGACATGTCTCTGGAGCAGTTGCCACAGCAGAGCTTGGCCCC 1031

QY 287 AlaAlaAlaProThrLeuSerProGluSerProAlaGlySerProAlaMetMetLeuGln 306

Db 1032 GCTGCTGCGCCCACTCTCGCCAGAGAGTCCCGCCGCTCGCCAGCATGATGCTGCAG 1091

QY 307 ProGlyProGlnLeuTyrAspValMetAspAlaValProAlaArgArgTrpLysGluPhe 326

Db 1092 CCGGGCCCGCAGCTTACGACGTGATGACCGCGCTCCAGCGCGCTGGAAGAGATTTC 1151

QY 327 ValArgThrLeuGlyLeuArgGluAlaGluIleGluAlaValGluValGluIleGlyArg 346

Db 1152 GTGCGACAGCTGGGCTGCGCGAGGAGAGATCGAAAGCCGTGAGGTGGAGATCGGCCGC 1211

QY 347 PheArgAspGlnGlnTyrGluMetLeuLysArgTrpArgGlnGlnProAlaGlyLeu 366

Db 1212 TTCCGAGACAGCAGTACGAGATGCTCAAGCGCTGGCGCCAGCAGCAGCGCGGCGCTC 1271

QY 367 GlyAlaValTyrAlaAlaLeuGluArgMetGlyLeuAspGlyCysValGluAspLeuArg 386

Db 1272 GGAGCCGTTTACCGCGGCCCTTGAGCGCATGGGCTGGACGCGCTGCTGGAAGACTTGGCC 1331

QY 387 SerArgLeuGlnArgGlyPro 393

Db 1332 AGCGGCTGCAGCGCGGCCCG 1352

RESULT 13

AX331947 1743 bp DNA linear PAT 09-JAN-2002

LOCUS

DEFINITION Sequence 2456 from Patent WO0194629.

ACCESSION AX331947

VERSION AX331947.1 GI:18122581

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

REFERENCE

1 Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G., Horrihan, S., Soppet, D.R. and Weaver, Z. Cancer gene determination and therapeutic screening using signature gene sets

JOURNAL Patent: WO 0194629-A 2456 13-DEC-2001;

FEATURES

location/Qualifiers

1..1743

/organism="Homo sapiens"

/db_xref="taxon:9606"

BASE COUNT 347 a 543 c 549 g 304 t

ORIGIN

Alignment Scores:

Pred. No.: 5.16e-106 Length: 1743

Score: 2140.50 Matches: 389

Percent Similarity: 91.10% Conservative: 0
Best Local Similarity: 91.10% Mismatches: 4
Query Match: 96.90% Indels: 35
DB: 6 Gaps: 1
US-09-993-234-6_COPY_25_417 (1-393) x AX331947 (1-1743)

QY	1	GLNGLYGLYThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly	20
Db	141	CAGGGGGCACTCGTAGCCCCAGGTGTGACTGTGCCGGTGACTTCACAGAAGATTGGT	200
QY	21	LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro	40
Db	201	CTGTTTGTTCAGAGAGGTGCCAGGGGGGCACTACCTGAAGGCCCTTGACAGGAGCCC	260
QY	41	CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis	60
Db	261	TGCGGCACTCCACCTGCCCTGTGTGTCCCAAGACACCTTCTTGCGCTGGAGAACCCAC	320
QY	61	HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu	80
Db	321	CATAATCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCTCCAGGTGGCGCTG	380
QY	81	GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu	100
Db	381	GAGAACTGTCAAGAGTGGCCGACACCGCTGTGGCTGTAAGCCAGGCTGGTTGTGAG	440
QY	101	CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys	120
Db	441	TGCCAGGTCAAGCAATGTGTCAAGCAAGTCAACCTTCTACTGCCAACCATGCTAGACTGC	500
QY	121	GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr	140
Db	501	GGGGCCCTGCACCGCCACACACGGCTACTCTGTCCCGCAGAGATACTGACTGTGGACC	560
QY	141	CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu	160
Db	561	TGCTGTGCTGCTCTATGAACATGGCGATGGCTGCTGCTGCCCCACGAGCACCCCTG	620
QY	161	GlySerCysProGluArgCysAlaValCysGlyTrpArg	174
Db	621	GGAGCTGTCCAGAGCGCTGTGCCGTGTCTGTGGCTGAGGCGAGAGTAGGTGTGTGCT	680
QY	174		174
Db	681	GGGAATGCCCGTGGGAGACTGGGATGGACCGAGGGGAGCGGGTGAGGAGGGGGCAAC	740
QY	175	-----GlnMetPheTrpValGlnValLeuLeuAlaGlyLeu	186
Db	741	CACCCAACACCACACAGCTGCTTTCAGTG-TTCTGGGTCCAGGTGCTCTGGCTGGCCCTT	799
QY	187	ValValProLeuLeuLeuGlyAlaThrLeuThrTyrThrTyrArgHisCysTrpProHis	206
Db	800	GTGTCTCCCTCTCTGCTTGGGGCCACCTGACCTACACATACCGCACTGTGCGCTCAC	859
QY	207	LysProLeuValThrAlaAspGluAlaGlyMetGluAlaLeuThrProProAlaThr	226
Db	860	AAGCCCTGTGTACTGCAGATGAAGCTGGGATGGAGGCTGTGACCCACACCGCCACC	919
QY	227	HisLeuSerProLeuAspSerAlaHisThrLeuLeuAlaProProAspSerSerGluLys	246
Db	920	CATCTGTACACCTTGACAGCGCCACACCTTCTAGCACCTCCTGACAGCAGTAGAGAG	979
QY	247	IleCysThrValGlnLeuValGlyAsnSerTrpThrProGlyTyrProGluThrGlnGlu	266
Db	980	ATCTGCACCGTCCAGTGTGGTGGTAAACAGCTGGACCCCTGGCTACCCCGAAGACCAGAG	1039
QY	267	AlaLeuCysProGlnValThrTrpSerTrpAspGlnLeuProSerArgAlaLeuGlyPro	286
Db	1040	GGGCTTGGCCCGCAGGTGACATGCTCTGGGACCAAGTTGGCCACAGAGCTCTTGGCCCC	1099
QY	287	AlaAlaAlaProThrLeuSerProGluSerProAlaGlySerProAlaMetLeuGln	306

Db	1100	GCTGTGCGCCACACTCTCGCCAGAGTCCCCAGCCGGCTCGCCAGCCATGATGCTGCAG	1159
QY	307	ProGlyProGlnLeuTyrAspValMetAspAlaValProAlaArgArgTrpLysGluPhe	326
Db	1160	CCGGGCCCCAGCTCTACGACGTGATGAGCCGGTCCACGCGCGCTGGAAGAGATTTC	1219
QY	327	ValArgThrLeuGlyLeuArgGluAlaGluIleGluAlaValGluValGluIleGlyArg	346
Db	1220	GTGCGCACGCTGGGGCTGCGCGAGGACAGATGCAAGCCGTGGAGGTGGAGATCGTCTC	1279
QY	347	PheArgAspGlnGlnTyrGluMetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeu	366
Db	1280	TTCGAGACCAAGCAGTAGAGATGCTCAAGCACTGGCCGACAGACAGCCCGGGCTTC	1339
QY	367	GlyAlaValTyrAlaAlaLeuGluArgMetGlyLeuAspGlyCysValGluAspLeuArg	386
Db	1340	GGAGCCGTTACGGCGCCCTGGAGCGCATGGGGCTGGACGGCTGCGTGAAGACTTGGCC	1399
QY	387	SerArgLeuGlnArgGlyPro	393
Db	1400	AGCCGCTGCAGCGTGGCCCG	1420
RESULT 14			
HWSL1			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
MEDLINE			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
FEATURES			
source			
1. 1743			
/organism="Homo sapiens"			
/db_xref="taxon:9606"			
/cell_type="T-lymphocyte"			
/tissue_type="lymphoid"			
1. 1742			
/gene="WSL-1"			
1. 610			
/gene="WSL-1"			
/number=1			
join(69. 666,768. 1423)			
/gene="WSL-1"			
/codon_start=1			
/product="WSL-1R protein"			
/protein_id="CAA70561.1"			
/db_xref="GI:1669693"			
/db_xref="SWISS-PROT:Q93038"			
/translation="MEQRRCGAVAALLLVLLGARQGGTRSPRCDACGDFHKRTG			
LECCRGCPAGHYLKAPCTEBCGNSTCLVCPDFTLAWENHNHNSCARQACDEQASQV			
ALENCSAVADTRCGCKPGWFEVCQVSQCVCSSPFYQPCIDCGALHHRTRLCSRDPT			
DCGTLPGFEYEHGDCVSCPTSLGSCPERCAAVCGWRQWVQVLLAGLVVPLLGA			
TLTYTRHCWPHKPLVTADAEAMEALTPPATHLSPDSAHLLAPDSSEKICTYQL			
VGNSWTPGYETQALCPQYTWSDQLPSRALGPARAPLSPSPAGSPAMLDGPO			
LYDVMDAVPARRWKEFVRLGLEAEIEAVEVEIGLFRDQYEMLKHWROQOPAGIGA			
VYALERMGLDGCVEDLRSRLQRP"			
join(69. 610,768. 882)			
/gene="WSL-1"			
CDS			

```
/codon_start=1
/product="WSL-S1 protein"
/protein_id="CAA70560.1"
/db_xref="GI:1669692"
/db_xref="SWISS-PROT:Q93038"
/translation="MEQRPGCAVAALALLVLGARAQGGTRSPRCDCAGDFHKKIG
LFCRRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAMENHNHSECAQCACDEQASQY
ALENCSAVADTRCGCKPGEVVECOVSQCVSSPFYCQPCLDGALHRTLLCSRRDT
DCGTCLPGFYEHDGCVSCPTVLGPGAPGWPCCPPAWGHPDLHPIPLIASQAPGYCR
"
69.830
/gene="ws1-1"
/codon_start=1
/product="WSL-S2 protein"
/protein_id="CAA70559.1"
/db_xref="GI:1669691"
/db_xref="SWISS-PROT:Q93038"
/translation="MEQRPGCAVAALALLVLGARAQGGTRSPRCDCAGDFHKKIG
LFCRRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAMENHNHSECAQCACDEQASQY
ALENCSAVADTRCGCKPGEVVECOVSQCVSSPFYCQPCLDGALHRTLLCSRRDT
DCGTCLPGFYEHDGCVSCPTVLGPGAPGWPCCPPAWGHPDLHPIPLIASQAPGYCR
"
611.666
/gene="ws1-1"
/number=2
667.767
/gene="ws1-1"
/number=3
768.1742
/gene="ws1-1"
/number=4

BASE COUNT      347 a      543 c      549 g      304 t
ORIGIN
Alignment Scores:
Pred. No.:      5.16e-106      Length:      1743
Score:      2140.50      Matches:      389
Percent Similarity:      91.10%      Conservative:      0
Best Local Similarity:      91.10%      Mismatches:      4
Query Match:      96.90%      Indels:      35
DB:      9      Gaps:      1
US-09-993-234-6_COPY_25_417 (1-393) x HSWSL1 (1-1743)
QY      1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGly 20
Db      141 CAGGGCGGCACTCGTAGCCGCCAGGTGTGACTGTGCCGGTGACTTCCACAGAAGATTGGT 200
QY      21 LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
Db      201 CTGTTTGTGTGACAGAGCGTGCACGCGGACACTGACGAAGGCCCTTGCACGACGCC 260
QY      41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTyrGluAsnHis 60
Db      261 TCGGGCAACTCCACCTGCTGTGTGTCCCAAGACACCTTCTTGGCCTGGAGAACCCAC 320
QY      61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db      321 CATATTTCTGAATGTGCCCGCTGCCAGGCCCTGTGATGACGACGAGGCCCTCCAGGTGG 380
QY      81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTyrPheValGlu 100
Db      381 GAGAACTGTTACAGAGTGGCCGACACACCGCTGTGGCTGTAAAGCCAGGCTGTGTGGAG 440
QY      101 CysGlnValSerGlnCysValSerSerSerProPheTyrCysGlnProCysLeuAspCys 120
Db      441 TGCAGGTCAGCCAATGTGTACAGAGTTCACCTTCTACTGCCAACCAATGCTAGACTGC 500
QY      121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db      501 GGGGCCCTGCACCGCCACACACGCGTACTCTGTCCCGCAGAGATATGACTGTGGAGCC 560
QY      141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
```

```
Db      561 TGCCCTGCTGGCTTCTATGACATGGCGATGGCTGCGTGTCTGCCCCACGAGCACCTTG 620
QY      161 GlySerCysProGluArgCysAlaAlaValCysGlyTyrArg----- 174
Db      621 GGGAGCTGTCCAGAGCGCTGTGCCGCTGTGTGGCTGGAGGCAGAGTAGTGTGTGCT 680
QY      174 ----- 174
Db      681 GGGAAATGCCGCTGGAGAACTGGGATGACCCGAGGAGCGGGGTGAGAGGGGGGCAAC 740
QY      175 -----GlnMetPheTyrValGlnValLeuLeuAlaGlyLeu 186
Db      741 CACCCCAACACCACACAGCTGCTTTCAGTG-TTCTGGGTCCAGGTGCTCTGGCTGCTT 799
QY      187 ValValProLeuLeuLeuGlyAlaThrLeuThrTyrThrTyrArgHisCysTyrProHis 206
Db      800 GTGGTCCCCCTCTGCTTGGGGCCACCTGACCTACACATACCGCCACTGCTGGCTTCAC 859
QY      207 LysProLeuValThrAlaAspGluAlaGlyMetGluAlaLeuThrProProAlaThr 226
Db      860 AAGCCCCCTGTACTGCAGATGAAGCTGGGATGGAGGCTCTGACCCACACCGGCCAC 919
QY      227 HisLeuSerProLeuAspSerAlaHisThrLeuLeuAlaProProAspSerSerGlyLys 246
Db      920 CATCTGTACCCCTTGGACAGCGCCACACACCTTCTAGCACCTCTGACAGCAGTGAAGA 979
QY      247 IleCysThrValGlnLeuValGlyAsnSerTyrThrProGlyTyrProGluThrGlnGlu 266
Db      980 ATCTGCACCGCTCAGTTGGTGGTAAACAGCTGACCCCTGGCTACCCCGAGACCCAGAG 1039
QY      267 AlaLeuCysProGlnValThrTyrSerTyrAspGlnLeuProSerArgAlaLeuGlyPro 286
Db      1040 GCGCTGTGCCCCGAGGTGACATGCTCTGGAGCAGTTGCCACGACAGACTCTTGGCCCC 1099
QY      287 AlaAlaAlaProThrLeuSerProGluSerProAlaGlySerProAlaMetMetLeuGln 306
Db      1100 GCTGTGCGCCACACTCTCGCCAGAGTCCCGCCAGCGGCTCGCCAGCAGATGCTGCAG 1159
QY      307 ProGlyProGlnLeuTyrAspValMetAspAlaValProAlaArgArgTyrLysGluPhe 326
Db      1160 CCGGGCCCGCAGCTCTACGACGTGATGACGGGGTCCCAAGCGCGCTGGAAGAGATTG 1219
QY      327 ValArgThrLeuGlyLeuArgGluAlaGluIleGluAlaValGluValGluIleGlyArg 346
Db      1220 GTGCGCACGCTGGGGCTGCGGAGGACAGAGATCGAAGCCGTGGAGGTGAGATCGGTC 1279
QY      347 PheArgAspGlnGlnTyrGluMetLeuLysArgTyrPargGlnGlnGlnProAlaGlyLeu 366
Db      1280 TTCCGAGACACAGCATGACAGATGCTCAAGCACTGGCCGACAGCAGACCGCGGCTC 1339
QY      367 GlyAlaValTyrAlaAlaLeuGluArgMetCysGlyLeuAspGlyCysValGluAspLeuArg 386
Db      1340 GGAGCCGTTTACCGCGGCCCTGAGAGCGCATGGGGCTGACGCGCTGCTGGAAGACTTGC 1399
QY      387 SerArgLeuGlnArgGlyPro 393
Db      1400 AGCCGCTGTGACGCTGGCCG 1420
RESULT 15
AF026070      1669 bp      mRNA      linear      PRI 28-JAN-1998
LOCUS      AF026070
DEFINITION      Homo sapiens death receptor 3 beta (DR3) mRNA, complete cds.
ACCESSION      AF026070
VERSION      AF026070.1 GI:2570830
KEYWORDS
SOURCE
ORGANISM      Homo sapiens.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1669)
Warzocha,K., Ribeiro,P., Charlot,C., Renard,N., Colffier,B. and
Salles,G.
```

TITLE A new death receptor 3 isoform: expression in human lymphoid cell lines and non-Hodgkin's lymphomas
JOURNAL Biochem. Biophys. Res. Commun. 242 (2), 376-379 (1998)
MEDLINE 98113360
PUBMED 9446802
REFERENCE 2 (bases 1 to 1669)
AUTHORS Warzocha, K., Ribeiro, P., Renard, N., Charlot, C., Collier, B. and Sales, G.
TITLE Direct Submission
JOURNAL Submitted (19-SEP-1997) Hematology, Centre Hospitalier Lyon-Sud, Chemin du Grand Revoyet, Pierre Benite 69495, France
FEATURES
source location/Qualifiers
1. 1669
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Mieliki"
/note="Identified in human pre-B cell line Mieliki and in patients with non-Hodgkin's lymphoma"
1. 1669
/gene="DR3"
/note="Apo-3; TRAMP; LARD"
69. 1349
/gene="DR3"
/note="DR3"
/note="DR3 beta; TNF receptor family member; alternatively spliced product; contains 28 amino-acid extension to the extracellular domain of the ordinary DR3 molecule"
/codon_start=1
/product="death receptor 3 beta"
/protein_id="AAC39556.1"
/db_xref="GI:2570831"
/translation="MEORPRGCAVAALLLVLLGARAOGGTRSPDCAGDEHKKIG LFCRCGPAGHYLKAPCTEPCGNSTCLVCPDITFLAMENHNSECARQACDEQASQV ALENCASAVADTRCGCKPGWFEVCQVSSPFYQCPCLDGCALHRTLLCSRDY DCGTCLPGFYEHGDGCVSCPTPPSLAGAPVQSAVPLSVAGRGVFWOVLLAG LVVPLLGATLTYTRHGMWPKPLVADGMEALTPPATHTLSPLDSHTLLAPDS SEKICTVOLVGNWTPGYPEQALCPQYTWSDQLPSRALGPAPAPLSPESPAGSP AMMLQPGPOLYDMADAVPARMKFEVRLGLREAEIIEAVEVEIGLFRDQYEMLKHMV QQQPAGLGAVYALALERMGLDGCVEDLRSRLQRGP"
BASE COUNT 329 a 532 c 513 g 295 t
ORIGIN
Alignment Scores:
Pred. No.: 2.29e-105 Length: 1669
Score: 2128.00 Matches: 388
Percent Similarity: 96.53% Conservative: 1
Best Local Similarity: 96.28% Mismatches: 4
Query Match: 96.33% Indels: 11
DB: 9 Gaps: 2
US-09-993-234-6_COPY_25_417 (1-393) x AF026070 (1-1669)
QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
Db 141 CAGGGCGGCACCTCGTAGCCCAAGGTGACTGTGCCGGTGACTTCCACAAAGAGATTGGT 200
QY 21 LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
Db 201 CTGTTTGTGTGCAGAGGCTGCCAGCGGGGCACTACTGTAAGGCCCTTGACAGGAGCCC 260
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db 261 TGGGGCAACTCCACCTGCTGTGTGTCCCAAGACACCTTCTTGCCCTGGGAGAACAC 320
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db 321 CATTAATCTGATGTGCCCTGCGCAGGCTGTGATGAGCAGGCTCCCAAGGTGGCGCTG 380
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
Db 381 GAGAACTGTTACAGAGTGGCCGACACCGCTGTGCTGTAAAGCCAGGCTGTTGTGAG 440
QY 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120

Db 441 TGGCAGGTACGCCAATGTGTACAGAGTTCACCCTTCTACTGCCCAACCATGCTAGACTGC 500
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 501 GGGGCCCTGCACCCGCCACACAGCGCTACTGTTCGCCGACAGATACTGACTGTGGAGCC 560
QY 141 CysLeuProGlyPheTyrGlnHisGlyAspGlyCysValSerCysProThrSer----- 158
Db 561 TGCCTGCCTGGCTTCTATGAACATGCGATGGCTGCGTGCCTGCCCCACGCC -ACCCCC 619
QY 159 -----ThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTyr 173
Db 620 GTCCCTGCAGAGCACCCTGGGGAGCTGTCCAGAGCGCTGTGCCCTGTGTGGCTGG 679
QY 174 ArgGln-----MetPheTyrValGlnValLeuLeuAlaGlyLeuValAlaProLeuLe 191
Db 680 AGGCAGAGTAGGTGTGTCTGGGTCCAGGTGCTCTGGCGTGGCTGTGTCCTCCCTCT 739
QY 191 uLeuGlyAlaThrLeuThrTyrThrTyrArgHisCysTrpProHisLysProLeuValTh 211
Db 740 GCTTGGGGCCACCCCTGACCTACACATACCCGCACTGCTGGCTTCACAAGCCCTGTTAC 799
QY 211 rAlaAspGluAlaGlyMetGluAlaLeuThrProProProAlaThrHisLeuSerProle 231
Db 800 TGCAATGAAGCTGGATGAGGCTTGTACCCACCCACACCGGCAATCTGTACACCTT 859
QY 231 uAspSerAlaHisThrLeuLeuAlaProAspSerSerGluLysIleCysThrValG1 251
Db 860 GGACAGCGCCACACCCCTTCTAGACCTCTGACAGACAGTGAAGAATCTGCACCGTCA 919
QY 251 nLeuValGlyAsnSerTrpThrProGlyTyrProGluThrGlnGluAlaLeuCysProG1 271
Db 920 GTTGGTGGGTAAACAGCTGACCCCTGGCTAACCCGAGACCCAGAGGCGCTCTGCCCGCA 979
QY 271 nValThrTrpSerTrpAspGlnLeuProSerArgAlaLeuGlyProAlaAlaAlaProTh 291
Db 980 GGTGACATGGTCTCTGGGACCAAGTTCGCCAGAGAGCTCTTGCGCCGCTCGTGCGCCAC 1039
QY 291 rLeuSerProGluSerProAlaGlySerProAlaMetMetLeuGlnProGlyProGlnLe 311
Db 1040 ACTCTGCCACAGATCCCGACCGGCTGCCACCATGATGCTGCAGCGCGGCCGACGCT 1099
QY 311 uTyrAspValMetAspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuG1 331
Db 1100 CTACGAGTGAATGAGCGGCTGCCAGCGCGGCTGGAAGAGATTCTGCCGACGCTGG 1159
QY 331 yLeuArgGluAlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnG1 351
Db 1160 GCTCGCGGAGGACAGAGATCGAAGCGGTGGAGGTGGAGATCGGTCTTCCGAGACCA 1219
QY 351 nTyrGluMetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAl 371
Db 1220 GTACGAGATGCTCAAGCACTGGCGGCGCAGACAGCCCGGCGCTCGGAGCCGTTTAC 1279
QY 371 aAlaLeuGluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnAr 391
Db 1280 GGCCCTGGAGCGCATGGGGCTGGAGCGCTGCGAAGACTTGGCGCAGCGCTGCAGCG 1339
QY 391 gGlyPro 393
Db 1340 TGGCCCG 1346

Search completed: April 6, 2003, 21:07:51
Job time : 4591.25 secs

THIS PAGE BLANK (USPTO)

FT mat_peptide 73..1251
FT /*tag= b
XX
PN W09733904-A1.
XX 18-SEP-1997.
XX
PF 17-OCT-1996; 96WO-US16849.
XX
PR 12-MAR-1996; 96US-0013285.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (UNMI) UNIV MICHIGAN.
PI Dillon PJ, Dixit VM, Gentz RL, Ni J, Yu G;
XX
DR WPI; 1997-470812/43.
DR P-PSDB; AAW31517.
XX

PT Death domain containing receptor polypeptide(s) DR3 and DR3-V1
PT for activation of apoptosis and NF-kappaB, antagonists can be used
PT to treat inflammatory diseases
XX

PS Claim 6; Page 75-77; 108pp; English.
XX

CC This cDNA clone codes for human death domain containing receptor
CC DR3 (see AAW31517), a novel member of the tumour necrosis factor
CC receptor family. It was isolated from a HVEC cDNA library.
CC Related death domain containing receptor DR3-V1 cDNA (see AAT89426)
CC was isolated from a human testis tumour cDNA library. The genes
CC have also been identified in cDNA libraries of foetal liver,
CC foetal brain, tonsil and leukocyte. Nucleic acids encoding full-
CC length or mature DR3, or the extracellular, transmembrane,
CC intracellular or especially the death domain of DR3, can be used to
CC produce recombinant polypeptides in transformed host cells. These
CC polypeptides can be used to treat diseases and disorders associated
CC with the inhibition of apoptosis. Antagonists can be used to treat
CC diseases and disorders associated with increased apoptosis and for
CC treating inflammatory diseases and disorders.
XX

SQ Sequence 1254 BP; 201 A; 420 C; 407 G; 226 T; 0 other;
XX

Alignment Scores:

Pred. No.: 2,19e-117 Length: 1254
Score: 2209.00 Matches: 393
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-09-993-234-6_COPY_25_417 (1-393) x AAT89427 (1-1254)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGly 20
Db 73 CAGGGCGGCACTCGTAGCCCCAGGTGTGACTGTGCCGTGACTTCCACAGAAGATTGGT 132
QY 21 LeuPheCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
Db 133 CTGTTTGTGGCAGAGGCTGCCAGCGGGGCACTACCTGAAGGCCCTTGCCACGAGCC 192
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db 193 TCGGGCAACTCCACTGCTGTGTGTCCCAAGACACCTTCTTGCCCTGGGAGAACAC 252
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGlnAlaSerGlnValAlaLeu 80
Db 253 CATAAATCTGAATGTGCCGCTGCCAGGCTGTGATGAGCAGAGCCCTCCAGGTGGCGCTG 312
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTyrPheValGlu 100
Db 313 GAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGCTGTAAAGCCAGGCTGTGTGAG 372
QY 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120

Db 373 TGCCAGGTCAGCCAAATGTGTACAGAGTTCACCCCTTCTACTGCCAACCATGCTAGACTGC 432
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 433 GGGGCCCTGCACCCGCCACACAGGCTACTCTGTTCGCCAGAGATAGTACTGTGGACC 492
QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db 493 TGCCTGCTGCTGCTTCTATGAACATGGCGATGGCTGCGTGTCTGCCACAGACACCTG 552
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTyrPargGlnMetPheTyrValGln 180
Db 553 GGGAGCTGTCCAGAGCGGTGTGCCCTGTGTGTGGCTGGAGCAGATGTCTGGGTCCAG 612
QY 181 ValLeuLeuAlaGlyLeuValValProLeuLeuGlyAlaThrLeuThrTyrThrTyr 200
Db 613 GTGCTCTGGCTGGCTGTGTGTCCCTCCCTGCTGTGGGCCACCCCTGACCTACACATAC 672
QY 201 ArgHisCysTrpProHisLysProLeuValThrAlaAspGluAlaGlyMetGluAlaLeu 220
Db 673 CGCCACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 732
QY 221 ThrProProProAlaThrHisLeuSerProLeuAspSerAlaHisThrLeuLeuAlaPro 240
Db 733 ACCCCACACACCGGCCACCATCTGTACACCTTGACAGCGCCACACCTTCTAGCACCT 792
QY 241 ProAspSerSerGluLysIleCysThrValGlnLeuValGlyAsnSerTrpThrProGly 260
Db 793 CTTGACAGCAGTGAAGATCTGCACCGTCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 852
QY 261 TyrProGluThrGlnGluAlaLeuCysProGlnValThrTrpSerTrpAspGlnLeuPro 280
Db 853 TACCCGAGACCCAGAGGCGCTGTGCCCGCAGGTGACATGTCTGTGGACAGTTGCC 912
QY 281 SerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSerProAlaGlySer 300
Db 913 AGCAGAGCTCTGGCCCCGCTGTGCGCCACACTCTGCCACAGATGCCCGCCGCTCG 972
QY 301 ProAlaMetLeuGlnProGlyProGlnLeuTyrAspValMetAspAlaValProAla 320
Db 973 CCAGCATGATGCTGCAGCCGGGCCGAGCTTACGACGTGATGAGCGGCTCCACAGCG 1032
QY 321 ArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGluAlaGluIleGluAlaVal 340
Db 1033 CGGCGCTGGAAGAGTTCGTGCGCACCGCTGGCGCTGCCGAGGACAGATCGAAGCCGTG 1092
QY 341 GluValGluIleGlyArgPheArgAspGlnIleTyrGluMetLeuLysArgTrpArgGln 360
Db 1093 GAGGTGAGATCGCGCGCTTCCGAGACCCAGCAGATGATGCTCAAGCGCTGGCGCCAG 1152
QY 361 GlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMetCysLysAspGly 380
Db 1153 CAGCAGCCCGCGGCGCTCGAGCCGTTTACGCGGCGCTGGAGCGCATGGGCTGGAGCGC 1212
QY 381 CysValGluAspLeuArgSerArgLeuGlnArgGlyPro 393
Db 1213 TCGCTGGAAGACTTGGCAGCGCGCTGCAGCGCGCGCG 1251
RESULT 2
AAK00925
ID AAK00925 standard; cDNA; 1254 BP.
XX
AC AAK00925;
XX
DT 25-MAR-1999 (first entry)
XX
DE Death domain containing receptor polypeptide (DR3) encoding cDNA.
XX
KW Death domain; receptor; DR3-V1; DR3; recombinant; ds.
XX
OS Homo sapiens.
XX

```

FH Key      Location/Qualifiers
FT CDS      1..1254
FT          /*tag= a
FT          /product= "Death domain containing receptor DR3"
FT          1..72
FT          /*tag= b
FT          73..1251
FT          /*tag= c
FT          mat_peptide
FT          JP11000170-A.
XX PD       06-JAN-1999.
XX PF       12-MAR-1997; 97JP-0057503.
XX PR       06-FEB-1997; 97US-0037341.
XX PR       12-MAR-1996; 96US-0013285.
XX PR       17-OCT-1996; 96US-0028711.
XX PA       (HUMA-) HUMAN GENOME SCI INC.
XX PA       (UNMI ) UNIV MICHIGAN.
XX DR       WPI: 1999-124390/11.
XX DR       P-PSDB; AAW95538.
XX PT       New death domain containing receptor and recombinant vector -
XX PT       optionally comprising leader sequence
XX PS       Claim 6; Fig 3; 50pp; Japanese.
XX CC       The invention provides nucleotide sequences encoding death domain
XX CC       containing receptor polypeptides DR3-V1 and DR3. The DR3-V1 cDNA clone
XX CC       is contained in ATCC deposition No. 97456 and the DR3 cDNA clone is
XX CC       contained in ATCC deposition No. 97757. Recombinant vectors comprising
XX CC       the nucleic acid sequences and optionally the leader sequences are
XX CC       used for the recombinant production of the proteins. The present
XX CC       sequence represents a cDNA encoding the death domain containing
XX CC       receptor polypeptide (DR3).
XX SQ       Sequence 1254 BP; 201 A; 420 C; 407 G; 226 T; 0 other;

Alignment Scores:
Pred. No.:      2.19e-117      Length:      1254
Score:          2209.00        Matches:      393
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      100.00%      Indels:      0
DB:               20          Gaps:         0

US-09-993-234-6_COPY_25_417 (1-393) x AAX00925 (1-1254)
OY 1 GlnGlyGlyThrArgSerProAlaGlyAspCysAlaGlyAspPheHisLysLysIleGly 20
Db 73 CAGGGCGGCACTCGTAGCCCAAGGTGTGACTGTGCCGGTGAATTCCACAGAAGATTGGT 132
OY 21 LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
Db 133 CTGTTTGTGTGAGAGGCTGCCAGCGGGGCACTACTGTAAGCCCTTGACACGAGCC 192
OY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db 193 TGGGGCAACTCCACCTGCTGTGTGTCCCAAGACACCTTCTTGCCCTGGGAGAACAC 252
OY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db 253 CATTAATCTGAATGTCCCGCTGCCAGGCTGTGATGAGCAGGCCCTCCAGGTGGCGCTG 312
OY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
Db 313 GAGAACTGTTCAAGCAGTGCGCCACACCCGCTGTGGCTGTAAAGCCAGGCTGTTGTGAG 372
OY 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120

```

```

Db 373 TGGCAGGTACAGCCATGTGTACAGCAGTTCAACCCTTCTACTGCCCAACCATG CCTAGACTGC 432
OY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 433 GGGGCCCTGCACCGCCACACACAGGCTACTGTGTCCCGCAGAGATGACTGTGGACC 492
OY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db 493 TGCCTGCTGGCTTCTATGAACATGCGATGGCTGCGTGTCTGCCCCACGACACCCCTG 552
OY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArgGlnMetPheTrpValGln 180
Db 553 GGGAGCTGTCCAGAGCGCTGTGCCGCTGTGTGGCTGAGGCGAGATGTCTGGGTCCAG 612
OY 181 ValLeuLeuAlaGlyLeuValAlaProLeuLeuLeuGlyAlaThrLeuThrTyrThrTyr 200
Db 613 GTGCTCTGGCTGGCTGTGTGGTCCCTCTGCTTGGGGCCACCTGACCTACACATAC 672
OY 201 ArgHisCysTrpProHisLysProLeuValThrAlaAspGluAlaGlyMetGluAlaLeu 220
Db 673 CGCCACTGCTGGCTCACAAGCCCTGGTTACTGCAGATGAAGCTGGGATGGAGGCTCTG 732
OY 221 ThrProProProAlaThrHisLeuSerProLeuAspSerAlaHisThrLeuAlaPro 240
Db 733 ACCCCACACCGGCCACCCATCTGTACCCCTTGACAGCGCCCAACCCCTTCTAGACACT 792
OY 241 ProAspSerSerGluLysIleCysThrValGlnLeuValGlyAsnSerTrpThrProGly 260
Db 793 CCTGACAGCAGTGAGAAGATCTGCACCGCTCCAGTGTGGTGGTAAACAGCTGGACCCCTGGC 852
OY 261 TyrProGluThrGlnGluAlaLeuCysProGlnValThrTrpSerTrpAspGlnLeuPro 280
Db 853 TACCCCGAGACCCAGAGAGCGCTGTGCCCGCAGAGTGACATGGTCTGGACCAAGTTGCC 912
OY 281 SerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSerProAlaGlySer 300
Db 913 AGCAGACTCTTGGCCCCGCTGTGGCCCCACACTCTCGCCAGACTCCCAAGCCGGCTCG 972
OY 301 ProAlaMetMetLeuGlnProGlyProGlnLeuTyrAspValMetAspAlaValProAla 320
Db 973 CCAGCATGATGTGTGACAGCGGGGCCAGCTCTACGACGTGATGAGACGGGTCCAGCG 1032
OY 321 ArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGluAlaGluIleGluAlaVal 340
Db 1033 CGGCGCTGGAAGAGTTCGTGCGGACGCTGGGGCTGCGCGAGCGAGAGATCGAAGCCGTG 1092
OY 341 GluValGluIleGlyArgPheArgAspGlnGlnTyrGluMetLeuLysArgTrpArgGln 360
Db 1093 GAGGTGAGATCGGCCGCTTCCGAGACACAGACAGATGCTCAAGCGCTGGCCGACG 1152
OY 361 GlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMetGlyLeuAspGly 380
Db 1153 CAGCAGCCCGCGGGCTCGGAGCCGTTTACCGCGCCCTGGAGCGCATGGGGCTGAGCGGC 1212
OY 381 CysValGluAspLeuArgSerArgLeuGlnArgGlyPro 393
Db 1213 TGCGTGAAGACTTGCAGACCGCGCTGCAGCGGGCCG 1251

RESULT 3
AAC68777
ID AAC68777 standard; cDNA; 1254 BP.
XX AAC68777;
AC
XX 20-FEB-2001 (first entry)
DT
XX Human death domain containing receptor DR3 coding sequence.
DE
XX Human; death domain containing receptor; DR3; cancer;
KW autoimmune disorder; inflammation; cardiovascular disorder; infection;
KW neurodegenerative disease; angiogenesis; ss.
XX Homo sapiens.
OS

```


XX PN WO200064465-A1.
XX PD 02-NOV-2000.
XX PF 21-APR-2000; 2000WO-US10741.
XX PR 22-APR-1999; 99US-0130488.
XX PR 28-MAY-1999; 99US-0136741.
XX PA (HUMA-) HUMAN GENOME SCI INC.
PA (UNMI) UNIV MICHIGAN.
PA (YUGG/) YU G.
PA (NIJ/) NI J.
PA (GENT/) GENTZ R L.
PA (DILL/) DILLON P J.
PA (DIXI/) DIXIT V M.
XX PI YU G, NI J, Gentz RL, Dillon PJ, Dixit VM;
XX DR WPI: 2000-687263/67.
DR P-PSDB; AAB36265.
XX PT Treating graft-versus-host disease, cancer, immunodeficiency or an
PT autoimmune disease comprising administering an antibody to Death Domain
PT Containing Receptor proteins and a second therapeutic agent -
XX PS Example 2B; Fig 2; 273pp; English.
XX CC The present invention provides the protein and coding sequences for two
CC death domain containing receptors, designated DR3 and DR3-VI. These
CC receptors are involved in apoptosis, and the sequences given can be used
CC in the treatment of cancers, infections, cardiovascular disorders such as
CC arrhythmias, ischaemia, aneurysms, arterial occlusive diseases, embolisms
CC and congenital heart defects, neurodegenerative diseases including
CC Alzheimer's and Parkinson's diseases, autoimmune disease such as multiple
CC sclerosis, arthritis, diabetes, Graves' disease, asthma and psoriasis,
XX CC and to promote angiogenesis and wound healing.
SQ Sequence 1254 BP; 201 A; 420 C; 407 G; 226 T; 0 other;
Alignment Scores:
Pred. No.: 2,19e-117 Length: 1254
Score: 2209.00 Matches: 393
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0
US-09-993-234-6_COPY_25_417 (1-393) x AAC68777 (1-1254)
QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisIleGly 20
Db 73 CAGGGCGGCACTCGTAGCCGCCAGGTGTGACTGTGCCGGTGACTTCCACAGAAGATTGGT 132
QY 21 LeupheCysCysArgGlyCysProAlaGlyHisTyrLeuIleAlaProCysThrGluPro 40
Db 133 CTGTTTGTGTGAGAGGCTGCCAGCGGGGCACTACCTGAAGGCCCTTGACGAGGCC 192
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db 193 TGGGGCAATCCACCTGCTGTGTGTCTCCCAAGACACCTTCTTGCGCTGGGAGAACCAC 252
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db 253 CATAAATCTGAATGTGCCCGCTGCTGATGAGCAGGCGCTCCAGGTGGCGCTG 312
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
Db 313 GAGAACTGTTCAGCAGTGGCGGACACCGCTGTGCTGTAAAGCCAGGCTGTTGTGAG 372
QY 101 CysGlnValSerGlnCysValSerSerSerProPheTyrCysGlnProCysLeuAspCys 120
|||||

Db 373 TGCCAGGTCAGCCAAATGTGTGACGAGTTCACCCCTTCTACTGCCAACCATGCTAGACTGC 432
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 433 GGGGCCCTGCACCGCCACACAGGGCTACTCTGTTCGCCGAGAGATACTGACTGTGGAGCC 492
QY 141 CysLeuProGlyPheTyrGlnHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db 493 TGCCTGCTGGCTTCTATGACATGGCGATGGCTGCTGCTGCTGCCCCACGAGACCCCTG 552
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArgGlnMetPheTrpValGln 180
Db 553 GGGAGCTGTCCAGAGCGCTGTGCCGCTGTGTGGCTGAGGCGAGATGTCTGGGTCCAG 612
QY 181 ValLeuLeuAlaGlyLeuValValProLeuLeuLeuGlyAlaThrLeuThrTyrThrTyr 200
Db 613 GTGCTCTGGCTGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 672
QY 201 ArgHisCysTrpProHisLysProLeuValThrAlaAspGluAlaGlyMetGluAlaLeu 220
Db 673 CGCCACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 732
QY 221 ThrProProAlaThrHisLeuSerProLeuAspSerAlaHisThrLeuLeuAlaPro 240
Db 733 ACCCCACACCGCGCCACCACTGTGACCCCTTGATGAGATGAAGCTGGGATGAGGCTCTG 792
QY 241 ProAspSerSerGluLysIleCysThrValGlnLeuValGlyAsnSerTrpThrProGly 260
Db 793 CCTGACAGCAGTAGAGATCTGCACCGCTCCAGTTGGTGGTAAACAGCTGAGCCCTGGC 852
QY 261 TyrProGluThrGlnGluAlaLeuCysProGlnValThrTrpSerTrpAspGlnLeuPro 280
Db 853 TACCCGAGACCCAGAGCGGCTCTGCCCGGAGGTGACATGTCTCTGGGACCAAGTTGCC 912
QY 281 SerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSerProAlaGlySer 300
Db 913 AGCAGAGCTTGTGGCCCGCTGCTGCGCCACACTCTCGCCAGAGTCCCAAGCCGCTCG 972
QY 301 ProAlaMetLeuGlnProGlyProGlnLeuTyrAspValMetAspAlaValProAla 320
Db 973 CCAGCATGATGTGACAGCGGGCGCCGAGCTGTACGAGTGTGAGCGGGTCCACGCG 1032
QY 321 ArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGluAlaGluIleGluAlaVal 340
Db 1033 CGGCGCTGGAAGAGTTCGTGCGCACGCTGGCGCTGCGGAGGACAGATCGAAGCCGTG 1092
QY 341 GluValGluIleGlyArgPheArgAspGlnGlnTyrGluMetLeuLysArgTrpArgGln 360
Db 1093 GAGGTGAGATCGCGCTTCCGAGACACAGCAGTACGAGATGCTCAAGCGCTGGCGCCAG 1152
QY 361 GlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMetGlyLeuAspGly 380
Db 1153 CAGCAGCCCGGGGCTCGGAGCGCTTACGGCGCCCTGGAGCGCATGGGGCTGGACGGC 1212
QY 381 CysValGluAspLeuArgSerArgLeuGlnArgGlyPro 393
Db 1213 TGGGTGAAGACTTGGCGACGCCGCTGCAGCGCGGCCG 1251
RESULT 4
ID AAT91180 standard; cDNA; 1634 BP.
AC AAT91180;
XX 14-APR-1998 (first entry)
DE Human apoptosis protein Apo-3 cDNA clone FH20.57.
XX Apo-3; apoptosis; human; therapy; drug screening; ss.
KW Homo sapiens.
OS
XX
FH key location/Qualifiers

FT CDS 89..1342
FT /*tag= a
FT sig_peptide 89..160
FT /*tag= b
FT /note= "determined by hydropathy analysis"
FT mat_peptide 161..1339
FT /*tag= c
XX PN W09737020-A1.
XX PD 09-OCT-1997.
XX PF 31-MAR-1997; 97WO-US05230.
XX PR 23-SEP-1996; 96US-0710802.
XX PR 01-APR-1996; 96US-0625328.
XX PA (GETH) GENENTECH INC.
XX PI Ashkenazi AJ;
XX DR WPI; 1997-503105/46.
XX PT Polypeptide(s) Apo-3 and Apo-2LI - useful for regulating apoptosis
XX PT in mammalian cells
XX PS Example 1; Page 45-46; 70pp; English.
XX CC cDNA clone FH20.57 (ATCC 55820) codes for a novel polypeptide (see
XX CC W26709), designated Apo-3, that stimulates or induces apoptotic
XX CC activity in mammalian cells. It was isolated from a human foetal
XX CC heart cDNA library by screening with probes (see T91183-84) based
XX CC on an EST sequence (GenBank locus W71984) that showed homology to
XX CC the intracellular domain of human TNFR1 and CD95. Amino acid
XX CC residues 1-181 of Apo-3 are identical to another novel apoptosis
XX CC polypeptide, Apo-2LI (see W26708). Nucleic acids encoding Apo-3
XX CC can be used diagnostically for tissue-specific typing and to
XX CC produce recombinant Apo-3 polypeptides, especially the
XX CC extracellular domain (amino acids 1-198) or death domain (amino
XX CC acids 338-417). Apo-3 can be used to induce apoptosis or
XX CC NF-kappa-N- or JNK-mediated gene expression for therapeutic
XX CC purposes. Non-human transgenic animals containing cells that
XX CC express Apo-3 nucleic acid, and knockout animals containing
XX CC cells that have an altered Apo-3 gene, can be used in drug
XX CC screening and development.
XX SQ Sequence 1634 BP; 300 A; 528 C; 519 G; 287 T; 0 other;

Alignment Scores:
Pred. No.: 2.92e-117 Length: 1634
Score: 2209.00 Matches: 393
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-09-993-234-6_COPY_25_417 (1-393) x AAT91180 (1-1634)
QY 1 GlnGlyGlyThrArgSerProAlaGlyAspCysAlaGlyAspRheHisLysLysIleGly 20
Db |||||||
Db 161 CAGGGCGCACTCGTAGCCCCCAGGTGTGACTGTGCCGGTGACTTCCACAAGAAATTGGT 220
QY 21 LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
Db |||||||
Db 221 CTGTTTGTGTCAGAGGCTGCCAGGGGGGCACTACCTGAAGCCCCCTTGACGAGGCC 280
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db |||||||
Db 281 TGGCGCACTCCACCTGCTGTGTGTCCCAAGACACCTCTTGGCCTGGGAGAACAC 340
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db |||||||
Db 341 CATTAATCTGAATGTGCCCGCTGCCAGGCCCTGTGATGAGCAGAGCCCTCCAGGTGGCGCTG 400

QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
Db |||||||
Db 401 GAGAACTGTTCAGACAGTGGCCGACACCCGCTGTGGCTGTAAGCCAGGCTGTGTGGAG 460
QY 101 CysGlnValSerGlnCysValSerSerSerProPheTyrCysGlnProCysLeuAspCys 120
Db |||||||
Db 461 TGGCAGGTCAAGCAATGTGTGACAGACTTCAACCTTCTACTGCAACCATGCTAGACTGC 520
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db |||||||
Db 521 GGGGCCCTGCACCGCCACACACCGGCTACTCTGTTCCCGCAGAGATGACTGTGGACCC 580
QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db |||||||
Db 581 TGCCTGCTGGCTTCTATGAACATGGCGATGGCTGCGTGTCTGCCCCACGAGACCCTG 640
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArgGlnMetPheTrpValGln 180
Db |||||||
Db 641 GGGAGCTGTCCAGACGCGCTGTGCCGCTGTGCTGAGGCGAGATGTTCTGGTCCAG 700
QY 181 ValLeuLeuAlaGlyLeuValValProLeuLeuLeuGlyAlaThrLeuThrTyrThrTyr 200
Db |||||||
Db 701 GTGCTCTGGCTGGCCCTGTGTGCTGCCCTCTGCTGTGGGGCCACCTGACCTACACATAC 760
QY 201 ArgHisCysTrpProHisLysProLeuValThrAlaAspGluAlaGlyMetGluAlaLeu 220
Db |||||||
Db 761 CGCCACTGTGGCTCTACAAAGCCCTGTGTTACTGACAGATGAAGCTGGAGTAGAGCTCTG 820
QY 221 ThrProProAlaThrHisLeuSerProLeuAspSerAlaHisThrLeuLeuAlaPro 240
Db |||||||
Db 821 ACCCCACACCGGCCACCATCTGTCAACCTTGGACAGCGCCACACCCCTTCTAGCACCCT 880
QY 241 ProAspSerSerGluLysIleCysThrValGlnLeuValGlyAsnSerTrpThrProGly 260
Db |||||||
Db 881 CCTGACAGAGTGAAGAATGTGCACCGCTCCAGTTGGTGGGTACAGCTGAGCCCTGGC 940
QY 261 TyrProGluThrGlnGluAlaLeuCysProGlnValThrTrpSerTrpAspGlnLeuPro 280
Db |||||||
Db 941 TACCCCGAGACCCAGAGGCGCTGTGCCCGCAGGTGACATGGTCTGGAGACCATGTTGCC 1000
QY 281 SerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSerProAlaGlySer 300
Db |||||||
Db 1001 AGCAGAGCTCTTGGCCCCGCTGTGCCGCCACACTCTCGCCAGAGTCCCAAGCCGGCTCG 1060
QY 301 ProAlaMetMetLeuGlnProGlyProGlnLeuTyrAspValMetAspAlaValProAla 320
Db |||||||
Db 1061 CCAGCCATGATGCTGCAGCCGGGGCCGACGCTCTACGACGTGATGGAGCGGGTCCACAGCG 1120
QY 321 ArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGluAlaGluIleGluAlaVal 340
Db |||||||
Db 1121 CGGCGCTGAAGAGATTGTCGTCGCCACGCTGGGGCTGCGCGAGGCAAGATCGAAGCCGTG 1180
QY 341 GluValGluIleGlyArgPheArgAspGlnGlnTyrGluMetLeuLysArgTrpArgGln 360
Db |||||||
Db 1181 GAGGTGAGATCGGCCGCTTCCGAGACGACAGTACGAGATGCTCAAGCGCTGGCGCAG 1240
QY 361 GlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMetGlyLeuAspGly 380
Db |||||||
Db 1241 CAGCAGCCCGGGGCTCGGAGCCGTTTACGGCGGCCCTGAGCGCATGGGGCTGGACGGC 1300
QY 381 CysValGluAspLeuArgSerArgLeuGlnArgGlyPro 393
Db |||||||
Db 1301 TGCCTGGAAGACTTGGCAGACCCGCTGCAAGCGGGCCG 1339

RESULT 5
AAH27782
ID AAH27782 standard; DNA; 1634 BP.
XX AAH27782;
AC AAH27782;
XX
DT 15-AUG-2001 (first entry)
XX

DE Human genomic DNA encoding a rheumatoid arthritis associated protein.
XX
KW Rheumatoid arthritis; transmembrane protein; human; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 89..1342
FT /*tag= a
FT /product= "Rheumatoid arthritis associated protein"
XX
PN WO200132921-A2.
XX
PD 10-MAY-2001.
XX
PF 01-NOV-2000; 2000WO-JP07690.
XX
PR 01-NOV-1999; 99JP-0310805.
XX
PA (SHIO/) SHIOZAWA S.
XX
PI Shiozawa S, Konishi Y;
XX
DR WPI; 2001-308750/32.
DR P-PSDB; AAB97370.
XX
PT Diagnosing rheumatoid arthritis by probing digested human genomic DNA
PT or comparing expression of mRNA or polypeptide of a region of
PT transmembrane protein
XX
PS Claim 1; Page 14-18; 21pp; Japanese.
XX
CC This invention relates to a method of diagnosing chronic rheumatoid
CC arthritis by digesting human genomic DNA with EcoRI and hybridizing it
CC with a probe containing a fragment of the present sequence which
CC represents DNA encoding a transmembrane protein. The method is used for
CC the diagnosis of chronic rheumatoid arthritis, and for developing new
CC treatments.
XX
SQ Sequence 1634 BP; 300 A; 528 C; 519 G; 287 T; 0 other;
XX
Alignment Scores:
Pred. No.: 2,92e-117 Length: 1634
Score: 2209.00 Matches: 393
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0
US-09-993-234-6_COPY_25_417 (1-393) x AAH27782 (1-1634)
QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGly 20
DB 161 CAGGGCGGCACTCGTAGCCGCCAGGTGTGACTGTGCCGGTGACTTCCACAAGAATGGT 220
QY 21 LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
DB 221 CTGTTTGTGACAGAGGCTGCCACGGGGGCACTAAGGCCCCCTTGCACGGAGCCC 280
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTyrPgluAsnHis 60
DB 281 TGGGGCACTCCACTGCCTGTGTGTGTCTCCCAAGACACCTTCTTGGCCCTGGGAGAACAC 340
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
DB 341 CATAATCTGAAATGTGCCCGCTGCCAGGCTGTGATGAGCAGAGGCTCCAGGTGGCGCTG 400
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTyrPheValGlu 100
DB 401 GAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGTGCTGTAAAGCCAGGCTGTGTGAG 460
QY 101 CysGlnValSerGlnCysValSerSerSerProPheTyrCysGlnProCysLeuAspCys 120
|||||

DB 461 TGGCAGGTCAGCCAAATGTGTACAGCAGTTACCCCTTCTACTGCCAACCATGCTAGACTGC 520
QY 121 GAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
DB 521 GGGGCCCTGCACCGCCACACAGGCTACTCTGTTCGCCAGAGATACTGACTGTGGACC 580
QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
DB 581 TGCCTGCCTGGCTTCTATGACATGGCGATGGCTGCTGCTCTGCCCCACGAGACCCCTG 640
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTyrParGlnMetPheTyrValGln 180
DB 641 GGGAGCTGTCCAGAGCGCTGTGCCGCTGTCTGTGGCTGGAGGCAAGATGTTCTGGCTCCAG 700
QY 181 ValLeuLeuAlaGlyLeuValValProLeuLeuGlyAlaThrLeuThrTyrThrTyr 200
DB 701 GTGCTCTGGCTGGCTGTGTGTGTGTCCTGCTGTGGGGCCACCCCTGACCTACACATAC 760
QY 201 ArgHisCysTrpProHisLysProLeuValThrAlaAspGluAlaGlyMetGluAlaLeu 220
DB 761 CGCCACTGTGGCTGCACAGCCCTGTGTACTGCAATGAAGCTGGAGTGGAGGCTCTG 820
QY 221 ThrProProAlaThrHisLeuSerProLeuAspSerAlaHisThrLeuLeuAlaPro 240
DB 821 ACCCCACACCGCGCCACCATCTGTACCCCTGGACAGCGCCACACCCCTTACGACACT 880
QY 241 ProAspSerSerGluLysIleCysThrValGlnLeuValGlyAsnSerTyrThrProGly 260
DB 881 CTGACACAGCAGTAGAGATCTGCACCCCTGCACCTCCAGTTGGTGGTAACAGCTGGACCCCTGGC 940
QY 261 TyrProGluThrGlnGluAlaLeuCysProGlnValThrTrpSerTrpAspGlnLeuPro 280
DB 941 TACCCCGAGACCCAGAGGCGCTCTGCCCGCAGGTGACATGTCTCTGGACCAAGTTGCC 1000
QY 281 SerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSerProAlaGlySer 300
DB 1001 AGCAGAGCTTGTGGCCCGCTGCTGCGCCACACTCTGCCACAGATGCCACGCGGCTCG 1060
QY 301 ProAlaMetLeuGlnProGlyProGlnLeuTyrAspValMetAspAlaValProAla 320
DB 1061 CCAAGCATGATGCTGCAGCGCGGCGCCAGCTTACGACGTGATGAGCGGGTCCAGCG 1120
QY 321 ArgArgTyrLysGluPheValArgThrLeuGlyLeuArgGluAlaGluIleGluAlaVal 340
DB 1121 CGGCGCTGGAAGAGTTCGTGCGCACGCTGGGCTGCGCAGAGCAGATCGAAGCCGTG 1180
QY 341 GluValGluIleGlyArgPheArgAspGlnGlnTyrGluMetLeuLysArgTyrArgGln 360
DB 1181 GAGGTGAGATCGCGCTTCCGAGACACAGCAGATGATGCTCAAGCGCTGGCGCCAG 1240
QY 361 GlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMetGlyLeuAspGly 380
DB 1241 CAGCAGCCCGCGGGCTCGAGGCCGTTACGGCGCCCTGGAGCGCATGGGGCTGAGCGGC 1300
QY 381 CysValGluAspLeuArgSerArgLeuGlnArgGlyPro 393
DB 1301 TGGGTGAAGACTTGGCGACGCCCTGCAAGCGCGGCGCCG 1339
RESULT 6
AAL47186
ID AAL47186 standard; cDNA; 1634 BP.
XX
AC AAL47186;
XX
DT 22-AUG-2002 (first entry)
XX
DE Human rheumatoid arthritis associated DR3 gene related cDNA #1.
XX
KW Human; DR3; rheumatoid arthritis; antirheumatic; antiarthritic;
KW gene therapy; gene; ss.
XX
OS Homo sapiens.
XX

```

FH Key Location/Qualifiers
FT CDS 89..1342
FT /*tag= a
FT /product= "AAOI7879"
XX PN WO200234912-A1.
XX PD 02-MAY-2002.
XX PF 24-OCT-2001; 2001WO-JP09313.
XX PR 24-OCT-2000; 2000JP-0324296.
XX PR 27-MAR-2001; 2001JP-0090546.
XX PR 30-MAR-2001; 2001JP-0099990.
XX PA (NEMI-) NEW IND RES ORG.
XX PA (SHIO/) SHIOZAWA S.
XX PI Shiozawa S, Konishi Y;
XX DR WPI; 2002-417132/44.
XX DR P-PSDB; AAOI7879.
XX PT Genomes, particularly DR3 genomic DNA, participating in rheumatoid
XX PT arthritis via mutation, useful in evaluating disease onset and its
XX PT possibility and providing therapy and remedies -
XX PS Example 1; Page 66-69; 84pp; Japanese.
XX CC The present invention relates to the human DR3 gene, which is associated
XX CC with rheumatoid arthritis. Certain mutations in the gene can be linked to
XX CC the disease. The sequences can be used to evaluate disease onset and its
XX CC possibility and to provide therapy and remedies. The present sequence is
XX CC a coding sequence described in the exemplification of the invention.
XX SQ Sequence 1634 BP; 300 A; 528 C; 519 G; 287 T; 0 other;

Alignment Scores:
Pred. No.: 2.92e-117 Length: 1634
Score: 2209.00 Matches: 393
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 24 Gaps: 0

US-09-993-234-6_COPY_25_417 (1-393) x AAL47186 (1-1634)
QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGly 20
Db 161 CAGGGCGGACATGTAAGCCCAAGGTGTACTGTGCGGTGACTTCCACAAGATTGGT 220
QY 21 LeupheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
Db 221 CTGTTTGTGTCAGAGGCTGCCAGCGGGGCACTGAAAGGCCCTTGCACGGAGCCC 280
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db 281 TCGGGCAACTCCACTGCTTGTGTGTCGCCAAGACACCTTCTTGCCCTGGGAGAACAC 340
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db 341 CATATATCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCTCCAGGTGGCGCTG 400
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
Db 401 GAGAACTGTTCAAGAGTGGCCGACACCCGCTGTGCTGTAAAGCCAGGCTGTTGTGGAG 460
QY 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120
Db 461 TGCACAGTCAAGCCATGTGTGTCAGCAGTTCACCTTCTTACTGCCAACCATGCTTAGACTGC 520
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
```

```

Db 521 GGGGCCCTGCACCGCCACACAGGCTACTCTGTTCGCCGACAGATACTGACTGTGGACC 580
QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db 581 TGCCTGCTGCTTCTTATGAACATGCGCATGGCTGCTGCTGCCCCACAGCACCCTG 640
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArgGlnMetPheTrpValGln 180
Db 641 GGGAGCTGTCCAGAGCGCTGTGCCGCTGTGTGTGGCTGGAGCAGATGTTCTGGTCCAG 700
QY 181 ValLeuLeuAlaGlyLeuValValProLeuLeuLeuGlyAlaThrLeuThrTyrThrTyr 200
Db 701 GTGCTCCTGGCTGGCTGTGTGGTCCCTCCTGCTGTGGGGCCACCTGACCTACACATAC 760
QY 201 ArgHisCysTrpProHisLysProLeuValThrAlaAspGluAlaGlyMetGluAlaLeu 220
Db 761 CGCCACTGCTGGCTCACAAGCCCCCTGTACTGTGACATGAAGCTGGGATGGAGGCTCTG 820
QY 221 ThrProProAlaThrHisLeuSerProLeuAspSerAlaHisThrLeuLeuAlaPro 240
Db 821 ACCCCACACACCGGCCACCATCTGTACACCTTGACAGCGCCACACACCTTCTTACACACT 880
QY 241 ProAspSerSerGluLysIleCysThrValGlnLeuValGlyAsnSerTrpThrProGly 260
Db 881 CCTGACAGCAGTGAAGATCTGCACCGCTCAGTGTGGTAAACAGCTGACCCCTGGC 940
QY 261 TyrProGluThrGlnGluAlaLeuCysProGlnValThrTrpSerTrpAspGlnLeuPro 280
Db 941 TACCCCGAGACCCAGAGCGCTCTGCCCGCAGGTGACATGTCTCGGACACAGTTGCC 1000
QY 281 SerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSerProAlaGlySer 300
Db 1001 AGCAGAGCTCTTGGCCCGCTGTGCCGCCACACATCTGCCACAGAGTCCCGCAGCGCTCG 1060
QY 301 ProAlaMetMetLeuGlnProGlyProGlnLeuTyrAspValMetAspAlaValProAla 320
Db 1061 CCAGCCATGATGCTGCACCGCGGCCGCCGACAGCTCTACGACGTGATGGACGGCTCCACGCG 1120
QY 321 ArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGluAlaGluIleGluAlaVal 340
Db 1121 CGGCGCTGGAAGAGTTCGTGCGCACGCTGGGGCTGCGGAGGACAGATCGAACCGCTG 1180
QY 341 GluValGluIleGlyArgPheArgAspGlnGlnTyrGluMetLeuLysArgTrpArgGln 360
Db 1181 GAGGTGAGATCGCGCTTCCGAGACACAGCAGTACGAGATGCTCAAGCGCTGGCGCCAG 1240
QY 361 GlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMetGlyLeuAspGly 380
Db 1241 CAGCAGCCCGCGGGCTGCGGAGCCGTTTACGGCGGCCCTGGAGCGCATGGGGCTGAGCGCC 1300
QY 381 CysValGluAspLeuArgSerArgLeuGlnArgGlyPro 393
Db 1301 TCGCTGGAAGACTTGCAGCGCCGCTGACAGCGCGGCCCG 1339

RESULT 7
AAC91477
ID AAC91477 standard; cdna; 1662 BP.
XX
AC AAC91477;
XX
DT 21-MAR-2001 (first entry)
XX
DE Human PRO779 cdna.
XX
KW Human; PRO; antiinflammatory; dermatological; antiarthritic;
KW antirheumatic; cardiant; antianaemic; immunosuppressive; antithyroid;
KW antidiabetic; nootropic; neuroprotective; hepatotropic; virucide;
KW antiallergic; antiasthmatic; immune related disorder;
KW hepatobiliary disease; autoimmune disease; allergy; ss.
XX
OS Homo sapiens.
XX
PN WO200073452-A2.
```


XX 07-DEC-2000.
PD
XX
PF 02-JUN-2000; 2000WO-US15264.
XX
PR 02-JUN-1999; 99WO-US12252.
PR 20-JUL-1999; 99US-0144732.
PR 20-JUL-1999; 99US-0144758.
PR 28-JUL-1999; 99US-0146222.
PR 01-SEP-1999; 99WO-US20111.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 29-OCT-1999; 99US-0162506.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28634.
PR 09-DEC-1999; 99US-0170262.
PR 20-DEC-1999; 99WO-US30911.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Chan B, Goddard A, Godowski PJ, Gurney AL;
PI Hebert C, Henzel W, Kabakoff RC, Shelton DL, Tumas D, Watanabe CK;
PI Wood WI;
XX
XX WPI; 2001-025253/03.
DR P-PSDB; AAB50918.
XX
PT Thirty three nucleic acids encoding PRO polypeptides which are useful
PT in the diagnosis and treatment of immune related disorders, e.g.
PT systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
PT thyroiditis and diabetes mellitus .
XX
XX Claim 48; Fig 33; 218pp; English.
PS
XX The present sequence is one of thirty three nucleic acids encoding PRO
CC polypeptides. The PRO polypeptides, anti-PRO antibodies, agonists and
CC antagonists are useful for treating and diagnosing immune related
CC disorders such as systemic lupus erythematosus, rheumatoid arthritis,
CC osteoarthritis, juvenile chronic arthritis, spondyloarthritis,
CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
CC anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,
CC immune-mediated renal disease, demyelinating diseases of the central
CC and peripheral nervous systems (such as multiple sclerosis, idiopathic
CC demyelinating polyneuropathy or Guillain-Barre syndrome, and chronic
CC inflammatory demyelinating polyneuropathy), hepatobiliary diseases
CC (such as infectious, autoimmune chronic active hepatitis, primary
CC biliary cirrhosis, granulomatous hepatitis and sclerosing cholangitis),
CC inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's
CC disease, autoimmune or immune-mediated skin diseases (such as bullous
CC skin diseases, erythema multiforme, contact dermatitis, psoriasis),
CC allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,
CC food hypersensitivity and urticaria), immunological diseases of the
CC lung (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis
CC and hypersensitivity pneumonitis), transplantation associated diseases
CC including graft rejection and graft-versus-host diseases.
XX
SQ Sequence 1662 BP; 302 A; 540 C; 531 G; 289 T; 0 other;

Pred. No.: 2,97e-117 Length: 1662
Score: 2209.00 Matches: 393
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0
US-09-993-234-6_COPY_25_417 (1-393) x AAC91477 (1-1662)
QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
Db 175 CAGGGCGCACTCCAGAGGCTGCCAGCGGGGCACTACCTGAGAGCCCTTGCACGGAGCCC 234
QY 21 LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
Db 235 CTGTTTGTGTGACAGAGGCTGCCAGCGGGGCACTACCTGAGAGCCCTTGCACGGAGCCC 294
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db 295 TGCGGCACTCCACCCTGCCCTGTGTCTCCCAAGACACACTTCTTGCCCTGGAGAACCCAC 354
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db 355 CATATTCTGAATGTGCCCGCTGCCAGGCTGTGATGACAGAGCCCTCCAGGTGGGCTG 414
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
Db 415 GAGAACTGTTCAGCAGTGGCGACACCCGCTGTGGCTGTAAAGCCAGGCTGTTGTGGAG 474
QY 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120
Db 475 TGCCAGGTCCAGCCAAATGTGTACAGCATGTCACCCCTTACTGCCAACCATGCCCTAGACTGC 534
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 535 GGGGCCCTGCACCGCCACACAGGCTACTCTGTTCGCCGACAGATACTGACTGTGGAGCC 594
QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db 595 TGCCCTGGCTGGCTTCTATGACATGGCGATGGCTGTCTGCCCCACGACGACCCCTG 654
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArgGlnMetPheTrpValGln 180
Db 655 GGGAGCTGTCCAGAGCGCTGTCCGCTGTCTGTGGCTGAGGACAGATGTTCTGGGTCAG 714
QY 181 ValLeuLeuAlaGlyLeuValValProLeuLeuGlyAlaThrLeuThrTyrThrTyr 200
Db 715 GTGCTCTGGCTGGCTTGTGTGTCGCCCTCTGCTTGGGGCCACCCCTGACTTACACATAC 774
QY 201 ArgHisCysTrpProHisLysProLeuValThrAlaAspGluAlaGlyMetGluAlaLeu 220
Db 775 CGCCACTGCTGGCTTCACAAAGCCCTGTGTACTGACATGAAGCTGGAGTGGAGGCTCTG 834
QY 221 ThrProProProAlaThrHisLeuSerProLeuAspSerAlaHisThrLeuLeuAlaPro 240
Db 835 ACCCCACACCGCCGCCCATCTGTACACCCCTGGACAGCGCCACACACCCCTTACGACACT 894
QY 241 ProAspSerSerGluLysIleCysThrValGlnLeuValGlyAsnSerTrpThrProGly 260
Db 895 CCTGACAGCAGTGAAGAATCTGCACCGCTCCAGTTGGTGGTAACAGCTTGACACCCCTGGC 954
QY 261 TyrProGluThrGlnGluAlaLeuCysProGlnValThrTrpSerTrpAspGlnLeuPro 280
Db 955 TACCCGAGACCGAGAGGCGCTGTGCCGAGGTGACATGTCTCTGGAGACCAAGTTGCC 1014
QY 281 SerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSerProAlaGlySer 300
Db 1015 AGCAGAGCTTTGGCCCGCTGTGCGCCACACTCTGCGCAGAGTCCCAAGCCGCGCTCG 1074
QY 301 ProAlaMetLeuGlnProGlyProGlnLeuTyrAspValMetAspAlaValProAla 320
Db 1075 CCAGCCATGATGCTGCAGCGCGGCGCGAGCTTACGACGTGATGAGACGGGTCGCCAGCG 1134
Alignment Scores:

QY 321 ArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGluAlaGluIleGluAlaVal 340
Db 1135 CGCGCTGGAAGAGAGTTCGCGCACCGCTGGGGCTGCCGACGACAGATCGAAGCCGTG 1194
QY 341 GluValGluIleGlyArgPheArgAspGlnGlnTyrGluMetLeuLysArgTrpArgGln 360
Db 1195 GAGGTGAGATCGCGCTTCGAGACACAGCAGTACGATGCTCAAGCGCTGGCGCAG 1254
QY 361 GlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMetGlyLeuAspGly 380
Db 1255 CAGCAGCCCGCGGCTCGAGCGCTTACGCGGCGCTGAGCGCATGGGCTGACGCGC 1314
QY 381 CysValGluAspLeuArgSerArgLeuGlnArgGlyPro 393
Db 1315 TCGCTGGAAGACTTGCAGCGCGCTGACGCGCGCCG 1353
RESULT 8
ABK40265
ID ABK40265 standard; cDNA; 1662 BP.
XX
AC ABK40265;
XX
DT 15-JUL-2002 (first entry)
XX
DE cDNA encoding human PRO779 polypeptide.
XX
KW Human; PRO; benign tumour; malignant tumour; lymphoid malignancy;
KW leukaemia; neuronal disorder; stromal disorder; blastocoele disorder;
KW inflammatory disorder; immune disorder; angiogenic disorder;
KW gene therapy; cytostatic; neuroprotective; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200153486-A1.
XX
PD 26-JUL-2001.
XX
PF 11-FEB-2000; 2000WO-US03565.
XX
PR 08-MAR-1999; 99WO-US05028.
PR 11-MAR-1999; 99US-123972P.
PR 11-MAY-1999; 99US-133459P.
PR 02-JUN-1999; 99WO-US12252.
PR 22-JUN-1999; 99US-140650P.
PR 22-JUN-1999; 99US-140653P.
PR 20-JUL-1999; 99US-144758P.
PR 26-JUL-1999; 99US-145698P.
PR 28-JUL-1999; 99US-146222P.
PR 17-AUG-1999; 99US-149395P.
PR 31-AUG-1999; 99US-151689P.
PR 01-SEP-1999; 99WO-US20111.
PR 15-SEP-1999; 99WO-US21090.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.
PR 05-JAN-2000; 2000WO-US00219.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL, Hillan KJ;
PI Marsters SA, Pan J, Piltl RM, Roy MA, Smith V, Stone DM;
PI Watanabe CK, Wood WI;
XX
DR WPI; 2002-205567/26.
DR P-PSDB; AAU86139.
XX
PT Thirty five nucleic acids encoding PRO polypeptides, useful for
PT treating benign or malignant tumours, leukaemias and lymphoid
PT malignancies, inflammatory, angiogenic and immunologic disorders -
PS
XX Claim 50; Fig 23; 302pp; English.
XX
CC The present invention relates to the isolation of novel human PRO

CC polypeptides and the polynucleotide sequences encoding them. The
CC PRO polypeptides, agonists, antagonists or anti-PRO antibodies are
CC useful for treating benign or malignant tumours (e.g. renal, kidney,
CC bladder, breast, etc), leukaemias and lymphoid malignancies, other
CC disorders such as neuronal, glial, astrocytic, hypothalamic, glandular,
CC macrophagal, stromal and blastocoele disorders, inflammatory, immune
CC and angiogenic disorders. The polynucleotide sequences are also
CC useful in gene therapy. ABK40254-ABK40288 encode for the human PRO
CC polypeptides of the invention.
XX
SQ Sequence 1662 BP; 302 A; 540 C; 531 G; 289 T; 0 other;
SQ
Alignment Scores:
Pred. No.: 2.97e-117 Length: 1662
Score: 2209.00 Matches: 393
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 24 Gaps: 0
US-09-993-234-6_COPY_25_417 (1-393) x ABK40265 (1-1662)
QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
Db 175 CAGGCGGCACCTCGTAGCCCGCAGGTGTGACTGTGCCGGTGACTTCCACAAGAAGATTGGT 234
QY 21 LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
Db 235 CTGTTTGTGTGACAGAGGCTGCCAGCGGGGCACTACCTGAAGGCCCTTGACAGAGCCC 294
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db 295 TCGGCGCACTCCACCTGCTGTGTGTCCCAAGACACCTTCTTGCGCTGGAGAACCCAC 354
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db 355 CATTAATTCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCTCCAGGTGGCGCTG 414
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
Db 415 GAGAACTGTTCAGCAGTGGCCGACACCGCTGTGGCTGAAGCCAGGCTGTGTGAGAG 474
QY 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120
Db 475 TGCCAGTCCAGCAATGTGTACAGACTTCAACCTTCTACTGCCAACCATGCTAGACTGC 534
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 535 GGGGCCCTGCACCGCCACACAGGCTACTGTGTCCCGCAGAGATGACTGTGGGACC 594
QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db 595 TGCCCTGCTGCTTCTATGACACATGGCATGGCTGCGTGTCTTCCCCACGAGCACCCTG 654
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTyrPargGlnMetPheTrpValGln 180
Db 655 GGGAGCTGTCCAGAGCGCTGTGCTGTGTGGCTGGAGGAGATGTCTGGGTCCAG 714
QY 181 ValLeuLeuAlaGlyLeuValValProLeuLeuGlnGlyAlaThrLeuThrTyrThrTyr 200
Db 715 GTGCTCTGGCTGGCTGTGTGTGCTCCCTCTGCTGTGGGGCCACCTGACCTACACATAC 774
QY 201 ArgHisCysTrpProHisLysProLeuValThrAlaAspGluAlaGlyMetGluAlaLeu 220
Db 775 CGCCACTGTGGCTGCACACAGCCCTGTACTGCAGATGAAGCTGGGATGGAGGCTCTG 834
QY 221 ThrProProAlaThrHisLeuSerProLeuAspSerAlaHisThrLeuLeuAlaPro 240
Db 835 ACCCCACCAACCGCCACCATCTGTACACCTTGACAGCGGCCACACCTTCTAGACACT 894
QY 241 ProAspSerSerGluLysIleCysThrValGlnLeuValGlyAsnSerTrpThrProGly 260
Db 895 CCGTACAGCAGTAGAAGATCTGCACCGCTCCAGTTGTTGGTTAACAGCTGAGCCCTGGC 954

QY 261 TyrProGluThrGlnGluAlaLeuGlyProGlnValThrTrpSerTrpAspGlnLeuPro 280
Db 955 TACCCGAGACCCAGAGAGCGCTGCGCCGACAGGTGACATGTCCTGGGACCCAGTTGCC 1014
QY 281 SerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSerProAlaGlySer 300
Db 1015 AGCAGAGCTCTGGCCCCGCTGCTGCGCCACACTCTGCGCAGAGTCCCGCGGCTCG 1074
QY 301 ProAlaMetMetLeuGlnProGlyProGlnLeuTyrAspValMetAspAlaValProAla 320
Db 1075 CCAGCCATGATGCTGACAGCCGGGCGCAGCTTACGACGTGATGACGCGGTCGCCAGCG 1134
QY 321 ArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGluAlaGluLeuAlaVal 340
Db 1135 CGGCGTGGAGAGAGTTCGTGCGCAGCTGGGGCTGCGGAGGACAGATCGAAGCCGTCG 1194
QY 341 GluValGluIleGlyArgPheArgAspGlnGlnTyrGluMetLeuLysArgTrpArgGln 360
Db 1195 GAGGTGAGATCGCGCTTCCGAGACAGACAGTACGAGATGCTCAAGCGCTGGCGCCAG 1254
QY 361 GlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMetGlyLeuAspGly 380
Db 1255 CAGCAGCCCGCGGCGCTCGGAGCGGTTTACGCGGCCCTGGAGCGCATGGGGCTGGAGCGC 1314
QY 381 CysValGluAspLeuArgSerArgLeuGlnArgGlyPro 393
Db 1315 TGGGTGGAAGACTTGGCGCAGCGCCCTGCAGCGCGCGCCG 1353

RESULT 9
AAT89426
ID AAT89426 standard; cDNA; 1783 BP.

AC AAT89426;
DT 02-MAR-1998 (first entry)
DE Death domain containing receptor DR3-V1 cDNA.
KW Death domain containing receptor; DR3-V1; human; apoptosis;
KW Inflammation; NF-kappaB; ds.
XX Homo sapiens.

OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 198..1484
FT sig_peptide /*tag= a
FT mat_peptide /*tag= b
FT 304..1481
FT /*tag= c

PN WO9733904-A1.
XX 18-SEP-1997.
PD 17-OCT-1996; 96WO-US16849.
XX 12-MAR-1996; 96US-0013285.
PR (HUMA-) HUMAN GENOME SCI INC.
PA (UNMT) UNIV MICHIGAN.
XX Dillon PJ, Dixit VM, Gentz RL, Ni J, Yu G;
PI WPI; 1997-470812/43.
DR P-PSDB; AAW31516.
XX Death domain containing receptor polypeptide(s) DR3 and DR3-V1
PT for activation of apoptosis and NF-kappaB, antagonists can be used
PT to treat inflammatory diseases
XX Claim 2; Page 71-73; 108pp; English.

XX This cDNA clone, deposited as ATCC 97456, codes for human death
CC domain containing receptor DR3-V1 (see AAW31516), a novel member of
CC the tumour necrosis factor receptor family. It was isolated from a
CC cDNA library derived from cells of a human testis tumour. Related
CC death domain containing receptor DR3 cDNA (see AAT89427) was isolated
CC from a HUVEC cDNA library. The genes have also been identified in
CC cDNA libraries of foetal liver, foetal brain, tonsil and leukocyte.
CC Nucleic acids encoding full-length or mature DR3-V1 can be used to
CC produce recombinant polypeptides in transformed host cells. These
CC polypeptides can be used to treat diseases and disorders associated
CC with the inhibition of apoptosis. Antagonists, such as antibodies
CC raised against DR3-V1, can be used to treat diseases and disorders
CC associated with increased apoptosis and for treating inflammatory
CC diseases and disorders.

SO Sequence 1783 BP; 330 A; 562 C; 564 G; 327 T; 0 other;

Alignment Scores:

Pred. No.: 3.21e-117 Length: 1783
Score: 2209.00 Matches: 393
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-09-993-234-6_COPY_25_417 (1-393) x AAT89426 (1-1783)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGly 20
Db 303 CAGGGCGGCACTCGTAGCCCAAGGTGTGACTGTGCGGGTACTTCCACAGAAGATTGGT 362
QY 21 LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
Db 363 CTGTTTGTGACAGAGGCTGCCAGCGGGGCACTTAAGAGCCCTTGCACGAGGCC 422
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db 423 TGGGCACTCCACCTGCTTGTGTGTCGCCAAGACACCTTCTGGCCGCGAGAACAC 482
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db 483 CATATTTGATGTGCGCGCTGCCAGGCTGTGATGAGCAGGCGCTCCAGGTGGCGCTG 542
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
Db 543 GAGAACTGTTCAAGCAGTGGCGGACACCCGCTGTGCTGTAAAGCCAGCGCTGTTGTGAG 602
QY 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120
Db 603 TGGCAGGTACCAATGTGTACAGACATCACCTTCTACTGCCAACCATGCTAGACTGC 662
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 663 GGGGCCCTGACCGCCACACACAGGCTACTGTTCGCCGACAGATACTGACTGTGGACC 722
QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db 723 TGGCTGCTGGCTTCTATGACATGCGCATGGCTGCTGCTGCTGCCACGACACCTTG 782
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArgGlnMetPheTrpValGln 180
Db 783 GGGAGCTGTCCAGAGCGCTGTGCGCTGTGCTGTGAGGACAGATGTTCTGGGTCCAG 842
QY 181 ValLeuLeuAlaGlyLeuValValProLeuLeuLeuGlyAlaThrLeuThrTyrThrTyr 200
Db 843 GTGCTCTGGCTGGCTTGTGTGTCCTCTGCTGCTGGGGCCACCTGACCTACACATAC 902
QY 201 ArgHisCysTrpProHisLysProLeuValThrAlaAspGluAlaGlyMetGluAlaLeu 220
Db 903 CGGCACTGTGGCTCACAAGCCCTGTTACTGACAGATGAAGCTGGGATGGAGGCTCTG 962
QY 221 ThrProProAlaThrHisLeuSerProLeuAspSerAlaHisThrLeuLeuAlaPro 240

|||||
Db 963 ACCCCACCACGGCCACCATCTGTCAACCTTGACAGCGCCACACCCCTTACGACT 1022
QY 241 ProaspSerSerGluYsIleCysThrValGlnLeuValGlyAsnSerTrpThrProGly 260
Db 1023 CCTGACAGCAGTAGAAGATCTGCACACCGTCCAGTTGGTGGTAACAGCTGAGACCCCTGCC 1082
QY 261 TyrProGluThrGlnGlnAlaLeuCysProGlnValThrTrpSerTrpAspGlnLeuPro 280
Db 1083 TACCCCGAGAGACCCAGAGCGGCTCTGCCCGCAGGTGACATGCTCCTGGAGCCAGTTGCC 1142
QY 281 SerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSerProAlaGlySer 300
Db 1143 AGCAGAGCTCTGGCCCCCGCTGCTGCCGCCACACTCTCCGCCAAGAGTCCCCAGCCGCTCG 1202
QY 301 ProAlaMetMetLeuGlnProGlyProGlnLeuTyrAspValMetAspAlaValProAla 320
Db 1203 CCAGCCATGATGTGCAGCGCGGCCCGCAGCTCTACGAGTGATGGACGCGGTCCAGCG 1262
QY 321 ArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGluAlaGluIleGluAlaVal 340
Db 1263 CGCGCGTGAAGAGATTGCGGCACAGCTGGGGCTGCCGAGCAGAGATCGAAGCCGCTG 1322
QY 341 GluValGluIleGlyArgPheArgAspGlnGlnIntyrgluMetLeuLysArgTrpArgGln 360
Db 1323 GAGGTGAGATCGCGCGCTCCGAGACGACAGTAGAGTGTCTCAAGCGCTGGCGCCAG 1382
QY 361 GlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGlnArgMetGlyLeuAspGly 380
Db 1383 CAGCAGCCCGCGCGCTCGGAGCCGTTTACGCGGCGCTGGAGCGCATGGGCTGGAGCGC 1442
QY 381 CysValGluAspLeuArgSerArgLeuGlnArgGlyPro 393
Db 1443 TGGGTGAAGACTTGGCGAGCGCGCTGCAGCGCGGCCG 1481

RESULT 10
AAx00924

ID AAx00924 standard; cDNA; 1783 BP.

XX AAx00924;

XX 25-MAR-1999 (first entry)

DE Death domain containing receptor polypeptide (DR3-V1) encoding cDNA.

XX Death domain; receptor; DR3-V1; DR3; recombinant; ds.

XX Homo sapiens.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 198..1484

FT sig_peptide /*tag= a /product= "Death domain containing receptor DR3-V1"

FT mat_peptide /*tag= b 301..1481

FT /*tag= c

PN JP11000170-A.

XX 06-JAN-1999.

XX 12-MAR-1997; 97JP-0057503.

XX 06-FEB-1997; 97US-0037341.

PR 12-MAR-1996; 96US-0013285.

PR 17-OCT-1996; 96US-0028711.

XX (HUMA-) HUMAN GENOME SCI INC.

PA (UNMI) UNIV MICHIGAN.

XX WPI; 1999-124390/11.

DR P-PSDB; AAW95537.

XX New death domain containing receptor and recombinant vector -
PT optionally comprising leader sequence
XX Claim 2; Fig 1, 2; 50pp; Japanese.
PS
XX The invention provides nucleotide sequences encoding death domain
CC containing receptor polypeptides DR3-V1 and DR3. The DR3-V1 cDNA clone
CC is contained in ATCC deposition No. 97456 and the DR3 cDNA clone is
CC contained in ATCC deposition No. 97757. Recombinant vectors comprising
CC the nucleic acid sequences and optionally the leader sequences are
CC used for the recombinant production of the proteins. The present
CC sequence represents a cDNA encoding the death domain containing
CC receptor polypeptide (DR3-V1).

SQ Sequence 1783 BP; 330 A; 562 C; 564 G; 327 T; 0 other;

Alignment Scores:

Pred. No.:	3.21e-117	Length:	1783
Score:	2209.00	Matches:	393
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	20	Gaps:	0

US-09-993-234-6_COPY_25_417 (1-393) x AAx00924 (1-1783)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGly 20

Db 303 CAGGGCGGCACTCGTAGCCCCAGGTGTGACTGTGCCGGTACTTCCACAAGAAGATTGGT 362

QY 21 LeuPheCysCysArgGlyCysProAlaGlyHisIstyrLeuLysAlaProCysThrGluPro 40

Db 363 CTGTTTGTGTGACAGAGGCTGCGCCAGCGGGGCACTACCTGAAGGCCCTTGCACGAGGCC 422

QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60

Db 423 TGGGCACTCCACCTGCGCTGTGTGTCCCAAGACACCTTGTGGCTGGAGAACCAC 482

QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80

Db 483 CATATTTCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCCCTCCAGGTGGCGCTG 542

QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100

Db 543 GAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGGCTGTAAAGCCAGGCTGTGTGGAG 602

QY 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120

Db 603 TGGCAGTCCAGCAATGTGTACAGATGCACCCCTTCTACTGCCAACCATGCCCTAGACTGC 662

QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140

Db 663 GGGGCCCTGCACCGCCACACAGGCTACTGTTCGCCGACAGATACTGACTGTGGAGCC 722

QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160

Db 723 TGGCTGCTGGCTTCTATGACATGGGATGGCTGCGTGTCCGCCACGAGACCCCTG 782

QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTyrPargGlnMetPheTrpValGln 180

Db 783 GGGAGCTGTCCAGAGCGCTGTGCCGTGTGGCTGGAGGACAGATGTTCTGGGTCCAG 842

QY 181 ValLeuLeuAlaGlyLeuValValProLeuLeuGluGlyAlaThrLeuThrTyrThrTyr 200

Db 843 GTGCTCTGGCTGGCTGTGTGTCCCTCTGCTTGGGGCCACCTGACCTACACATAC 902

QY 201 ArgHisCysTrpProHisLysProLeuValThrAlaAspGluAlaGlyMetGluAlaLeu 220

Db 903 CGCCACTGCTGGCTCACAAGCCCTGTGTACTGCAGATGAAGCTGGGATGAGGCTCTG 962

QY 221 ThrProProAlaThrHisLeuSerProLeuAspSerAlaHisThrLeuAlaPro 240

Db 963 ACCCCACCACCGGCCACCACTGTACACCTTGACACAGCGCCACACACCTTCTAGCACCT 1022
QY 241 ProaspserserGlulysilecysThrValGlnLeuValGlyAsnSerTrpThrProGly 260
Db 1023 CCGTACAGCAGTGAAGAATCTGCACACCGTCCAGTGTGGGTAAACAGCTGAGACCCCTGGC 1082
QY 261 TyrProGluThrGlnGlnAlaLeuCysProGlnValThrTrpSerTrpAspGlnLeuPro 280
Db 1083 TAACCCGAGAGACCCAGAGAGCGCTCTGCCCGCAGGTGACATGCTCTGGAGACAGTGGCC 1142
QY 281 SerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSerProAlaGlySer 300
Db 1143 ACCAGAGCTCTGGCCCCCGCTGCTGCGCCACACTCTCCGCCAGAGTCCCGCAGCGCTCG 1202
QY 301 ProAlaMetMetLeuGlnProGlyProGlnLeuTyrAspValMetAspAlaValProAla 320
Db 1203 CCAGCCATGATGTCTGACGCGCGGCCCGCAGCTCTACGACGTGATGAGCGCGTCCACGCG 1262
QY 321 ArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGluAlaGluIleGluAlaVal 340
Db 1263 CGGCGCTGGAAGAGATTCTGCGCACGCTGGGGCTGCGGAGGACAGATCGAAGCCGTG 1322
QY 341 GluValGluIleGlyArgPheArgAspGlnGlnTyrGluMetLeuLysArgTrpArgGln 360
Db 1323 GAGGTGAGATCGCGCGCTTCCGAGACACGACGACGATGATGCTCAAGCGCTGCGCCAG 1382
QY 361 GlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMetGlyLeuAspGly 380
Db 1383 CAGCAGCCCGCGGCTCGGAGCGCTTACGCGCGCTTGAGCGCATGGGGCTGGACGGC 1442
QY 381 CysValGluAspLeuArgSerArgLeuGlnArgGlyPro 393
Db 1443 TGGCTGGAAGACTGCGCAGCGCGCTGACGCGCGCGCG 1481
RESULT 11
AAC68776
ID AAC68776 standard; cDNA; 1783 BP.
AC AAC68776;
XX 20-FEB-2001 (first entry)
DE Human death domain containing receptor DR3-V1 coding sequence.
XX
KW Human; death domain containing receptor; DR3-V1; cancer;
KW autoimmune disorder; inflammation; cardiovascular disorder; infection;
KW neurodegenerative disease; angiogenesis; ss.
XX
OS Homo sapiens.
XX
PN WO200064465-A1.
XX 02-NOV-2000.
PD 21-APR-2000; 2000WO-US10741.
PF
XX 22-APR-1999; 99US-0130488.
PR 28-MAY-1999; 99US-0136741.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (UNMI) UNIV MICHIGAN.
PA (YUG/) YU G.
PA (NIJ/) NI J.
PA (GENT/) GENTZ R L.
PA (DILL/) DILLON P J.
PA (DIXI/) DIXIT V M.
XX
PI YU G, NI J, Gentz RL, Dillon PJ, Dixit VM;
XX
DR WPI; 2000-687263/67.
DR P-PSDB; AAB36264.
XX
PT Treating graft-versus-host disease, cancer, immunodeficiency or an

PT autoimmune disease comprising administering an antibody to Death Domain
PT Containing Receptor proteins and a second therapeutic agent -
XX
PS Example 1; Fig 1; 273pp; English.
XX
CC The present invention provides the protein and coding sequences for two
CC death domain containing receptors, designated DR3 and DR3-V1. These
CC receptors are involved in apoptosis, and the sequences given can be used
CC in the treatment of cancers, infections, cardiovascular disorders such as
CC arrhythmias, ischemia, aneurysms, arterial occlusive diseases, embolisms
CC and congenital heart defects, neurodegenerative diseases including
CC Alzheimer's and Parkinson's diseases, autoimmune disease such as multiple
CC sclerosis, arthritis, diabetes, Graves' disease, asthma and psoriasis,
CC and to promote angiogenesis and wound healing.
XX
SQ Sequence 1783 BP; 330 A; 562 C; 564 G; 327 T; 0 other;

Alignment Scores:
Pred. No.: 3, 21e-117 Length: 1783
Score: 2209.00 Matches: 393
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-09-993-234-6_copy_25_417 (1-393) x AAC68776 (1-1783)
QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGly 20
Db 303 CAGGCGGCACCTCTAGCCGCCAGGTGTGACTGTCCGGTACTTCCACAAGAATGGT 362
QY 21 LeuPheCysCysArgGlyCysProAlaGlnHisTyrLeuLysAlaProCysThrGluPro 40
Db 363 CTGTTTGTTCAGAGGCTGCCAGCGGGCACTACCTGAAGGCCCTTGACAGGAGCCC 422
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db 423 TCGGCAACTCCACCTGCTGTGTGTCCCAAGACACACCTTCTGGCCGGAGAACCCAC 482
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db 483 CATAAATCTGATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCGCTCCAGGTGGCGCTG 542
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
Db 543 GAGAACTGTTCAGCAGTGGCGGACACCGCTGTGGCTGTAAAGCCAGGCTGTGTGAG 602
QY 101 CysGlnValSerGlnCysValSerSerSerProPheTyrCysGlnProCysLeuAspCys 120
Db 603 TGCCAGGTACGCCAATGTGTACAGCATTCACCTTCTACTGCCAACCATGCTAGACTGC 662
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 663 GGGGCCCTGCACCGCCACACAGGCTACTGTCTCCGACAGATTAAGTACTGTGGAGCC 722
QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db 723 TGCCTGCTGGCTTCTATGAACATGGCGATGGCTGCGTGTCTGCCACGAGACACCTG 782
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArgGlnMetPheTrpValGln 180
Db 783 GGAGCTGTCCAGAGCGCTGTGCCGCTGTCTGTGGCTGAGGAGATGTCTGGGTCCAG 842
QY 181 ValLeuLeuAlaGlyLeuValValProLeuLeuLeuGlyAlaThrLeuThrTyrThrTyr 200
Db 843 GTGCTCCTGGCTGGCTGTGTGTCCCTCTGCTTGGGGCCACCTGACCTACACATAC 902
QY 201 ArgHisCysTrpProHisLysProLeuValThrAlaAspGluAlaGlyMetGluAlaLeu 220
Db 903 CGGCACTGCTGGCTCACAAGCCCTGTTACTGACATGAAGCTGGATGAGGCTCTG 962
QY 221 ThrProProAlaThrHisLeuSerProLeuAspSerAlaHisThrLeuLeuAlaPro 240

Db 963 ACCCCACGACGGCCACCATCTGTGCACCTTGACAGCGCCACACCCCTTACACCT 1022

QY 241 ProAspSerSerGluLysIleCysThrValGlnLeuValGlyAsnSerTrpThrProGly 260
|||||
Db 1023 CCTGCACAGCAGTGAGAGATCTGCACCGCTCCAGTTGGTGGGTACACGCTGCACCCCTGGC 1082

QY 261 TyrProGluThrGlnGlnAlaLeuCysProGlnValThrTrpSerTrpAspGlnLeuPro 280
|||||
Db 1083 TACCCCGAGACCCAGAGAGCGCTGCTCCGCGAGGTGACATGGTCTGGGACACAGTTGCC 1142

QY 281 SerArgAlaLeuGlyProAlaAlaProThrLeuSerProGluSerProAlaGlySer 300
|||||
Db 1143 AGCAGAGCTCTTGCGCCCGCTGCTGCGCCACACTCTCGCAGAGTCCACAGCCGCTCG 1202

QY 301 ProAlaMetMetLeuGlnProGlyProGlnLeuTyrAspValMetAspAlaValProAla 320
|||||
Db 1203 CCAGCCATGATGCTGCAGCCGCGCCGAGCTCTACGACGTGATGAGCGGCTCCACGCG 1262

QY 321 ArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGluAlaGluIleGluAlaVal 340
|||||
Db 1263 CGGCGCTGGAAGAGTTCGTGCGCACGCTGGGGCTGCGCGAGGACAGATCGAAGCCGTG 1322

QY 341 GluValGluIleGlyArgPheArgAspGlnGlnIleTyrGluMetLeuLysArgTrpArgGln 360
|||||
Db 1323 GAGGTGAGATCGCGCGCTTCCGAGACAGCAGTACGAGATGCTCAAGCGCTGGCGCCAG 1382

QY 361 GlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMetGlyLeuAspGly 380
|||||
Db 1383 CAGCAGCCCGCGCGCTCGGAGCCGTTACGCGCGCCCTGAGCGCATGGGGCTGAGCGCG 1442

QY 381 CysValGluAspLeuArgSerArgLeuGlnArgGlyPro 393
|||||
Db 1443 TGCCTGAGACTTGCAGCAGCCGCTGCAGCGCGCGCG 1481

RESULT 12
AAV28700
ID AAV28700 standard; cDNA; 1847 BP.
XX
AC AAV28700;
XX
DT 20-AUG-1998 (first entry)
XX
DE Human apoptosis inducing receptor coding sequence.
XX
KW Apoptosis inducing receptor; AIR protein; human; cell death regulator;
KW Type I transmembrane protein; tumour cell death; autoimmune disease;
KW therapy; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 236..1489
FT /*tag= a
FT /product= AIR
XX
PN WO9814565-A1.
XX
PD 09-APR-1998.
XX
PE 03-OCT-1997; 97WO-US17876.
XX
PR 04-OCT-1996; 96US-0044456.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Perkins PA;
XX
DR WPI; 1998-240077/21.
DR P-PSDB; AAW57045.
XX
PT DNA encoding apoptosis inducing receptor - which is Type I
PT transmembrane protein, useful for regulating cell death
XX

PS Claim 2; page 28-30; 45pp; English.
XX
CC This sequence encodes the human apoptosis inducing receptor (AIR) of the
CC invention. AIR is a Type I transmembrane protein, soluble forms of which
CC can be used to regulate cell death in a therapeutic setting. Soluble AIR
CC can also be used in vitro to block apoptosis or AIR-expressing cells, or
CC to screen agonists or antagonists of AIR activity. The cytoplasmic domain
CC of AIR can be used to develop assays for inhibitors of AIR-induced cell
CC death, which is useful to regulate cell death in a therapeutic setting as
CC well as in vitro. Agonists of AIR activity can be used to kill tumour
CC cells that express AIR, or T cells expressing AIR in autoimmune diseases.
XX
SQ Sequence 1847 BP; 316 A; 605 C; 579 G; 347 T; 0 other;

Alignment Scores:
Pred. No.: 3.33e-117 Length: 1847
Score: 2209.00 Matches: 393
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 19 Gaps: 0

US-09-993-234-6_COPY_25_417 (1-393) x AAV28700 (1-1847)

QY 1 GlnGlyLysThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGly 20
|||||
Db 308 CAGGCGGACATGCTAGCCGCCAGGTGTGACTGTGCCGTGACTTCCACAGAAGATTGGT 367

QY 21 LeupheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
|||||
Db 368 CTGTTTGTGTCAGAGGCTGCCAGCGGGGCACTACTGAAGGCCCCGTGACGAGAGCC 427

QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
|||||
Db 428 TCGGCACTCCACCTGCTGTGTGTGCCAAGACACACTTCTTGCGCTGGAGAACCAC 487

QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
|||||
Db 488 CATATTCTGAATGTGCCCGCTGCCAGGCTGTGATGACAGGCGCTCCACGCTGGCGCTG 547

QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
|||||
Db 548 GAGAACTGTTCAGCAGTGGCCGACACACCGCTGTGCTGAAGCCAGGCTGTGTGGAG 607

QY 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120
|||||
Db 608 TGCCAGGTGACCAATGTGTACAGAGTACACCTTCTACTGCCAACCATGCTTAGACTGC 667

QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
|||||
Db 668 GGGGCCCTGCACGCCACACACAGGCTACTCTGTCCCGCAGAGATACTGATGGGACC 727

QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
|||||
Db 728 TGCCTGCTGGCTTCTATGAACATGGCGATGGCTGCTGCTGCCCCACGAGCACCCCTG 787

QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTyrPargGlnMetPheTrpValGln 180
|||||
Db 788 GGGAGCTGTCCAGACGCGCTGTGCCGTGTGTGGCTGGAGGAGATGTCTGGGTCCAG 847

QY 181 ValLeuLeuAlaGlyLeuValAlaProLeuLeuGlyAlaThrLeuThrTyrThrTyr 200
|||||
Db 848 GTGCTCTGGCTGCTGTGTGTCCTGCTGTGGGGCCACCTGACTACACATAC 907

QY 201 ArgHisCysTrpProHisLysProLeuValThrAlaAspGluAlaGlyMetGluAlaLeu 220
|||||
Db 908 CGCCACTGTGCTGCACAAGCCCTGTGTACTGACAGATGAAGCTGGATGGAGGCTCTG 967

QY 221 ThrProProAlaThrHisLeuSerProLeuAspSerAlaHisThrLeuLeuAlaPro 240
|||||
Db 968 ACCCCACGACCGCCACCATCTGTACACCTTGGACAGCGCCACACACCTTCTAGCACCT 1027

QY 241 ProAspSerSerGluLysIleCysThrValGlnLeuValGlyAsnSerTrpThrProGly 260

Db 1028 CCTGACAGAGTGAAGATCTGCACCGTCCAGTTGGTGGTAACTGACCCCTGGC 1087
QY 261 TyrProGluThrGlnGluAlaLeuCysProGlnValThrTrpSerTrpAspGlnLeuPro 280
Db 1088 TACCCCGAGACCAGAGAGCGCTGCGCCGACAGTACATGGTCTGGGACACAGTGGCC 1147
QY 281 SerArgAlaLeuGlyProAlaAlaProThrLeuSerProGluSerProAlaGlySer 300
Db 1148 AGCAGAGCTCTGGCCCCGCTGCGCCACACTCTCGCCAGACTCCCCAGCCGCTCG 1207
QY 301 ProAlaMetMetLeuGlnProGlyProGlnLeuTyrAspValMetAspAlaValProAla 320
Db 1208 CCAGCCATGATGCTGCAGCCGGCCGACAGCTTACGACCGTGTGACCGCGGTCAGCG 1267
QY 321 ArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGluAlaGluIleGluAlaVal 340
Db 1268 CGGCGCTGGAAGAGAGTTCGTGCCACCGCTGGGGCTGCCGAGGCGAGATCGAAGCCGTG 1327
QY 341 GluValGluIleGlyArgPheArgAspGlnGlnTyrGluMetLeuLysArgTrpArgGln 360
Db 1328 GAGGTGAGATCGGCCCTTCGAGACCAAGCAGTACGAGATGCTCAAGCGCTGGCGCCAG 1387
QY 361 GlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMetGlyLeuAspGly 380
Db 1388 CAGCAGCCCGCGGCGCTCGAGCCGTTTACGCGGCCCTGAGCGCATGGGGCTGAGCGCC 1447
QY 381 CysValGluAspLeuArgSerArgLeuGlnArgGlyPro 393
Db 1448 TCGGTGGAAGACTTGCAGCCGCGCTGAGCGCGCGCCG 1486

RESULT 13
ABL64119
ID ABL64119 standard; DNA; 1743 BP.

XX ABL64119;
DT 15-MAY-2002 (first entry)
XX DE Breast cancer related gene sequence SEQ ID NO:2456.
XX KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW cytosstatic; gene therapy; antineoplastic; wilm's tumour; adenocarcinoma;
XX gene; ds.
OS Homo sapiens.
XX WO200194629-A2.
PN 30-MAY-2001; 2001WO-US10838.
XX 13-DEC-2001.
PF 05-JUN-2000; 2000US-209473P.
XX 05-JUN-2000; 2000US-209531P.
PR 18-SEP-2000; 2000US-233133P.
PR 18-SEP-2000; 2000US-233617P.
PR 20-SEP-2000; 2000US-234009P.
PR 20-SEP-2000; 2000US-234034P.
PR 20-SEP-2000; 2000US-234052P.
PR 22-SEP-2000; 2000US-234509P.
PR 22-SEP-2000; 2000US-234567P.
PR 25-SEP-2000; 2000US-234923P.
PR 25-SEP-2000; 2000US-234924P.
PR 25-SEP-2000; 2000US-235077P.
PR 25-SEP-2000; 2000US-235082P.
PR 25-SEP-2000; 2000US-235134P.
PR 25-SEP-2000; 2000US-235280P.
PR 26-SEP-2000; 2000US-235637P.
PR 26-SEP-2000; 2000US-235638P.
PR 27-SEP-2000; 2000US-235711P.
PR 27-SEP-2000; 2000US-235720P.

PR 27-SEP-2000; 2000US-235840P.
PR 27-SEP-2000; 2000US-235863P.
PR 28-SEP-2000; 2000US-236028P.
PR 28-SEP-2000; 2000US-236032P.
PR 28-SEP-2000; 2000US-236033P.
PR 28-SEP-2000; 2000US-236034P.
PR 28-SEP-2000; 2000US-236109P.
PR 28-SEP-2000; 2000US-236111P.
PR 29-SEP-2000; 2000US-236842P.
PR 29-SEP-2000; 2000US-236891P.
PR 02-OCT-2000; 2000US-237172P.
PR 02-OCT-2000; 2000US-237173P.
PR 02-OCT-2000; 2000US-237278P.
PR 02-OCT-2000; 2000US-237294P.
PR 02-OCT-2000; 2000US-237295P.
PR 02-OCT-2000; 2000US-237316P.
PR 03-OCT-2000; 2000US-237425P.
PR 03-OCT-2000; 2000US-237598P.
PR 03-OCT-2000; 2000US-237604P.
PR 03-OCT-2000; 2000US-237606P.
PR 03-OCT-2000; 2000US-237608P.
PR 01-NOV-2000; 2000US-244867P.
PR 01-NOV-2000; 2000US-245084P.
PA (AVAL-) AVALON PHARM.
XX
PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppet DR, Weaver Z;
XX
DR WPI; 2002-188264/24.

Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set -
Claim 1; SEQ ID 2456; 44pp; English.

The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL6164 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytosstatic activity and can be used in gene therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, CC oesophageal, ovarian, kidney, prostate or pancreatic cancer, CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine CC carcinoma, papillary carcinoma and wilm's tumour.

Sequence 1743 BP; 347 A; 543 C; 549 G; 304 T; 0 other;

Alignment Scores:
Pred. No.: 2.5e-113 Length: 1743
Score: 2140.50 Matches: 389
Percent Similarity: 91.10% Conservative: 0
Best Local Similarity: 91.10% Mismatches: 4
Query Match: 96.90% Indels: 35
DB: 24 Gaps: 1

US-09-993-234-6_COPY_25_417 (1-393) x ABL64119 (1-1743)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGly 20
Db 141 CAGGGCGGCACTCGTAGCCCGCAGGTGTGACTGTGCGGCTGACTTCCACAGAAGATTGGT 200
QY 21 LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
|||||

Db 201 CTGTTTGTGCAGAGCGTGCACGGGGGCGACTACCTGAAGCCCCCTGCACGAGGCC
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db 261 TCGGGCAACTCCACCTGCTTGTGTCTCCCAAGACACCTTCTTGCCCTGGAGAACCCAC 320
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db 321 CATAACTCTGAATGTGCCCGCTGCCAGGCCCTGTGATGAGAGGCCCTCCAGGTGGCGCTG 380
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
Db 381 GAGAACTGTTCAGCAGTGGCGGACACCCGCTGTGGCTGTAGCCAGGCTGTTGTGGAG 440
QY 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120
Db 441 TGGCAGGTTCAGCAATGTGTACAGAGTTCACCCCTTCTACTGCCCAACCATGCGCTAGACTGC 500
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 501 GGGGCCCTGCACCGCCACACAGGCTACTCTGTTCGCCAGAGATACTGACTGTGGACC 560
QY 141 CysLeuProGlyPheTyrGlnHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db 561 TGCCTGCTGGCTTCTATGACATGGCGATGGCTGCTGCTGCCACGACGACCCCTG 620
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArg----- 174
Db 621 GGGAGCTGTCCAGAGCGGTGCCCTGTCTGTGGCTGGAGGCGAGAGTAGTGTGTGCT 680
QY 174 ----- 174
Db 681 GGGAAATGCGCGTGGAGAACTGGGATGGACCGAGGGGAGCGGGTGAGAGGGGGCAAC 740
QY 175 -----GlnMetPheTrpValGlnValLeuLeuAlaGlyLeu 186
Db 741 CACCCCAACACCCACAGCTGCTTTCAGTG-TTCTGGGTCCAGAGTGTCTGCTGGCTT 799
QY 187 ValValProLeuLeuLeuGlyAlaThrLeuThrTyrThrTyrArgHisCysTrpProHis 206
Db 800 GTGGTCCCCCTCTGCTGGGGCCACCCCTGACCTACACATACCGCCACTGTGGCTCTAC 859
QY 207 LysProLeuValThrAlaAspGluAlaGlyMetGluAlaLeuThrProProProAlaThr 226
Db 860 AAGCCCTGGTTACTGCAGATGAAGCTGGGATGAGGCTGTGACCCACACCGGCCACC 919
QY 227 HisLeuSerProLeuAspSerAlaHisThrLeuLeuAlaProProAspSerSerGlyLys 246
Db 920 CATCTGTACACCTTGACAGCGGCCACACCTTCTAGCAGCTCCTGACAGAGTAGAAG 979
QY 247 IleCysThrValGlnLeuValGlyAsnSerTrpThrProGlyTyrProGluThrGlnGlu 266
Db 980 ATCTGCACCGTCCAGTTGGTGGTAACAGCTGGACCCCTGGCTAACCCGAGACCCAGAG 1039
QY 267 AlaLeuCysProGlnValThrTrpSerTrpAspGlnLeuProSerArgAlaLeuGlyPro 286
Db 1040 GCGCTCTGCCCGCAGGTGACATGGTCTGGGACCAAGTTGCCACAGAGCTCTTGCCCC 1099
QY 287 AlaAlaAlaProThrLeuSerProGluSerProAlaGlySerProAlaMetLeuGln 306
Db 1100 GCTGCTGCCCGCACACTCTGCCAGAGTCCCGACCGCGCTGCCAGCCATGATGCTGCAG 1159
QY 307 ProGlyProGlnLeuTyrAspValMetAspAlaValProAlaArgArgTrpLysGluPhe 326
Db 1160 CCGGGCCCGCAGCTCTACGACGTGATGACGCGGTCCCGCGCGCTGGAAGAGATTTC 1219
QY 327 ValArgThrLeuGlyLeuArgGluAlaGluIleGluAlaValGluValGluIleGlyArg 346
Db 1220 GTGGCGACGCTGGGCTGCGGAGGACAGAGATCGAAGCCGTGGAGGTGAGATCGGTCTC 1279
QY 347 PheArgAspGlnGlnTyrGluMetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeu 366
Db 1280 TTCCGAGACACAGAGTAGAGATGCTCAAGCACTGGCGCCAGACAGACCGCGGGGCTTC 1339

QY 367 GlyAlaValTyrAlaAlaLeuGluArgMetGlyLeuAspGlyCysValGluAspLeuArg 386
Db 1340 GGAGCCGTTTACGCGGCCCTGGAGCCCATGGGGCTGACCGGCTGCTGGAAGACTTGGCC 1399
QY 387 SerArgLeuGlnArgGlyPro 393
Db 1400 AGCGCGCTGCAGCGTGGCCCG 1420
RESULT 14
AAF83770
ID AAF83770 standard; DNA; 1250 BP.
XX
AC AAF83770;
XX
DT 06-AUG-2001 (first entry)
XX
IDE Nucleotide sequence of human TR3 gene.
XX
KW TR3; cell proliferation; leukemia; immunosuppressive; cytostatic; dermatological; antiarthritic; antidiabetic; neuroprotective; cardiant; antithyroid; antiinflammatory; antiallergic; T-cell-inhibitor; ds.
XX
OS Homo sapiens.
XX
FH
FH Key Location/Qualifiers
FT CDS 1..1250
FT /tag= a
FT /transl_except= "(pos:481..482, aa:Asp)"
FT /note= "this codon has an apparent 1 nucleotide
FT deletion which alters the reading frame"
FT /transl_except= "(pos:558..559, aa:Cys)"
FT /note= "this codon has an apparent 1 nucleotide
FT deletion which alters the reading frame"
FT /transl_except= "(pos:638..639, aa:Leu)"
FT /note= "this codon has an apparent 1 nucleotide
FT deletion which alters the reading frame"
FT /transl_except= "(pos:718..719, aa:Met)"
FT /note= "this codon has an apparent 1 nucleotide
FT deletion which alters the reading frame"
FT sig_peptide 1..72
FT /tag= b
FT mat_peptide 73..1247
FT /tag= c
PN WO200135995-A2.
XX
XX 25-MAY-2001.
PD
XX
PF 17-NOV-2000; 2000WO-US31692.
XX
XX 19-NOV-1999; 99US-0166583.
PR
XX
PA (TITT/) TITILE T V.
PA (WEGM/) WEGMANN K W.
XX
PI Tittle TV, Wegmann KW;
XX
XX WPI: 2001-343711/36.
DR P-PSDB; AAB84941.
DR
XX
PT Composition for treatment of T-cell mediated disease e.g. arthritis,
PT cancer comprises a biologically active TR3-specific binding agent
PT especially a monoclonal antibody -
XX
PS Disclosure; Page 72; 77pp; English.
XX
CC The invention relates to a composition comprising a biologically active
CC TR3-specific binding agent (I) that binds to TR3 and inhibits the
CC proliferation of cells expressing TR3. (I) identified by the methods are
CC useful for treating a subject suspected of having a disease associated
CC with a proliferation of cells expressing TR3 especially leukemias or
CC lymphomas or a T-cell mediated disease especially autoimmune diseases

FT /tag= j
FT /number= 5
FT Intron 1822..3068
FT /tag= k
FT /number= 5
FT exon 3069..3124
FT /tag= l
FT /number= 6
FT Intron 3125..3225
FT /tag= m
FT /number= 6
FT exon 3226..3333
FT /tag= n
FT /number= 7
FT Intron 3334..3529
FT /tag= o
FT /number= 7
FT exon 3530..3577
FT /tag= p
FT /number= 8
FT Intron 3578..4021
FT /tag= q
FT /number= 8
FT exon 4022..4202
FT /tag= r
FT /number= 9
FT Intron 4203..4433
FT /tag= s
FT /number= 9
FT exon 4434..4825
FT /tag= t
FT /number= 10

WO200234912-A1.

02-MAY-2002.

24-OCT-2001; 2001WO-JP09313.

XX 24-OCT-2000; 2000JP-0324296.
PR 27-MAR-2001; 2001JP-0090546.
PR 30-MAR-2001; 2001JP-0099990.

PA (NEMI-) NEW IND RES ORG.
PA (SHIO/) SHIOZAWA S.

PI Shiozawa S, Konishi Y;

XX WPI; 2002-417132/44.

XX Genomes, particularly DR3 genomic DNA, participating in rheumatoid
PT arthritis via mutation, useful in evaluating disease onset and its
PT possibility and providing therapy and remedies -

XX Claim 1; Page 64-66; 84pp; Japanese.

XX The present invention relates to the human DR3 gene, which is associated
CC with rheumatoid arthritis. Certain mutations in the gene can be linked to
CC the disease. The sequences can be used to evaluate disease onset and its
CC possibility and to provide therapy and remedies. The present sequence is
CC the gene of the invention.

XX Sequence 4825 BP; 921 A; 1378 C; 1521 G; 1005 T; 0 other;

Alignment Scores:

Pred. No.: 2.76e-76 Length: 4825
Score: 1498.50 Matches: 389
Percent Similarity: 28.46% Conservative: 0
Best Local Similarity: 28.46% Mismatches: 4
Query Match: 67.84% Indels: 978
DB: 24 Gaps: 8

US-09-993-234-6_COPY_25_417 (1-393) x AAL47185 (1-4825)

OY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
DB 669 CAGGGCGGCACTGCTAGCCGCCAGGCTGTGACTGTGCCGGTGACTTCACAAGAAATTGGT 728
OY 21 LeupheCysCysArgGlyCysProAla----- 29
DB 729 CTGTTTGTTCAGAGAGCTGCCAGCGGTAAGTGCCACAGGGGTGGAGAGCATGGG 788
OY 29 ----- 29
DB 789 GCAGGCAGGCTGAGAGAGTGCGCGGCGACGCCCGGAGGTAAGAGAGCGCTGCCAGGGGA 848
OY 29 ----- 29
DB 849 GGTAGGGGTAGGCTGACAGAGAAGTAGGAGCTGAGAGAAAGAGGAGGAGGCGAGGG 908
OY 29 ----- 29
DB 909 TGGGAAGCAGGTGCGGGGTTGCTGGCGACGCCCTCTGCCCTGACCCCTGCTGTTTC 968
OY 30 ----GlyHisTyrLeuLysAlaProCysThrGluProCysGlyAsnSerThrCysLeuVa 48
DB 969 CACAGGGCACTACCTGAAGGCCCTTGCACGAGAGCCCTGCGGCACTCCACCTGCCCTGT 1028
OY 48 ICysProGlnAspThrPheLeuAlaTrpGluAsnHisHisAsnSerGluCysAlaArgCy 68
DB 1029 GTGTCCCAAGACACACTTCTTGCGCTGGAGAAACACCATATTTCTGAATGTGCCCGCTG 1088
OY 68 sGlnAlaCysAspGlu----- 73
DB 1089 CCAGGCTGTGATGAGCAGGGGTAGGGGCTTCTCAGTGCTTGCGCAGGAGATTCTTAAGGA 1148
OY 73 ----- 73
DB 1149 CAGGCTTCTGAAGGAAGTGGCTGGCTGGGCCCCAAACTTGGGTGTGAGGCTCTGCA 1208
OY 73 ----- 73
DB 1209 CCCACCTTGCAGAAACCTCCACCTGATCCTCTTACAGGTTGCCCTTGCCCTTCTCT 1268
OY 73 ----- 73
DB 1269 CTTCCTGTGACCTTCCCATCTCTCATGTGCTTGCCCTGTGCGCCTTAATCTCTG 1328
OY 73 ----- 73
DB 1329 AGCTTCTCTTTTTTTAAAGGTAGCCCTGTACCTGTCTGTCTTTCGCTATTCTGTCTCC 1388
OY 73 ----- 73
DB 1389 ATTATCTTGGGATAATGCTCTGTGCTTCCATGGAGCCCTTGGCCCTGACTACTCTCC 1448
OY 74 -----GlnAlaSerGlnValAlaLeuGluAsnCysSerAl 85
DB 1449 ACTCCCACTCTCCCTGCACCCGCCACAGGCC-TCCCAAGTGGCGGTGAGAATGTTACGC 1507
OY 85 aValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGluCysGlnValSerG 105
DB 1508 AGTGGCCGACACCCGCTGTGGCTGTAGCCAGCGCTGTTGTGTGAGTCCCAAGTCAAGCCA 1567
OY 105 nCysValSerSerSerProPheTyrCysGlnProCysLeuAspCysGlyAlaLeuHisAr 125
DB 1568 ATGTGTACAGATTACCCCTTCTACTGCCAACCATGCTAGACTGGGGGCCCTGCACCCG 1627
OY 125 gHisThrArgLeuLeuCysSer----- 132
DB 1628 CCACACACGCTACTCTGTGA-GTACCCTCCACCCAGGGCTCTTACTCCAGACCCCTTT 1686
OY 132 ----- 132
DB 1687 CTCCCTGCTGACCCCACTCCTGTGCCAATGGTGAAGCATGCTCTCTGATTCAGAGTTTC 1746

QY 133 -ArgArgaspThrAspCysglyThrCysIeuProglyPheTyrgIuHisglyAspIyCy 152
Db 1747 CCGCAGAGATGACTGACTGTGGACCTGCCTGCTTCTATGACATGGCGATGGCTG 1806
QY 152 sValSerCysProThrSer----- 158
Db 1807 CGTGTCTCTGCCCAACGTA-ATTCTAGCTGTCTGGATGGAGGAAGCGCGCTGGAG 1865
QY 158 ----- 158
Db 1866 CAGAGCAGGGGCTGGGGTGGGCGAGTCTGCTGTTACAGAAATAGGAAGAGGGATAG 1925
QY 158 ----- 158
Db 1926 GGAGAGGAGCCCTTGGCCCTGTGATGGGTGGGCCCCCAGCTTCAGGCCAACTTAGATGCA 1985
QY 158 ----- 158
Db 1986 AAAGAGCAATCTGATCCGCCCTTAGCCAGATACATTAAGGTAATTGCCCTTCACTTTCAGC 2045
QY 158 ----- 158
Db 2046 CAGCATTCGCCCCAGCGATCCAGCCAGATATTACAGATGATTTGTCACTTACACAGAGA 2105
QY 158 ----- 158
Db 2106 GTCACATGTGATATAGCTTTAAAACTTGGGCTGAAGGAGTTGAGGCTGCAGTGAGCTATG 2165
QY 158 ----- 158
Db 2166 ATCGTCCCACTGCACCTTCAGCCCTGGGCAACAGAGCGAGACTATTAAATAAATAATAA 2225
QY 158 ----- 158
Db 2226 TATTAAATCTATTAAATATTAAATATTAAATCTATTAAATAATAATAAAGGCTGA 2285
QY 158 ----- 158
Db 2286 GAGTCAGGACTGTGCTGCTAGTCTCTAGGGGATCTTGGGCAAGTGCAGAGAAATCGCGT 2345
QY 158 ----- 158
Db 2346 CTCTGATGTGTGTGTCCTTCTCAACATGGGATGTTAGCAGCTAATTACAGGCTTT 2405
QY 158 ----- 158
Db 2406 GATCAGAGGTAAAGGACTTCTGTAGCTATTCAAGTCTTTTTTTTTTTTTTTTTTTTT 2465
QY 158 ----- 158
Db 2466 TTTTGGAGATGAGACTTGTCTGTACCCAGGCTGAGTGCAGTGGCAGATCTTGGCT 2525
QY 158 ----- 158
Db 2526 CACTACAACCTTGTGCTGCTGGGTCAAGTGAATTCTCTGCTCAGCCTCCCAAGTAGCT 2585
QY 158 ----- 158
Db 2586 GGGACTACAGAGCCCAACCAACCCCGGCTAATTTTTGTATTTTTTGTAGTAGACGGG 2645
QY 158 ----- 158
Db 2646 GTTTCACCGTGTAGCCAAAGATGTCCTTGATACACCTGACCTCGTGATCCACCCGCTTG 2705
QY 158 ----- 158
Db 2706 CCTCCCAAAGTGTGGATTACAGGCAAGCCACCGCGCGGCTCCATTCAAGTCTT 2765
QY 158 ----- 158
Db 2766 TATTGAATATCTGCTATGTCTACACACTGTCTAGGTGCTGGGATGCAACAGGGGACA 2825
QY 158 ----- 158

Db 2826 AAATAGGCAAAATCCCTGTCTTTTGGGGTTGACATTCTAGTACTCTTCATGTAGTCTA 2885
QY 158 ----- 158
Db 2886 GAAGAAGCTCAGTGAATAGTGTGTGTGTTGTACCAGGACACAATGACAGAAACATTC 2945
QY 158 ----- 158
Db 2946 TTGGTAGAGTGAGAGGCTTGGGAGGGAAGGTCCTTAGATGGAGCAGATGCTGGGCA 3005
QY 158 ----- 158
Db 3006 GTCTTAGGAGACCCCTCTGCGATGCACCCCTCATCCCTCAGGCCACCCCGTCCCTTG 3065
QY 159 -----ThrLeuGlySerCysProGluArgCysAlaIaValCysGlyTyrArg----- 174
Db 3066 CAGGACACCCCTGGGAGCTGTCCAGAGCGCTGTGCCGTGTCTGTGGCTGAGGCGAGAG 3125
QY 174 ----- 174
Db 3126 TAGGTGTGTCTGGGAATGCGAGTGGGAGAACTGGGATGGACCGAGGGGAGCGGGTGA 3185
QY 175 -----GlnMetPheTyrValGlnValle 182
Db 3186 GGAAGGGGGCAACCAACCAACCAACCAACCAAGCTGCTTTCAGTG-TTCTGGGTCCAGGTGCT 3244
QY 182 uLeuAlaGlyLeuValValProLeuLeuGlyAlaThrLeuThrTyrThrTyrArgH1 202
Db 3245 CCTGGCTGGCTGTGTGTGTCCTCTCTGCTTGGGCAACCTGACCTACACATACCGCA 3304
QY 202 sCysTrpProHisIysProLeuValThr----- 211
Db 3305 CTGCTGGCTCACAAGCCCTGTTACTGTGTAAGTACACACACCACACACCAACCA 3364
QY 211 ----- 211
Db 3365 AGCCTGGGTGAGATGGGTAGCCAGAGTCTACTCAACCTGATACAGAAAGGAAACT 3424
QY 211 ----- 211
Db 3425 GAGGAGGAGTGTGGGGTGCAGAGGAACCTTAGAGAGCTGTACAGCAACCAAGTCCA 3484
QY 212 -----AlaAspGluAlaGlyM 217
Db 3485 GGAGGCTTGCCTGGTGGCTGACCGCAATCTCTGTCTGTCTGACGATGAAGCTGGGA 3544
QY 217 etGluAlaLeuThrProPro----- 223
Db 3545 TGGAGGCTGTGACCCCAACCAACCGTGAAGAACTCACTGTGTGATTTGCGCTGCTTCTG 3604
QY 223 ----- 223
Db 3605 GAGCTGGAAGATCAAGCCTTACTATGATCCCTGGAGCTTGGCACCGGGCCAGACCGGGT 3664
QY 223 ----- 223
Db 3665 AGCCCTAGTGACAGAGGTGTGGGAGCAGATCATCAGTGAAGACCAAGACAGACTGC 3724
QY 223 ----- 223
Db 3725 CTGCCCTCAAGGGGTGCTCAGTCAAGCTGAGTTCAGATTCTGTAACAGAGAGCTAACAGTT 3784
QY 223 ----- 223
Db 3785 CAATGAAGAAGAGCCCATGTGCTGGGGGACAAAGAGAAAGGCGGGGACAGGGGAC 3844
QY 223 ----- 223
Db 3845 TCAAGGCAAGAAGCAAGAGTTCTGCTGGGCTACAGTGAGAGCAGGCGCAACTGTGGAGGT 3904
QY 223 ----- 223

Db 3905 GTCAATTGGGGGTGTCTGTGCTGACTGAACGAGGACTGTCCCTCTGGAGAGGCACTGC 3964
QY 224 -----Pro-Ala 225
Db 3965 GGGTAAGGGCCCTTACTTGGCAAGCAGGGCTGACCTGGGGCCCTCTTGCTTCCAGGCC 4024
QY 226 ThrHisLeuSerProLeuAspSeraIahisThrLeuLeuAlaProProAspSerSerglu 245
Db 4025 ACCCATCTGTCAACCTTGAGACGCGCCACACACCTTCTAGCACTCTTGACAGCAGTGAG 4084
QY 246 LysIleCysThrValGlnLeuValGlyAsnSerTrpThrProGlyTyrProGluThrGln 265
Db 4085 AAGATCTGCACCGTCCAGTTGGTGGTAACAGCTGAGACCCCTGACTACCCGAGACCCAG 4144
QY 266 GluAlaLeuCysProGlnValThrTrpSerTrpAspGlnLeuProSerArgAlaLeu--- 284
Db 4145 GAGCGCTTGTGCGCAGAGTGAATGCTCTGGAGACAGTGGCCACAGAGCTCTTGGT 4204
QY 284 ----- 284
Db 4205 AAGGACATCAGTGGCCTGAGGCTTGACCCCATTTCTCTGTCTGCGGTGGAGATTGTG 4264
QY 284 ----- 284
Db 4265 GTTTCACAAGCTGTCCCTTCTGTGCCCCCTAACTGACGAGTCCGCCCTATGCCCTGACC 4324
QY 284 ----- 284
Db 4325 CACCGGATCCAGCGGGCTTACGCCCTGGGGTACCCGACAGACGCCCTGACTCTGCCCTC 4384
QY 285 -----GlyProAlaAla 288
Db 4385 CCGACCGCGGCCACAGTACCCCAATTGGCTCTCTGTGCCCCCTGCCAGCCCGCTGCT 4444
QY 289 AlaProThrLeuSerProGluSerProAlaGlySerProAlaMetMetLeuGlnProGly 308
Db 4445 GCGCCACACTCTCGCCAGAGTCCCAAGCCGCGCTCGCCAGCATGATGCTGCAGCCGGGC 4504
QY 309 ProGlnLeuTyrAspValMetAspAlaValProAlaArgArgTrpLysGluPheValArg 328
Db 4505 CCGCAGCTCTACGACGTGATGGACGCGGCTCCCAAGCGCGCTGGAAGGAGTTCTGTCGC 4564
QY 329 ThrLeuGlyLeuArgGluAlaGluIleGluAlaValGluValGluIleGlyArgPheArg 348
Db 4565 ACCTGGGGCTGCGCGAGGCAAGATCGAAGCCGTGGAGTGAGATCGCGCTTCCGA 4624
QY 349 AspGlnGlnTyrGluMetLeuysArgTrpArgGlnGlnProAlaGlyLeuGlyAla 368
Db 4625 GACCAGCAGTACGAGATGCTCAAGCCTGGCGCCAGCAGACGCCCGGCGCTCGAGGCC 4684
QY 369 ValTyrAlaAlaLeuGluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArg 388
Db 4685 GTTACGCGGGCCCTGAGCGCATGGGGCTTGACGGCTGCTGGAAGACTTGCGCAGCCGC 4744
QY 389 LeuGlnArgGlyPro 393
Db 4745 CTGCAGCGCGGCCG 4759

Search completed: April 6, 2003, 16:52:30
Job time : 436.927 secs

26

THIS PAGE BLANK (USPTO)

GenCore version 5.1.4_p5-4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 6, 2003, 21:08:18 ; Search time 149.643 Seconds
(without alignments)
2303.655 Million cell updates/sec

Title: US-09-993-234-6_COPY_25_417

Perfect score: 2209
Sequence: 1 QGTRSPRCDCAGDFHKKIG.....ERMGLDGCVEDLRSRLQRP 393

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Dgapop 6.0 , Delext 7.0

Searched: 593429 seqs, 438583890 residues

Total number of hits satisfying chosen parameters: 1186858

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ .p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US09993234/runat_27032003_115459_15466/app_query.fasta_1.2346
-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bites -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09993234_@CGN_1_1_249_@runat_27032003_115459_15466
-NCPU=6 -ICPU=3 -NO_XLPHY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2209	100.0	1254	10	US-09-333-966-3
2	2209	100.0	1634	9	US-10-081-280-9
3	2209	100.0	1634	9	US-10-112-793-9
4	2209	100.0	1634	9	US-10-112-193-11

5	2209	100.0	1634	10	US-09-993-234-9	Sequence 9, Appl1
6	2209	100.0	1783	10	US-09-333-966-1	Sequence 1, Appl1
7	2140.5	96.9	1743	9	US-09-954-531-1389	Sequence 1389, Ap
8	1498.5	67.8	10797	9	US-10-092-154-1577	Sequence 1577, Ap
9	1498.5	67.8	10797	10	US-09-764-847-1577	Sequence 1577, Ap
10	957.5	43.3	816	10	US-09-964-824A-292	Sequence 292, App
11	952	43.1	1438	9	US-10-081-280-5	Sequence 5, Appl1
12	952	43.1	1438	9	US-10-112-793-5	Sequence 5, Appl1
13	952	43.1	1438	9	US-10-112-193-5	Sequence 5, Appl1
14	952	43.1	1438	10	US-09-884-733-5	Sequence 5, Appl1
15	952	43.1	1438	10	US-09-993-234-5	Sequence 5, Appl1
16	666	30.1	433	9	US-10-081-280-2	Sequence 2, Appl1
17	666	30.1	433	9	US-10-112-793-2	Sequence 2, Appl1
18	666	30.1	433	9	US-10-112-193-2	Sequence 2, Appl1
19	666	30.1	433	10	US-09-884-733-2	Sequence 2, Appl1
20	666	30.1	433	10	US-09-993-234-2	Sequence 2, Appl1
21	383.5	17.4	2130	10	US-09-917-800A-1601	Sequence 1601, Ap
22	383.5	17.4	2440	10	US-09-970-532-1	Sequence 1, Appl1
23	369.5	16.7	2173	9	US-09-898-234-14	Sequence 14, Appl
24	369.5	16.7	2173	9	US-09-899-429A-24	Sequence 24, Appl
25	369.5	16.7	2173	9	US-09-792-356-14	Sequence 14, Appl
26	369.5	16.7	2173	10	US-09-899-422-14	Sequence 14, Appl
27	369	16.7	1368	9	US-09-898-234-1	Sequence 1, Appl1
28	369	16.7	1368	9	US-09-899-429A-1	Sequence 1, Appl1
29	369	16.7	1368	9	US-09-792-356-1	Sequence 1, Appl1
30	369	16.7	1368	10	US-09-899-422-1	Sequence 1, Appl1
31	369	16.7	2111	10	US-09-880-107-2360	Sequence 2360, Ap
32	369	16.7	2141	9	US-09-898-234-16	Sequence 16, Appl
33	369	16.7	2141	9	US-09-899-429A-26	Sequence 26, Appl
34	369	16.7	2141	9	US-09-792-356-16	Sequence 16, Appl
35	369	16.7	2141	10	US-09-899-422-16	Sequence 16, Appl
36	369	16.7	2175	12	US-10-120-397-1	Sequence 1, Appl1
37	330	14.9	191	9	US-09-796-692-2549	Sequence 2549, Ap
38	256	11.6	1334	9	US-09-898-234-11	Sequence 11, Appl
39	256	11.6	1334	9	US-09-792-356-11	Sequence 11, Appl
40	256	11.6	1334	10	US-09-899-422-11	Sequence 11, Appl
41	255	11.5	1334	9	US-09-899-429A-21	Sequence 21, Appl
42	229	10.4	1704	12	US-10-020-787-1	Sequence 1, Appl1
43	226.5	10.3	1724	10	US-09-924-231-1	Sequence 1, Appl1
44	226.5	10.3	1724	10	US-09-934-289A-14	Sequence 14, Appl
45	216.5	9.8	1834	10	US-09-934-289A-41	Sequence 41, Appl

ALIGNMENTS

RESULT 1
US-09-333-966-3
Sequence 3, Application US/09333966

Patent No. US20020009773A1
GENERAL INFORMATION:

APPLICANT: Yu, Guo-Liang
APPLICANT: Ni, Jian
APPLICANT: Dixit, Vishva
APPLICANT: Gentz, Reiner L.
APPLICANT: Dillon, Patrick J.
TITLE OF INVENTION: Death Domain Containing Receptors
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/333,966
FILING DATE:
CLASSIFICATION:

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/815,469
; FILING DATE:
; APPLICATION NUMBER: No. US2002000973A1 yet Assigned
; FILING DATE: 06-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,711
; FILING DATE: 17-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,285
; FILING DATE: 12-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Steife, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1254 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1251
; US-09-333-966-3

Alignment Scores:
Pred. No.: 9.64e-190 Length: 1254
Score: 2209.00 Matches: 393
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-993-234-6_COPY_25_417 (1-393) x US-09-333-966-3 (1-1254)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGly 20
Db 73 CAGGGCGGCACTCGTACGCCCCAGGCTGTGACTGTGCGGGTGACTTCCACAGAGATTGGT 132
QY 21 LeuPheCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
Db 133 CTGTTTGTTCAGAGGCTGCCAGCGGGGCACTTGAAGCCCCCTTGCACGAGCCCC 192
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db 193 TCGGCAACTCCACTGCCCTTGTGTGTCGCCAAGACACCTTCTTGCGCTGGAGAACAC 252
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluAlaSerGlnValAlaLeu 80
Db 253 CATAAATTCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCTCCACAGGTGGCGCTG 312
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTyrPheValGlu 100
Db 313 GAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGGCTGTAAGCCAGGCTGGTTTGTGAG 372
QY 101 CysGlnValSerGlnCysValSerSerSerProPheTyrCysGlnProCysLeuAspCys 120
Db 373 TGGCAGGTACGCCAATGTGTACAGCACTTCAACCTTCTACTGCCAACCAATGCTAGACTGC 432
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 433 GGGGCGCTGCACCGCCACACAGGCTACTCTGTCCCGCAGAGATACTGACTGTGGACC 492
QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db 493 TGCCTGCGCTGCTTATGAACATGGCGATGGCTGCGTGTCTGCCCCACGAGACCCCTG 552
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTyrPargGlnMetPheTrpValGln 180
```

```

Db 553 GGAGCTGTCCAGAGCGCTGTGCCGCTGTCTGTGGCTGAGGCGAGATGTCTGGGTCCAG 612
QY 181 ValLeuAlaGlyLeuValValProLeuLeuLeuGlyAlaThrLeuThrTyrThrTyr 200
Db 613 GTGCTCTGGCTGGCCTGTGTGTGTCCTCCCTCTGCTGTGGGGCCACCTGACCTACACATAC 672
QY 201 ArgHisCysTrpProHisLysProLeuValThrAlaAspGluAlaGlyMetGluAlaLeu 220
Db 673 CGCCACTGTGGCTGCCTCACAGACCCCTGTACTGCAGATGAAGCTGGATGAGAGCTCTG 732
QY 221 ThrProProProAlaThrHisLeuSerProLeuAspSerAlaHisThrLeuAlaPro 240
Db 733 ACCCCACCAACCGGCCACCATCTGTCAACCTTGACACAGCCACACCTTCTAGACCT 792
QY 241 ProAspSerSerGluLysIleCysThrValGlnLeuValGlyAsnSerTrpThrProGly 260
Db 793 CCTGACAGCAGTGAGAAGATCTGCACCGTCCAGTTGGTGGTAAACAGCTGAGACCCCTGAC 852
QY 261 TyrProGluThrGlnGluAlaLeuCysProGlnValThrTrpSerTrpAspGlnLeuPro 280
Db 853 TACCCCGAGACCCAGAGAGCGCTGTGCCCGCAGAGTGACATGTCCTGGAGCACGTTGCC 912
QY 281 SerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSerProAlaGlySer 300
Db 913 AGCAGAGCTCTTGCCCGCTGTGCTGCGCCACACACTCTGCGCAAGATGCCACGCGCTCG 972
QY 301 ProAlaMetMetLeuGlnProGlyProGlnLeuTyrAspValMetAspAlaValProAla 320
Db 973 CCAGCATGATGCTGCAGCGCGGCGCCGACGCTCTACGACGTGATGACGCGGCTGCCAGCG 1032
QY 321 ArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGluAlaGluAlaVal 340
Db 1033 CGGCGCTGGAAGAGATTCGTGCGCACGCTGGGCTGCGCGAGCAGAGATGAGCCGCTG 1092
QY 341 GluValGluIleGlyArgPheArgAspGlnGlnTyrGluMetLeuLysArgTrpArgGln 360
Db 1093 GAGGTGAGATCGCGCGCTTCCGAGACACAGCAGACAGATGATGCTCAAGCGCTGCGCCAG 1152
QY 361 GlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMetGlyLeuAspGly 380
Db 1153 CAGCAGCCCGCGGCTCGGAGCCGTTTACGCGCGCTTGAGCGCATGGGCTGAGACGGC 1212
QY 381 CysValGluAspLeuArgSerArgLeuGlnArgGlyPro 393
Db 1213 TCGGTGAAGACTTGCAGCAGCCGCTGCAGCGCGCGCCG 1251

RESULT 2
US-10-081-280-9
; Sequence 9, Application US/10081280
; Patent No. US20020165157A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/081,280
; FILING DATE: 21-Feb-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/829,270
```

FILING DATE: 31-Mar-1997
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5416
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1634 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-081-280-9

Alignment Scores:
Pred. No.: 1.31e-189 Length: 1634
Score: 2209.00 Matches: 393
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-993-234-6_COPY_25_417 (1-393) x US-10-081-280-9 (1-1634)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
DB 161 CAGGCGCGCACTCGTAGCCCGAGGTGTGACTGTGCCGCTGACTTCCACAAGAAGATTGGT 220
QY 21 LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
DB 221 CTGTTTGTGACAGAGGCTGCCAGCGGGGCACTACCTGAAGGCCCTTGACGAGACCC 280
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
DB 281 TGGCGCACTCCACCTGCTGTGTGTCCCAAGACACCTTCTTGCGCTGGAGAACCCAC 340
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
DB 341 CATTAATTCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCTCCAGGTGGCGCTG 400
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
DB 401 GAGAACTGTTCAGCAGTGGCGGCAACCCGCTGTGCTGAAGCCAGGCTGTTGTGAG 460
QY 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120
DB 461 TGGCAGGTCAAGCAATGTGTACAGACTTCTACTGCAACCATGCTAGACTGC 520
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
DB 521 GGGGCCCTGCACCGCCACACAGGCTACTCTGTCCCGCAGAGATACTGACTGTGGGACC 580
QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
DB 581 TGCCTGCTGGCTTCTATGAACATGGCGATGGCTGCTGCTGCCCCACGAGCACCCTG 640
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTyrPargGlnMetPheTrpValGln 180
DB 641 GGGAGCTGTCCAGAGCGGTGTGCCCTGTGTGGCTGGAGGAGATGTCTGGGTCCAG 700
QY 181 ValLeuLeuAlaGlyLeuValValProLeuLeuGlyAlaThrLeuThrTyrThrTyr 200
DB 701 GTGCTCCTGGCTGGCTTGTGTGTCCTCTCTGCTGGGCGCCACCTGACCTACACATAC 760
QY 201 ArgHisCysTrpProHisLysProLeuValThrAlaAspGluAlaGlyMetGluAlaLeu 220
DB 761 CGGCACTGCTGGCTCACAAGCCCTGGTTACTGCAGATGAAGCTGGGATGAGGCTCTG 820
QY 221 ThrProProAlaThrHisLeuSerProLeuAspSerAlaHisThrLeuLeuAlaPro 240

DB 821 ACCCCACACCGGCCACCATCTGTACCCCTTGACAGCGCCACACCTTCTAGCACCT 880
QY 241 ProAspSerSerGluLysIleCysThrValGlnLeuValGlyAsnSerTrpThrProGly 260
DB 881 CCTGACAGCAGTGAGAAGATCTGCACCCGCTCCAGTTGGTGGTAAACAGCTGACCCCTGGC 940
QY 261 TyrProGluThrGlnGluAlaLeuCysProGlnValThrTrpSerTrpAspGlnLeuPro 280
DB 941 TACCCCGAGACCCAGGAGCGCTCTGCCCGCAGGTGACATGTGTCTGGAGACCAGTTGCC 1000
QY 281 SerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSerProAlaGlySer 300
DB 1001 AGCAGAGCTCTTGGCCCGCTGTGCGCCACACTCTCGCCAGAGTCCACAGCCGCTCG 1060
QY 301 ProAlaMetLeuLeuGlnProGlyProGlnLeuTyrAspValMetAspAlaValProAla 320
DB 1061 CCAGCCATGATGTGTGACAGCGCGGCCGCTCTACGACGTGATGAGACCGGCTCCAGCG 1120
QY 321 ArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGluAlaGluIleGluAlaVal 340
DB 1121 CGGCGCTGAGAGAGTTCGTGCCGACAGCTGGGGCTGCGCGAGGCGAGACATCGAAGCCGTG 1180
QY 341 GluValGluIleGlyArgPheArgAspGlnGlnTyrGluMetLeuLysArgTrpArgGln 360
DB 1181 GAGGTGAGATCGGCCGCTTCCGAGACCAAGACTAGAGATGCTCAAGCGCTGGCGCCAG 1240
QY 361 GlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMetGlyLeuAspGly 380
DB 1241 CAGCAGCCCGCGGCTCGGAGCGCTTTCAGCGCGCCCTGAGCGCGCATGGGCGCTGACGCG 1300
QY 381 CysValGluAspLeuArgSerArgLeuGlnArgGlyPro 393
DB 1301 TGCCTGGAAGCTTGCAGCGCCGCTGCAGCGCGCGCCG 1339

RESULT 3
US-10-112-793-9
: Sequence 9, Application US/10112793
: Publication No. US20020192729A1
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi J.
: TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
: NUMBER OF SEQUENCES: 28
: CORRESPONDENCE ADDRESS:
: ADDRESS: Genentech, Inc.
: STREET: 1 DNA Way
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Winpatin (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/10/112,793
: FILING DATE: 28-Mar-2002
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/828,683A
: FILING DATE: 31-Mar-1997
: APPLICATION NUMBER: 08/625328
: FILING DATE: 1-Apr-1996
: APPLICATION NUMBER: 08/710802
: FILING DATE: 23-Sep-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Marschang, Diane L.
: REGISTRATION NUMBER: 35,600
: REFERENCE/DOCKET NUMBER: P1007P1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650/225-5416
: TELEFAX: 650/952-9881

Score: 2209.00 Matches: 393
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-993-234-6_COPY_25_417 (1-393) x US-10-112-193-11 (1-1634)

OY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
Db 161 CAGGGCGGCACTCGTAGCCCAAGGTGTGACTGTGCGGTGACTTCCACAAGAAGATTGGT 220
OY 21 LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
Db 221 CTGTTTGTGTGACAGAGCGTGGCCAGCGGGGCACTACCTGAAGGCCCTTGACAGGAGCCC 280
OY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db 281 TGGCGCACTCCACCTGCTGTGTGTCACCAAGACACCTTCTGGCCCTGGAGAACCCAC 340
OY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db 341 CATATTTCTGAATGTGCCCGCTGCCAGGCCCTGTGATGAGCAGCCCTCCAGGTGGCGCTG 400
OY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
Db 401 GAGAACTGTTTCAGCAGTGGCCGACACCCGCTGTGGTGTAAAGCCAGGCTGGTTGTGAG 460
OY 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120
Db 461 TGGCAGGTCAAGCAATGTGTAGCAGTTACACCTTCTACTGCCAACCATGCTAGACTGC 520
OY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 521 GGGGCCCTGCACCGCCACACAGGCTACTCTGTCCCGCAGAGATACTGACTGTGGGACC 580
OY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db 581 TGCCTGCTGGCTTCTATGAACTGGCGATGGCTGCTGCTGCCCCACGAGCACCCCTG 640
OY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArgGlnMetPheTrpValGln 180
Db 641 GGGAGCTGTCCAGAGCGGTGTGCGCTGTGTGGTGAGCAGATGTTCTGGGTCCAG 700
OY 181 ValLeuLeuAlaGlyLeuValValProLeuLeuGlyAlaThrLeuThrTyrThrTyr 200
Db 701 GTGCTCTGTGGCTGGCTGTGTGTGCTCCCTGCTGTGGGCCACCTGACCTACACATAC 760
OY 201 ArgHisCysTrpProHisLysProLeuValThrAlaAspGluAlaGlyMetGluAlaLeu 220
Db 761 CGCCACTGTGCTGCCTCACAGCCCTGCTTACTGCAGATGAAGCTGGATGGAGGCTCTG 820
OY 221 ThrProProProAlaThrHisLeuSerProLeuAspSerAlaHisThrLeuLeuAlaPro 240
Db 821 ACCCCACCAACCGGCCACCACTGTGTACACCTTGACAGCGCCCAACCCCTTCTAGCACCT 880
OY 241 ProAspSerSerGluLysIleCysThrValGlnLeuValGlyAsnSerTrpThrProGly 260
Db 881 CTTGACAGCAGTAGAAGATGTGCACCTCCAGTTGTGGTAAACAGCTGGAGCCCTGTGC 940
OY 261 TyrProGluThrGlnGluAlaLeuCysProGlnValThrTrpSerTrpAspGlnLeuPro 280
Db 941 TACCCCGAGAGCCAGAGCGGTGTGCGCGAGGTGACATGTCTCTGGGACAGTGGCCC 1000
OY 281 SerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSerProAlaGlySer 300
Db 1001 AGCAGAGCTCTTGGCCCGGTGTGCGCCACACTCTGCGCAGAGTCCCGAGCGGCTCG 1060
OY 301 ProAlaMetMetLeuGlnProGlyProGlnLeuTyrAspValMetAspAlaValProAla 320
Db 1061 CCAGCCATGATGCTGCAGCGCGCGCCGACAGCTCTACGACGTGATGGACGCGGCTCCAGCG 1120
OY 321 ArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGluAlaGluIleGluAlaVal 340

Db 1121 CGGCGCTGGAAGAGTTCGTGCGCAGCTGGGGCTGCGCGAGGCGAGATCGAAGCCGTG 1180
OY 341 GluValGluIleGlyArgPheArgAspGlnGlnTyrGluMetLeuLysArgTrpArgGln 360
Db 1181 GAGGTGAGATCGGGCGCTTCCGAGACAGCAGTAGTACGATGCTCAAGCCCTGCGCCAG 1240
OY 361 GlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMetGlyLeuAspGly 380
Db 1241 CAGCAGCCCGGGCCCTCGAGGCCGTTTACGGCGCCCTGAGAGCGCATGGGGCTGAGCGGC 1300
OY 381 CysValGluAspLeuArgSerArgLeuGlnArgGlyPro 393
Db 1301 TGGTGGAGACTTGGCAGCGCGCTTGCAGCGCGGCCG 1339

RESULT 5

US-09-993-234-9
Sequence 9, Application US/09993234
Patent No. US20020146768A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
City: South San Francisco
STATE: California
COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 Inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/993,234
FILING DATE: 19-No. US20020146768A1-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/828,683
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:

NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007P1
TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-5416
TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 1634 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-09-993-234-9

Alignment Scores:

Pred. No.: 1.31e-189 Length: 1634
Score: 2209.00 Matches: 393
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-993-234-6_COPY_25_417 (1-393) x US-09-993-234-9 (1-1634)

OY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
Db 161 CAGGGCGGCACTCGTAGCCCAAGGTGTGACTGTGCGGTGACTTCCACAAGAAGATTGGT 220

Db 303 CAGGGCGGCACTCGTAGCCCCAGGTGTGACTGTGCCGGTGACTTCCACAGAAGATTGGT 362
QY 21 LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
Db 363 CTGTTTGTGTGCAGAGGCTGCCAGCGGGGCACTACCTGAAGGCCCTTGACAGGAGCCC 422
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db 423 TCGGGCAACTCCACCTGCTTGTGTGTCCCAAGACACCTTCTTGCGCTGGAGAACCAAC 482
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db 483 CATAAATTCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCTCCAGAGTGGCGCTG 542
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
Db 543 GAGAACTGTTCAAGAGTGGCGGACACCGGCTGTGGCTGTAAAGCCAGGCTGTTGTGAG 602
QY 101 CysGlnValSerGlnCysValSerSerSerProPheTyrCysGlnProCysLeuAspCys 120
Db 603 TGGCAGGTCAGCCAAATGTGTACAGAGTTCACCCCTTCTACTGCCAACCATGCGCTAGACTGC 662
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 663 GGGGGCCCTGCACCGCCACACAGGCTACTCTGTCCCGCAGAGATACTGACTGTGGAGCC 722
QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db 723 TGCCTGCTGGCTTCTATGAACATGGCGATGGCTGCGTCTGCCCCACAGACACCCCTG 782
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArgGlnMetPheTrpValGln 180
Db 783 GGGAGCTGTCCAGAGCGCTGTGCCCTGTCTGTGGCTGGAGCAGATGTCTGTGGTCCAG 842
QY 181 ValLeuLeuAlaGlyLeuValValProLeuLeuLeuGlyAlaThrLeuThrTyrThrTyr 200
Db 843 GTGCTCTGGCTGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 902
QY 201 ArgHisCysTrpProHisLysProLeuValThrAlaAspGluAlaGlyMetGluAlaLeu 220
Db 903 CGCCACTGCTGGCTCACAAGCCCCCTGTACTGCAGATGAAGCTGGGATGGAGCGCTCTG 962
QY 221 ThrProProAlaThrHisLeuSerProLeuAspSerAlaHisThrLeuLeuAlaPro 240
Db 963 ACCCCACCACCGGCCACCATCTGTCAACCTTGACAGCGCCACACCCCTTCTAGCACCT 1022
QY 241 ProAspSerSerGluLysIleCysThrValGlnLeuValGlyAsnSerTrpThrProGly 260
Db 1023 CTTGACAGCAGTAGAAGATGTCAACCGTCCAGTTGGTGTAAACAGCTGGACCCCTGGC 1082
QY 261 TyrProGluThrGlnGluAlaLeuCysProGlnValThrTrpSerTrpAspGlnLeuPro 280
Db 1083 TACCCCGAGACCCAGAGGGCTGTGCCCGCAGGTGACATGTCTCTGGGAGCAGTTGCC 1142
QY 281 SerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSerProAlaGlySer 300
Db 1143 AGCAGAGCTCTTGGCCCCGCTGTGCCCCACACTCTGCCCAGAGTCCCCAGCGGCTGC 1202
QY 301 ProAlaMetLeuLeuGlnProGlyProGlnLeuTyrAspValMetAspAlaValProAla 320
Db 1203 CCAGCCATGATGCTGCAGCGCGGCGCCGAGCTCTACGACGTGATGAGCGCGGTCCAGCG 1262
QY 321 ArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGluAlaGluIleGluAlaVal 340
Db 1263 CGGGCTGGAAGAGTTCTGTGCCACAGCTGGGGCTGCGCGAGCAGAGATCGAAGCCGCTG 1322,
QY 341 GluValGluIleGlyArgPheArgAspGlnGlnTyrGluMetLeuLysArgTrpArgGln 360
Db 1323 GAGGTGAGATCGCGCGCTTCCGAGACACAGCAGTACGAGATGCTCAAGCGCTGCGCCAG 1382
QY 361 GlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMetGlyLeuAspGly 380
Db 1383 CAGCAGCCCGCGGCGCTCGAGCGCTTACGCGGCGCTGAGCGCATGGGGCTGACGCGC 1442

QY 381 CysValGluAspLeuArgSerArgLeuGlnArgGlyPro 393
Db 1443 TGGGTGGAAGACTTGGCAGCGGCTTGCAGCGGCGCCG 1481
RESULT 7
US-09-954-531-1389
; Sequence 1389, Application US/09954531
; Patent No. US20020165180A1
; GENERAL INFORMATION:
; APPLICANT: weaver, Zoe
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C
; TITLE OF INVENTION: Gene Sets
; FILE REFERENCE: 689290-77
; CURRENT APPLICATION NUMBER: US/09/954,531
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: US/60/233,133
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,009
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,034
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,509
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US/60/234,567
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 1392
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1389
; LENGTH: 1743
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-531-1389
Alignment Scores:
Pred. No.: 2,01e-183 Length: 1743
Score: 2140.50 Matches: 389
Percent Similarity: 91.10% Conservative: 0
Best Local Similarity: 91.10% Mismatches: 4
Query Match: 96.90% Indels: 35
DB: 9 Gaps: 1
US-09-993-234-6_copy_25_417 (1-393) x US-09-954-531-1389 (1-1743)
QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
Db 141 CAGGGCGGCACTCGTAGCCCCAGGCTGTGACTGTGCCGGTACTTCCACAAGAAGATTGGT 200
QY 21 LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
Db 201 CTGTTTGTGTGCAGAGGCTGCCAGCGGGCACACTGAAGGCCCTTGACAGGAGCCC 260
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db 261 TGGGGCACTCCACCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 320
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db 321 CATAAATTCTGAATGTGCCCGCTGTGCCAGGCTGTGATGAGCAGGCGCTCCAGGTGGCGCTG 380
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
Db 381 GAGAACTGTTCAAGAGTGGCGGACACCGGCTGTGGCTGTAAAGCCAGGCTGTTGTGAG 440
QY 101 CysGlnValSerGlnCysValSerSerSerProPheTyrCysGlnProCysLeuAspCys 120
Db 441 TGGCAGGTCAGCCAAATGTGTACAGAGTTCACCCCTTCTACTGCCAACCATGCGCTAGACTGC 500
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 501 GGGGGCCCTGCACCGCCACACAGGCTACTGTGTCCCGCAGAGATACTGACTGTGGAGCC 560
QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160


```
|||||
Db 561 TGCTGCTGGCTTCTATGACATGCGGATGGCTGCTGCTGCCACGACACCTG 620
QY 161 glySerCysProGluArgCysAlaValCysGlyTyrParg----- 174
Db 621 GGGAGCTGTCCAGAGCGCTGCGGCTGTCTGTGGCTGGAGGCAAGTAGGTGTGCT 680
QY 174 ----- 174
Db 681 GGGATGCGCGTGGAGAACTGGGATGGACCGAGGGGAGCGGGTGAGAGCGGGCAAC 740
QY 175 -----GlnMetPheTyrValGlnValLeuAlaGlyLeu 186
Db 741 CACCCACACACCACACGCTGCTTCAAGTGTCTGGGTCCAGGTGCTGCTGGCTGCT 799
QY 187 ValValProLeuLeuLeuGlyAlaThrLeuThrTyrThrTyrArgHisCysTyrProHis 206
Db 800 GTGGTCCCCCTCTGCTTGGGGCCACCCCTGACCTACACATACCGCCACTGCTGGCTCAC 859
QY 207 LysProLeuValThrAlaAspGluAlaGlyMetGluAlaLeuThrProProProAlaThr 226
Db 860 AAGCCCCCTGTTACTGACAGATGAAGCTGGGATGAGGCTCTGACCCACACCGGCGCAC 919
QY 227 HisLeuSerProLeuAspSerAlaHisThrLeuLeuAlaProProAspSerSerGluLys 246
Db 920 CATCTGTACCCCTTGACAGCGCCACACCCCTTACACCTCTGACAGCAGTGAAG 979
QY 247 IleCysThrValGlnLeuValGlyAsnSerTyrThrProGlyTyrProGluThrGlnGlu 266
Db 980 ATCTGCACCGCTCAGTTGGTGTAAACAGCTGACCCCTGGCTACCCCGAGACCCAGAG 1039
QY 267 AlaLeuCysProGlnValThrTyrSerTyrPaspGlnLeuProSerArgAlaLeuGlyPro 286
Db 1040 GCGCTGCGCCCGCAGAGTGACATGGTCTCTGGGACACAGTTGCCACAGAGCTCTGGCCC 1099
QY 287 AlaAlaAlaProThrLeuSerProGluSerProAlaGlySerProAlaMetLeuGln 306
Db 1100 GCTGCTGCGCCACACTCTCGCAGAGTCCCGACCGGCTCGCCAGCATGATGCTGAC 1159
QY 307 ProGlyProGlnLeuTyrAspValMetAspAlaValProAlaArgTyrPlyGluPhe 326
Db 1160 CCGGGCCCGCAGCTCTACGACGTGATGACGCGGTCCCGACCGCGGCTGGAAGAGTTT 1219
QY 327 ValArgThrLeuGlyLeuArgGluAlaGluIleGluAlaValGluValGluIleGlyArg 346
Db 1220 GTGGCAGCGCTGGGGCTGCGGAGGCAAGATCGAAGCCGTGGAAGTGAATCGGTCTC 1279
QY 347 PheArgAspGlnGlnTyrGlnMetLeuLysArgTyrPargGlnGlnProAlaGlyLeu 366
Db 1280 TTCGAGACACAGCAGTACGAGTGTCAAGCACTGGCGCAGCAGCAGCGGCGCTC 1339
QY 367 GlyAlaValTyrAlaAlaLeuGluArgMetGlyLeuAspGlyCysValGluAspLeuArg 386
Db 1340 GGAGCGCTTACGCGCGCTGGAGCGCATGGGCTGAGCGCTGCGTGAAGACTGTGCG 1399
QY 387 SerArgLeuGlnArgGlyPro 393
Db 1400 AGCGCGCTGACAGCTGGCCG 1420
```

RESULT 8

```
US-10-092-154-1577
; Sequence 1577, Application US/10092154
; Publication NO. US20030054375A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009C1
; CURRENT APPLICATION NUMBER: US/10/092,154
; NUMBER OF SEQ ID NOS: 2003
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1577
```

```
; LENGTH: 10797
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-092-154-1577

Alignment Scores:
Pred. No.: 7.87e-125 Length: 10797
Score: 1498.50 Matches: 389
Percent Similarity: 28.46% Conservative: 0
Best Local Similarity: 28.46% Mismatches: 4
Query Match: 67.84% Indels: 978
DB: 9 Gaps: 8

US-09-993-234-6_COPY_25_417 (1-393) x US-10-092-154-1577 (1-10797)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGly 20
Db 5268 CAGGGCGCAGCTGTAGCCCCCAGAGGTGTACTGTGCGGTACTTCCACAGAAGATTGT 5327
QY 21 LeuPheCysCysArgGlyCysProAla----- 29
Db 5328 CTGTTTGTGTGACAGAGGCTGCCAGCGGGGTAAAGTGCCACAGGGGTGGAGAGCATGG 5387
QY 29 ----- 29
Db 5388 GCAGCGAGGCTGAGAGGTGCGGGCAGGCCCGGAGGTAAAGAGAGGCTGGCAGGGGA 5447
QY 29 ----- 29
Db 5448 GGTAGGGGTAGCTGACAGAGAAGTAGGAGCTGAGAGAAGAGGAGGAGGAGGAGG 5507
QY 29 ----- 29
Db 5508 TGGAAAGCAGGTGCGGGGTTGCTGGGACAGCCCTTGCTGCTGACCCCTGCTGTTTC 5567
QY 30 ----GlyHisTyrLeuLysAlaProCysThrGluProCysGlyAsnSerThrCysLeuVal 48
Db 5568 CACAGGGCAGCTACCTGAAGGCCCCCTTGCACGAGAGCCCTGGCGACACTGCCCTGTGT 5627
QY 48 ICysProGlnAspThrPheLeuAlaTyrGluAsnHisHisAsnSerGluCysAlaArgCys 68
Db 5628 GTGTCCCAAGACACTTCTTGGCTGGGAGAACCAACATAATTCTGAATGTGCCCGCTG 5687
QY 68 sGlnAlaCysAspGlu----- 73
Db 5688 CCAGGCGCTGATGACAGAGGTGAGGGGCTTCTCAGTGTGTCAGAGGAGTTCTTAAGGA 5747
QY 73 ----- 73
Db 5748 CAGGCTTCTGAAGGAAGTGGCTGCTGCGGCCAAACTTGGGGTGTGAGGCTCTGCA 5807
QY 73 ----- 73
Db 5808 CCCACCCCTTGCCAGAACCTCCACCCCTGATCTCTTCAAGGTGCCCTTGCCCTTCTCT 5867
QY 73 ----- 73
Db 5868 CTTCCTGTGACCTTCCCATCTCTCCATGTGCCCTTGCCCTTGAATCTCTG 5927
QY 73 ----- 73
Db 5928 AGCTTCTCTTTTAAAGGTAGCCCTGTACCTGTCTTCTTCCGCTAATTCTGTCTCC 5987
QY 73 ----- 73
Db 5988 ATTATCTTGGATATGCTCTGCTCTCTCCATGAGGAGCCCTTGGCCCTGACTACTCTCC 6047
QY 74 -----GlnAlaSerGlnValAlaLeuGluAsnCysSerAl 85
Db 6048 ACTCCCATCTCCCTGCAGACCCACACAGCC-TCCTCAGGTGGCGCTGAGAACTGTTCAGC 6106
QY 85 aValAlaAspThrArgCysGlyCysLysProGlyTyrPheValGluCysGlnValSerGlu 105
|||||
```


Db 6107 AGTGGCCGACACCCGCTGGCTGTAAAGCCAGGCTGGTTGTGAGTGCCAGGTACGCCA 6166
QY 105 ncysValserSerProphetylrcysglProCysleuaspCysglAlaLeuHisar 125
|||||
Db 6167 ATGTGTACAGAGTTACACCTTCTACTGCCAACCATGCTAGACTGGGGCCCTGCACCG 6226
QY 125 gh1ThrargLeuLeuCysSer----- 132
|||||
Db 6227 CCACACACGGCTACTCTGTGA-GTACCCCCACCCAGGGCTCTCTACTCCAGACCCCTT 6285
QY 132 ----- 132
Db 6286 CTCCCTGCCTGACCCACATCCTGTCCCATGGTGACGCATGCCCTCTCCGATTGCAGTTTC 6345
QY 133 -ArgArgAspThrAspCysglYthrCysleuProglYpHeTyrGlUHisGlyAspGlyCy 152
|||||
Db 6346 CCGCAGAGATACTACTGTGGGAACTGCCTGCCTGCTTCTATGAACATGGCGATGGCTG 6405
QY 152 sValSerCysProThrSer----- 158
|||||
Db 6406 CGTGTCTCTGCCCCACGTA-ATTCTAGCTGTCTGGGATGAGGGAAGGGCGCTGGGAG 6464
QY 158 ----- 158
Db 6465 CAGAGCAGGGCCCTGGGGTGGGCAAGTGTCTGCTGTTCAAGAATAGGAAGAGGGGATAG 6524
QY 158 ----- 158
Db 6525 GGAGGAGGAGCCTTGGCCCTGTGATGGGTGGGCCCCACTTCAGGCAAACTTAGATGCA 6584
QY 158 ----- 158
Db 6585 AAAGAGCAATCTGATCCGCTTAGCCAGATACATTAAGGTATTGCTTCACCTTCAGC 6644
QY 158 ----- 158
Db 6645 CAGCATTCCCCCAGCGATCCTAGCCAGATATTACAGATGATTTGTCACTTACACAGAGA 6704
QY 158 ----- 158
Db 6705 GTACATTTGATATAGCTTTAAACTTGGGCTGAAGAGGTTGAGGCTGCAGTGAGCTATG 6764
QY 158 ----- 158
Db 6765 ATCGTGCCACTGCACCTTCAGCCTGGGCAACAGAGCGACCTATTAAATAAATAATAA 6824
QY 158 ----- 158
Db 6825 TATTAAATCTATTAAATATTAAATATTAAATCTATTAAATAAATAACAAAGGCGTGA 6884
QY 158 ----- 158
Db 6885 GAGTCAGGACTGTGCTGTAGTCTCTTAGGGATCTTGGGCAAGTGACAGAATTGCGGT 6944
QY 158 ----- 158
Db 6945 CTCTGATGTGTGTCCCTTCTCAACATGGGATGTAGCAGCTAATTACAGGCCCTTT 7004
QY 158 ----- 158
Db 7005 GATCAGAGGTAAGGACTTCTCTAGCTATTCAAGTCTTTTTTTTTTTTTTTTTTTTTT 7064
QY 158 ----- 158
Db 7065 TTTTGTGAGATGAGACTTGTCTGTACCCAGGCTGAGTGCAGTGGCAGCATCTTGCT 7124
QY 158 ----- 158
Db 7125 CACTACAACCTCTGTGCTGGGTTCAAAGTATTCCTGCTCAGCCTCCCAAGTAGCT 7184
QY 158 ----- 158
Db 7185 GGGACTACAGAGCCACCAACCCCGGCTAATTTTTTTTGTATTTTATAGAGACGGG 7244

QY 158 ----- 158
Db 7245 GTTTCACCGTGTAGCCAAAGATGGTCTGATCACCTGACCTCGTGATCCACCGCCTTGG 7304
QY 158 ----- 158
Db 7305 CCTCCAAAGTGTGGATTACAGGATGAGCCACCGCGCGGCTCCATTCAGTCTT 7364
QY 158 ----- 158
Db 7365 TATTGAATATCTGCTATGTCTTACACACTGTTCTAGGTGCTGGGATGCAACAGGGACA 7424
QY 158 ----- 158
Db 7425 AAATAGCAAAATCCCTGTCTTTTGGGTTGACATTCTAGACTCTTCATGTAGTCTA 7484
QY 158 ----- 158
Db 7485 GAAGAGCTCAGTGAATAGTGTCTGTGTGTATTACCAGGACACAATGACAGAAATTC 7544
QY 158 ----- 158
Db 7545 TTGGGTAGAGTGAGAGCGCTGGGAGGGAAGGCTCTTAGATGAGACAGATGCTGGGA 7604
QY 158 ----- 158
Db 7605 GTCTTAGGGAGCCCTCCTGGCATGCACCCCTCATCCCTCAGGCCACCCCGTCCCTTG 7664
QY 159 -----ThrLeuGlySerCysProgluArgCysAlaAlaValCysGlyTrrArg----- 174
|||||
Db 7665 CAGGACACCCCTGGGAGCTGTCCAGAGCGCTGTGCCGTGTGTGTGGCTGGAGGCAGAG 7724
QY 174 ----- 174
Db 7725 TAGGTGTGTCTGGGAATGCGATGGGAGAACTGGGATGACCGAGGGGCGGTGA 7784
QY 175 -----GlnMetPheTrrValGlnValLe----- 182
|||||
Db 7785 GGAGGGGGCAACCACCAACCAACCAAGCTGCTTTCAGTG-TTCTGGGTCCAGGTGCT 7843
QY 182 uLeuAlaGlyLeuValValProLeuLeuGlyAlaTThrLeuThrTrrTrrArgH1 202
|||||
Db 7844 CCTGGCTGGCTTGTGTGCTCCCTGCTGCTTGGGCCACCCCTGACCTACACATACCGCCA 7903
QY 202 scysTrrProHisLysProLeuValThr----- 211
|||||
Db 7904 CTGCTGGCTCACAAAGCCCTGTGTTACTGTGAATACACACACACACACGACCCAGA 7963
QY 211 ----- 211
Db 7964 AGCTGGGGTCAAGATGGGTAGCCAGAGTCTACTCAACCTGTATACAGAAAGGAAACT 8023
QY 211 ----- 211
Db 8024 GAGGCAAGGAGTGTGGGTGACAGGAACCTTAGAGAGCTGTACCAAGCAGCCAGTCCA 8083
QY 212 -----AlaAspGluAlaGlyM----- 217
|||||
Db 8084 GGAGGCTTGCCGTGGCTGACCGCAATCTCTGTGTCTGTCAAGATGAAGCTGGGA 8143
QY 217 etGluAlaLeuThrProPro----- 223
|||||
Db 8144 TGGAGCTCTGACCCACCAACCGTAAAGAACCTCACTGTGTGATTTCTGGGCTGCCCTTCTG 8203
QY 223 ----- 223
Db 8204 GAGCTGAAGATCAAGCCTTACTATGATCCCTGGAGCTTGGCAGCGGGCCAGCAGCGGT 8263
QY 223 ----- 223
Db 8264 AGCCCTAGTGACAGAGGTGTGGGAGCAGAGTCATCAGTGAAGAGACGACAGCAGTGC 8323

Db 5928 AGCTTCTCTTTT TAGGGTAGCCCTGTACCTGTCTGTCTTCGCTATTCTGTCTCC 5987
QY 73 ----- 73
Db 5988 ATTATCTTGGATAATGCCCTGCTCCCTCCATGGAGCCCTTGGCCCTGACTAATCTCC 6047
QY 74 -----GlnAlaSerGlnValAlaLeuGluAsnCysSerAl 85
Db 6048 ACTCCCCATCTCCCTGCACCCCCACCAAGCC-TCCCAGGTGGCGCTGGAGAATCTTCAGC 6106
QY 85 aValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGluCysGlnValSerG 105
Db 6107 AGTGGCCGACACCCGCTGTGGCTGTAAGCCAGGCTGTTGTGGAGTGCACAGTCCAGCA 6166
QY 105 nCysValSerSerSerProPheTyrCysGlnProCysLeuAspCysGlyAlaLeuHisAr 125
Db 6167 ATGTGTCAGCAGTTCACCCCTTCTACTGCCAACCATGCTGACTGCGGGCCCTGCACCG 6226
QY 125 gHisThrArgLeuLeuCysSer----- 132
Db 6227 CCACACACGGCTACTCTGTGA-GTACCCCCACCCAGGCGCTCTACTCCACAGACCCCTT 6285
QY 132 ----- 132
Db 6286 CTCCCTGCCCTGACCCACTCCTGCCCATGGGTGACGCATGCCCTCTCCTGATTCAGGTTTC 6345
QY 133 -ArgArgAspThrAspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCy 152
Db 6346 CCGCAGAGATACTGACTGTGGGACCTGCTGCTGCTTCTATGAACATGGCGATGGCTG 6405
QY 152 sValSerCysProThrSer----- 158
Db 6406 CGTGTCTCTGCCCCACGTA-ATTCTAGCTGTCTGGTGGATGGAGGGAAGCGCGCTGGAG 6464
QY 158 ----- 158
Db 6465 CAGAGCAGGGGCTGGGTGGGCGAGGTGCTGCTGTTCAGGAATAGAAAGGGGATAG 6524
QY 158 ----- 158
Db 6525 GGAGAGGAGCCTTGCCCTGTGATGGGTGGGCCCACTTCAGGCAAACTTAGATGGCA 6584
QY 158 ----- 158
Db 6585 AAAGACCAATCTGGATCCGCCCTTAGCCAGATACATTAAGGGTATTGCCCTTCACTTTCAGC 6644
QY 158 ----- 158
Db 6645 CAGCATTCCTCCCGAGATCCTAGCCAGATATTACAGATGATTGTCACTTACACAGAGA 6704
QY 158 ----- 158
Db 6705 GTACATTTGATATAGCTTTAAACTTGGGCTGAAGGAGTTGAGGCTGCAGTGAATAG 6764
QY 158 ----- 158
Db 6765 ATCGTCCACTGCACCTTCAGCCCTGGGCAACAGAGCAGACCTATTAAATAAATAAA 6824
QY 158 ----- 158
Db 6825 TATTAAATCTATTAAATATTAAATCTATTAAATAAATAAATAAAGGCTGA 6884
QY 158 ----- 158
Db 6885 GAGTCAGACTGTGCTGTAGTTCCTAGGGGATCTTGGGCAAGTGCAGAGAATTGCGCT 6944
QY 158 ----- 158
Db 6945 CTCTGATGTGTGTCCCTTTCACACATGGGATGTTAGCAGCTAATTACAGGCCCTTT 7004
QY 158 ----- 158

Db 7005 GATCAGAGTAAGGACTTCTGTAGCTATTCAAGTCTTTTTTTTTTTTTTTTTTTT 7064
QY 158 ----- 158
Db 7065 TTTTGAATGAGACTTGTCTGTTCACCCAGGCTGAGTGCAGTGGCACGATCTTGCT 7124
QY 158 ----- 158
Db 7125 CACTACAACCTCTGCTGCCCTGGTTCAAGTATTCCTGCTCCTCAGCTCCCAAGTAGCT 7184
QY 158 ----- 158
Db 7185 GGGACTACAGAGACCCACCAACCCCGGCTAATTTTGTATTTTGTAGAGACGGG 7244
QY 158 ----- 158
Db 7245 GTTTCACCGTGTAGCCAAGATGGTCTTGATCACCCTGACCTCGTGATCCACCCGCTTGG 7304
QY 158 ----- 158
Db 7305 CCTCCCAAAGTCTGGGATTACAGGCATGAGCCACCGCGCGGCTCCATTCAAGTCTT 7364
QY 158 ----- 158
Db 7365 TATTGAATATCTCTATGTCTTACACACTGTCTAGGTGTGGGATGCAACAGGGGACA 7424
QY 158 ----- 158
Db 7425 AAATAGCAAAATCCCTGTCTTTTGGGTTGACATTCTAGTGACTTTCATGTAGTCTA 7484
QY 158 ----- 158
Db 7485 GAAGAAGTCAAGTGAATAGTGTCTGTGGTGTACCAGGACACAATGACAGAACAATTTC 7544
QY 158 ----- 158
Db 7545 TTGGGTAGACTGAGAGCCCTGGGAGGGAAGGCTCTTAGGATGAGACAGATGCTGGGA 7604
QY 158 ----- 158
Db 7605 GTCTTAGGAGCCCTCCTGGCATGACCCCTCATCCCTCAGGCCACCCCGTCCCTTG 7664
QY 159 -----ThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTrpArg----- 174
Db 7665 CAGAGCACCCCTGGGAGCTGTCCAGACGCTGTGCCGCTGTCTGTGCTGAGGCGAGAG 7724
QY 174 ----- 174
Db 7725 TAGGTGTGTGCTGGGAATGCGAGTGGGAGAACTGGGATGGACCGAGGGGAGCGGTGA 7784
QY 175 -----GlnMetPheTrpValGlnValLe 182
Db 7785 GGAGGGGGCAACCAACCAACACACCAAGCTGCTTTCAGTG-TTCTGGGTCCAGGTGCT 7843
QY 182 uLeuAlaGlyLeuValValProLeuLeuGlyAlaThrLeuThrTyrTrpArgH 202
Db 7844 CCTGGCTGGCTTGTGTCCCTCTCTGCTTGGGGCCACCTGACCTACACATACCGCCA 7903
QY 202 sCysTrpProHisLysProLeuValThr----- 211
Db 7904 CTGTGGCTTCACAAGCCCTGTACTGTGAAGTACACACACCAACACACACCAAGCA 7963
QY 211 ----- 211
Db 7964 AGCTGGGTCAGGATGGGTAGCCCAAGTCTACTCAACCCGTGATACAGAAAGGGAACCT 8023
QY 211 ----- 211
Db 8024 GAGCAGGAGTGTGGGTGCAGAGGAACCTAGAGAGCTGTACCAACCAAGGTCCA 8083
QY 212 -----AlaAspGluAlaGlyM 217
Db 8084 GGAGGCTTGCTGTGGCTGACCGCAATCTCTGTGTCTGTACGACAGATGAAGCTGGGA 8143

QY 217 etGlualaleuThrPro----- 223
Db 8144 TGGAGGCTCTGACCCACCACCGGTAGAACTCTACTGTGTGATCTGGGCTGCTTCTG 8203
QY 223 ----- 223
Db 8204 GAGCTGGAAGATCAAGCCTTACTATGATCCCTGGAGCTTGGACGCGCCAGCACCGGGT 8263
QY 223 ----- 223
Db 8264 AGCCCTAGTGAGACAGAGGTGTGGGAGACAGTCAATGAGATGAGACCAGACAGTGC 8323
QY 223 ----- 223
Db 8324 CTGCCCTCAAGGGGTGCTCAGTCACTGGAGTTCAGATTCGTACACAGAGCTAACAGTT 8383
QY 223 ----- 223
Db 8384 CAATGGAAGAGAGCCCATGTGCTGGGGGACAGAGAGAGAGCGGGGGGAGCGGAC 8443
QY 223 ----- 223
Db 8444 TCAAGGCAAGAGCAAGAGTCTGCTGGGCTACAGTGAAGCAGGCGCAACTGTGGAGGT 8503
QY 223 ----- 223
Db 8504 GTCATTCGGGGGTGTCTGCTGACTGAACCAAGGAGTGTCCCTCTGAGAGGCACTGC 8563
QY 224 -----Pro-Ala 225
Db 8564 GGCTAAGGGGCTTACTTGGCAAGCAGGGCTGACCTGGGGCCCTCTTGGCTTCCAGCC 8623
QY 226 ThrHisLeuSerProLeuAspSerAlaHisThrLeuLeuAlaProProAspSerSerGlu 245
Db 8624 ACCCATCTGTCAACCTTGGACAGCGCCACACACCTTCTAGCACCTCTGACAGCAGTGA 8683
QY 246 LysIleCysThrValGlnLeuValGlyAsnSerTrpThrProGlyTrpGlnThrGln 265
Db 8684 AAGATCTGACACCGTCCAGTGTGGTAAACAGCTGACACCCCTGGCTACCCCGAGACCCAG 8743
QY 266 GluAlaLeuCysProGlnValThrTrpSerTrpAspGlnLeuProSerArgAlaLeu--- 284
Db 8744 GAGCGCTCTGCCCGCAGGTACATGTGCTGGGACCAAGTTGCCAGAGCTCTTGGT 8803
QY 284 ----- 284
Db 8804 AAGGACATCAGTGCCTGAGGCTTGACCCCATTTCTCTGTCTGGGTGGGAAGTTGTG 8863
QY 284 ----- 284
Db 8864 GTTTCACAACGTGTCCCTTCTGCCCCCTAAGTACGAGAGTCCGCCCTATGCCCTGACC 8923
QY 284 ----- 284
Db 8924 CACCGGATCCAGCGGGCTTACGCCCTGGGGTAAACCGACAGACGCCCTGACTCTGCCTC 8983
QY 285 -----GlyProAlaAla 288
Db 8984 CCGACCGCGGGCCAGTACCCCAATGTGCTCTCTGCCCCCTGCCAGGCCCGCTGCT 9043
QY 289 AlaProThrLeuSerProGlnSerProAlaGlySerProAlaMetMetLeuGlnProGly 308
Db 9044 GCGCCACACTCTCGCCAGAGTCCCGCAGCGGCTCGCCAGCCATGATGCTGCAGCGGGC 9103
QY 309 ProGlnLeuTrpAspValMetAspAlaValProAlaArgArgTrpLysGlnPheValArg 328
Db 9104 CCGCAGCTCTACGACGTGATGAGCGGCTCCAGCGCGGCTGGAAGAGATTGTCGCGC 9163
QY 329 ThrLeuGlyLeuArgGluAlaGluIleGluAlaValGluValGluIleGlyArgPheArg 348
Db 9164 ACGTGGGGCTGCGCGAGGAGAGATCGAAGCCGTGAGGTGGAATCGGCCGCTTCCGA 9223

QY 349 AspGlnInTyRgluMetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAla 368
Db 9224 GACCAGCAGTACGAGATGTCTCAAGGCTGGCGCCAGACAGACGCCCGGCTCGAGACC 9283
QY 369 ValTyraAlaAlaLeuGluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArg 388
Db 9284 GTTACCGCGCCCTGGAGCGCATGGGGCTTGACGCGCTGCGTGAAGACTTGCAGACCCG 9343
QY 389 LeuGlnArgGlyPro 393
Db 9344 CTGACGCGGGCCCG 9358

RESULT 10

US-09-964-824A-292
; Sequence 292, Application US/09964824A
; Patent No. US20020102531A1
; GENERAL INFORMATION:
; APPLICANT: Horriqan, Stephen
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Sign
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-73
; CURRENT APPLICATION NUMBER: US/09/964, 824A
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/60/236, 033
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236, 032
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236, 028
; NUMBER OF SEQ ID NOS: 583
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 292
; LENGTH: 816
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-824A-292

Alignment Scores:
Pred. No.: 1.48e-77 Length: 816
Score: 957.50 Matches: 187
Percent Similarity: 72.66% Conservative: 7
Best Local Similarity: 70.04% Mismatches: 48
Query Match: 43.35% Indels: 26
DB: 10 Gaps: 4

US-09-993-234-6_copy_25_417 (1-393) x US-09-964-824A-292 (1-816)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGly 20
Db 57 CAGGGCGGCACTGCTAGACCCCGAGGTGACTGTGCGGGTGAAGTCCACAAGAAGATTGGT 116
QY 21 LeuPheCysSerArgGlyCysProAlaGlyHisTyRleuLysAlaProCysThrGluPro 40
Db 117 CTGTTTGTGGCAGAGGCTGCCAGCGGGCACTGAAAGGCCCTTGACAGGAGACC 176
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db 177 TCGGCAACTCCACTGCTGTGTGTGCCCAAGACACCTTCTTGCGCTGGGAGAACAC 236
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db 237 CATAAATCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCGCTCCAGGTGGCGCTG 296
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
Db 297 GAGAACTGTTCAGCAGTGGCGGACACCGGCTGTGGCTGTAAGCAGGCTGTTGTGAG 356
QY 101 CysGlnValSerGlnCysValSerSerProPheTyRcysGlnProCysLeuAspCys 120
Db 357 TGCAGGTCAAGCAATGTGTACAGAGTTCAACCTTCTACTGCAACCATGCTAGACTGC 416
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140

Db 417 GGGGCCCTGCACCGCCACACAGGCTACTCTGTTCGCCGACAGATACTGACTGTGGACC 476
QY 141 CysleuProglyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db 477 TGCCCTGCGCTGCTCTATGACATGGCGATGGCTGCGTGTCTGCCACGTAATTCCTA 536
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTyrPargln-MetPheTyrValG1 180
Db 537 -----GCTGTCTGGGATGGAGGGAAGGGCGGCTGGAGCA 572
QY 180 nValleuLeuAlaGlyLeuValValProLeuLeu-----LeuG1 193
Db 573 GAGCAGGGGACCTGGGTGGGCGAGTGTCTGTTCAGGAATAGGAAGAGGGGATAGG 632
QY 193 yAlaThrLeuThrTyrThrTyrArgHisCysTrpPro-----HisLysProLeuVa 210
Db 633 GAGG-----AGGAGCCCTTGGCCCTGTGATGGGTGGGCCCCACTTCA 674
QY 210 lThrAlaAspGluAlaGlyMetGluAlaLeuThrProProProAlaThrHisLeuSerPr 230
Db 675 GGCAACTTAGATGGCAA-AMGACAACTCTGATCCGCCCTTAGCCAGATACATAAGGTA 733
QY 230 oleuAspSerAlaHisThrLeuLeuAlaProProAspSerSerGluLysIleCysThyVa 250
Db 734 TTGCTCTTCACTTTCAGCCAGCAATTCGCCCCAGCGATCCTAGCCAGATATTACAGATGCT 793
QY 250 lGlnLeuValGlyAsnSer 256
Db 794 AACCTCTGTGCCGAATTC 812

RESULT 11
US-10-081-280-5
; Sequence 5, Application US/10081280
; Patent No. US20020165157A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/081,280
; FILING DATE: 21-Feb-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/829,270
; FILING DATE: 31-Mar-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1007R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5416
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1438 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-081-280-5

Alignment Scores:
Pred. No.: 8.98e-77 Length: 1438
Score: 952.00 Matches: 163
Percent Similarity: 93.71% Conservative: 1
Best Local Similarity: 93.14% Mismatches: 3
Query Match: 43.10% Indels: 8
DB: 9 Gaps: 1

US-09-993-234-6_COPY_25_417 (1-393) x US-10-081-280-5 (1-1438)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
Db 449 CAGGGCGCACCTCGTAGCCCCAGGTGTGACTGTGCCGGTGACTTCACCAAGAAGATTGGT 508
QY 21 LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
Db 509 CTGTTCCTGTGCAGAGGCTGCCACGGGGGCACTACCTGAAGGCCCTTGACAGGAGCC 568
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db 569 TGCGGCACTCCACCTGCTGTGTGTCCCAAGACACCTTCTGGCCTGGGAGAACCA 628
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db 629 CATATTCGATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCGCTCCAGGTGGCGCTG 688
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
Db 689 GAGACTGTTCAGCAGTGGCGCCGACACCCGCTGTGGCTGAAGCCAGGCTGTTGTGGAG 748
QY 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120
Db 749 TGCCAGGTGACCAATGTGTACAGATTCACCCCTTCTACTGCCAACCATGCTAGACTGC 808
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 809 GGGGCCCTGCACCGCCACACACAGGCTACTCTGTTCGCCGACAGATACTGACTGTGGACC 868
QY 141 CysLeuProglyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db 869 TGCCCTGCGCTCTCTATGACATGGCGATGGCTGCGTGTCTGCCACGTAATTCCTA 928
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTyrPargln 175
Db 929 -----GCTGTCTGGGATGGAGGGA 949

RESULT 12
US-10-112-793-5
; Sequence 5, Application US/10112793
; Publication No. US20020192729A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/112,793
; FILING DATE: 28-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,683A

FILING DATE: 31-Mar-1997
APPLICATION NUMBER: 08/625328
FILING DATE: 1-Apr-1996
APPLICATION NUMBER: 08/710802
FILING DATE: 23-Sep-1996
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1438 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-112-793-5

Alignment Scores:
Pred. No.: 8.98e-77 Length: 1438
Score: 952.00 Matches: 163
Percent Similarity: 93.71% Conservative: 1
Best Local Similarity: 93.14% Mismatches: 3
Query Match: 43.10% Indels: 8
DB: 9 Gaps: 1

US-09-993-234-6_COPY_25_417 (1-393) x US-10-112-793-5 (1-1438)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGly 20
DB 449 CAGGGCGGCACTCGTAGCCAGGTGTGACTGTGCCGGTGACTTCCACAGAAGATTGGT 508
QY 21 LeupheCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
DB 509 CTGTTTGTGTGACAGAGGCTGCCAGCGGGCAGTACTGAAGCCCCCTTGCACGAGGCC 568
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
DB 569 TCGGCACTCCACCTGCTGTGTGTCCCAAGACACTTCTTGCGCTGGAGAACAC 628
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
DB 629 CATATTCTGAATGTGCCCGCTGCCAGGCTGTGATGACAGGCTCCACAGGTGGCGCTG 688
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
DB 689 GAGAACTGTTCAGCAGTGGCCGACACACCCGCTGTGGCTGTAAAGCCAGGCTGGTGGAG 748
QY 101 CysGlnValSerGlnCysValSerSerSerProPheTyrCysGlnProCysLeuAspCys 120
DB 749 TGCAGGTCAAGCAATGTGTACAGAGTTCACCTTCTACTGCCAACCAATGCTAGACTGC 808
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
DB 809 GGGGCCCTGCACGCCACACACGCTACTCTGTCCCGCAGAGATACTGACTGTGGAGCC 868
QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
DB 869 TGCCTGCTGCTCTATGAACATGGCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTA 928
QY 161 GlySerCysProGluArgCysAlaValAlaCysGlyTrpArgGln 175
DB 929 -----GCTGTCTGTGGATGAGGGAA 949

RESULT 13
US-10-112-193-5
; Sequence 5, Application US/10112193
; Publication No. US20030004313A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.

TITLE OF INVENTION: Apo-3 POLYPEPTIDE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/112,193
FILING DATE: 28-Mar-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/928,069
FILING DATE: 11-Sep-1997
APPLICATION NUMBER: 60/026943
FILING DATE: 23-Sep-1996
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1052R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1438 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-112-193-5

Alignment Scores:
Pred. No.: 8.98e-77 Length: 1438
Score: 952.00 Matches: 163
Percent Similarity: 93.71% Conservative: 1
Best Local Similarity: 93.14% Mismatches: 3
Query Match: 43.10% Indels: 8
DB: 9 Gaps: 1

US-09-993-234-6_COPY_25_417 (1-393) x US-10-112-193-5 (1-1438)

QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGly 20
DB 449 CAGGGCGGCACTCGTAGCCAGGTGTGACTGTGCCGGTGACTTCCACAGAAGATTGGT 508
QY 21 LeupheCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
DB 509 CTGTTTGTGTGACAGAGGCTGCCAGCGGGCAGTACTGAAGCCCCCTTGCACGAGGCC 568
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
DB 569 TCGGCACTCCACCTGCTGTGTGTCCCAAGACACTTCTTGCGCTGGAGAACAC 628
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
DB 629 CATATTCTGAATGTGCCCGCTGCCAGGCTGTGATGACAGGCTCCACAGGTGGCGCTG 688
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
DB 689 GAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGCTGTAAAGCCAGGCTGGTGGAG 748
QY 101 CysGlnValSerGlnCysValSerSerSerProPheTyrCysGlnProCysLeuAspCys 120
DB 749 TGCAGGTCAAGCAATGTGTACAGAGTTCACCTTCTACTGCCAACCAATGCTAGACTGC 808

```

QY      121 GLYAlaLeuHISArgHISThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
      |||||||
Db      809 GGGGCCCTGCACCGCCACACACAGCGGTACTCTGTCCCGCAGAGATACTGACTGTGGAGCC 868

QY      141 CysLeuProGlyPheTyrgLuiHISGlyAspGlyCysValSerCysProThrSerThrLeu 160
      |||||||
Db      869 TGCGTCGCTGGCTCTATGACATGGCGATGGCTGCGTCTCCTGCCCGCAGTATTCCTA 928

QY      161 GlySerCysProGluArgCysAlaAlaValCysGlyTyrArgGln 175
      |||||
Db      929 -----GCTGTCGTGGATGAGGAA 949

RESULT 14
US-09-884-733-5
; Sequence 5, Application US/09884733
; Patent No. US20020123116A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-2 Ligand Inhibitor
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 Inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/884,733
; FILING DATE: 19-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/304,003
; FILING DATE: 14-JUNE-2000
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5416
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1438 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-884-733-5

Alignment Scores:
Pred. No.:      8.98e-77      Length:      1438
Score:          952.00      Matches:      163
Percent Similarity: 93.71%      Conservative: 1
Best Local Similarity: 93.14%      Mismatches: 3
Query Match:    43.10%      Indels:      8
DB:             10      Gaps:      1

US-09-993-234-6_COPY_25_417 (1-393) x US-09-884-733-5 (1-1438)
QY      1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHISLysLysIleGly 20
      |||||||
Db      449 CAGGGCGGCACACTCGTAGCCCCAGGTGTGACTGTGCCGGTGACTTCACAGAAAGATTGGT 508

QY      21 LeuPheCysCysArgGlyCysProAlaGlyHISLysTyrLeuLysAlaProCysThrGluPro 40
      |||||||
Db      509 CTGTTTGTGTGCAGAGGCTGCCCCAGGGGGGCACCTACCTGAAAGGCCCTTGACAGGAGCCC 568

```

```

QY      41  CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
         |||||||
Db      569  TGGCGCAACTCCACCTGCGCTGTGTGTCCCAAGACACACCTTCTTGCGCTGGAGAACCAC 628
QY      61  HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
         |||||||
Db      629  CATTAATTCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCGCTCCAGGTGGCGCTG 688
QY      81  GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
         |||||||
Db      689  GAGAACTGTTCAGCAGTGGCCGACACCGCTGTGGCTGTAAAGCCAGGCTGGTTGTGGAG 748
QY      101  CysGlnValSerGlnCysValSerSerProPheTrpCysGlnProCysLeuAspCys 120
         |||||||
Db      749  TGGCAGGTGACCAATGTGTACAGCAGTTCAACCTTCTACTGCCAACCAATGCTTACACTGC 808
QY      121  GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
         |||||||
Db      809  GGGGCGCTGCACCGCCACACAGGCTACTGTGTCCCGCAGAGATACTGACTGTGGACC 868
Db      869  TGGCTGCTGGCTTCTATGACATGGCGATGGCTGCGTGTCTGCCCCCAGCTAATTCCTA 928
QY      161  GlySerCysProGluArgCysAlaValCysGlyTrpArgGln 175
         |||||
Db      929  -----GCTGTCTGGATGGAGGAA 949

RESULT 15
US-09-993-234-5
; Sequence 5, Application US/09993234
; Patent No. US20020146768A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/993,234
; FILING DATE: 19-No. US20020146768A1-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/828,683
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1007P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5416
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1438 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-993-234-5

```

Alignment Scores:

Pred. No.:	8.98e-77	Length:	1438
Score:	952.00	Matches:	163
Percent Similarity:	93.71%	Conservative:	1
Best Local Similarity:	93.14%	Mismatches:	3
Query Match:	43.10%	Indels:	8
DB:	10	Gaps:	1

US-09-993-234-6_COPY_25_417 (1-393) x US-09-993-234-5 (1-1438)

```
QY      1  GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly  20
          |||||||
Db      449  CAGGGCGGCACACTCGTAGCCCCAGGTGTGACTGTGCCGGTGACTTCCACAGAAGATTGGT  508

QY      21  LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro  40
          |||||||
Db      509  CTGTTTGTGTGACAGAGGCTGCCAGCGGGGACACTACCTGAAGCCCCCTTGACAGGAGCCC  568

QY      41  CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis  60
          |||||||
Db      569  TCGGGCAACTCCACCTGCTGTGTGTCCCAAGACACCTTCTTGCGCTGGAGAACAC  628

QY      61  HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu  80
          |||||||
Db      629  CATTAATTCTGAATGTGCCCTGCCAGGCTGTGATGAGCAGGCCCTCCAGGTGGCGCTG  688

QY      81  GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu  100
          |||||||
Db      689  GAGAACTGTTCAGCAGTGGCGGACACACCCGCTGTGGCTGTAAAGCCAGGCTGTTGTGGAG  748

QY     101  CysGlnValSerGlnCysValSerSerSerProPheTyrCysGlnProCysLeuAspCys  120
          |||||||
Db      749  TGCCAGGTCAAGCCATGTGTGACAGATTCAACCCCTTCTACTGCCAACCATGCTAGACTGC  808

QY     121  GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr  140
          |||||||
Db      809  GGGGCCCTGCACCGCCACACAGGCTACTCTGTTCGCCAGAGATGACTGAGTGGAGCC  868

QY     141  CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu  160
          |||||||
Db      869  TGCCTGCCTGGCTTCTATGAACATGGCGATGGCTGTCTGCCGCCACGTAATTCCCTA  928

QY     161  GlySerCysProGluArgCysAlaAlaValCysGlyTrpArgGln  175
          |||||
Db      929  -----GCTGTCTGGGATGGAGGAA  949
```

Search completed: April 7, 2003, 03:58:32
Job time : 188.643 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 6, 2003, 16:19:54 ; Search time 2458.26 Seconds

(without alignments)
2589.161 Million cell updates/sec

Title: US-09-993-234-6_COPY_25_417

Perfect score: 2209

Sequence: 1 QGGTRSPRCDCAGDFHKKIG.....ERMGLDGCVEDLRSLQKGP 393

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL-frame+_p2n.model -DEV=xlh
-Q-/cgn2_1/USPTO_spool/US09993234/runat_27032003_115456_15362/app_query.fasta_1.2346
-DB-EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blissum62 -TRANS-human40.cdi -LIST=45
-DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09993234_cgn_1_1_4749_@runat_27032003_115456_15362 -NCPU=6 -ICPU=3
-NO_XLPHY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estln:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1423	64.4	1010	14	BQ068309
2	1211	54.8	698	9	AI807913
3	1179	53.4	681	10	BE563566
4	1166	52.8	767	13	BI909448
5	1090	49.3	632	10	AW268610
6	1082	49.0	651	13	BM009354
7	1066.5	48.3	647	14	BM794760
8	1026	46.4	688	9	AI424936
9	979	44.3	562	9	AI140043
10	968	43.8	539	12	BF726557
11	952	43.1	552	14	BM783972
12	952	43.1	585	10	AW517358
13	943	42.7	565	14	BM744307
14	937	42.4	514	14	BM756372
15	937	42.4	514	14	BM783979
16	932	42.2	492	14	BM741016
17	916	41.5	508	9	AI203624
18	893	40.4	488	14	BM770798
19	869.5	39.4	494	10	BE220347
20	839	38.0	673	13	BM251737
21	798.5	36.1	478	10	AW002222
22	781	35.4	427	12	BE696572
23	780.5	35.3	434	14	BM826048
24	698	31.6	439	14	BM824360
25	680	30.8	422	9	AI700459
26	666	30.1	433	14	HA1522
27	654	29.6	687	10	BE670189
28	639	28.9	572	10	BE668836
29	597.5	27.0	500	9	AA476747
30	591	26.8	432	14	N71143
31	560.5	25.4	345	14	BM853061
32	537	24.3	623	9	AI811528
33	518.5	23.5	443	14	HA6211
34	517	23.4	345	9	AA934992
35	486.5	22.0	372	14	W76376
36	479.5	22.7	435	10	AV664983
37	474.5	21.5	755	13	BI655045
38	472	21.4	587	9	AI380959
39	463	21.0	468	14	HA6374
40	455	20.6	633	10	BB212432
41	446	20.2	618	10	AW074008
42	445.5	20.2	582	10	AM182875
43	436.5	19.8	775	12	BG867742
44	420.5	19.0	322	9	AA971249
45	416	18.8	274	12	BF552058

ALIGNMENTS

RESULT 1	BQ068309	1010 bp	EST 02-APR-2002
LOCUS	AGENCOURT_6794093	NIH_MGC_121	Homo sapiens cDNA clone IMAGE:5770562
DEFINITION	5', mRNA sequence.		
ACCESSION	BQ068309		
VERSION	BQ068309.1	GI:19897355	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 1010)		
TITLE	NIH-MGC http://mgs.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)		

JOURNAL COMMENT

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12833 row: n column: 03
High quality sequence stop: 689.

FEATURES

source
1. .1010
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5770562"
/clone_lib="NIH_MGC_121"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH_MGC Library."
BASE COUNT 179 a 353 c 287 g 191 t
ORIGIN

Alignment Scores:

Pred. NO.: 3.45e-109 Length: 1010
Score: 1423.00 Matches: 257
Percent Similarity: 91.58% Conservative: 4
Best Local Similarity: 90.18% Mismatches: 13
Query Match: 64.42% Indels: 11
DB: 14 Gaps: 3

US-09-993-234-6_COPY_25_417 (1-393) x BQ068309 (1-1010)

QY 30 GLYHISTYRLLEULYSALAPROCYSTHRLUPROCYSGLYASNSETHRCYSLUVALCY 49
|||||
Db 50 GGGCACTACTGAGGCCCTTGACGAGGCCCTGCGCACTCCACCTGCTGTGTGT 109
QY 50 PROGLNAPTHRHELEUALATRPLUASNHISASNSETHRCYSLUVALCYSGLN 69
|||||
Db 110 CCCCAAGACACCTTCTTGCGCTGGAGAACCAATATCTGAATGTCGCCGCTGCCAG 169
QY 70 ALACYSASPLUGLINALASERGLNVALALALEUGLUASNYSSETHRALVALALASPTH 89
|||||
Db 170 GCCTGTGATGAGCAGGCCCTCCAGGTGGCGCTGGAGAACTGTTACAGCAGTGCCGACACC 229
QY 90 ARGCYSGLYCYSLYSPROGLYTRPHEVALGLUCYSGLNVALSERGLNYSVALSERSER 109
|||||
Db 230 CGCTGTGGCTGTAAGCCAGGCTGTTGTGAGTGCACAGGTCAATGTGTGACAGCAGT 289
QY 110 SERPROPHETRYCYSLNPROCYSLUASNPCYSGLYALALEUHNISARGHISTHARGLEU 129
|||||
Db 290 TCACCTTCTACTGCCAACCATGCTAGACTGCGGGCCCTGCACCGCCACACGCGCTA 349
QY 130 LEUCYSSERARGASPTHASPCYSGLYTHRCYSLUENPROGLYPHETRYGLUHNISGLY 149
|||||
Db 350 CTCTGTTCCTCCGACAGATACCTGAGCCTGCTGCTGCTCTATGAACATGGC 409
QY 150 ASPGLYCYVALSERCYSPROTHSERTHREUGLYSERCYSPROGLUARGCYSLAALA 169
|||||
Db 410 GATGCTGCGTGTCTGCTCCACGAGCACCCTGGGAGCTTCACAGAGCGCTGCTGCCGT 469
QY 170 VALCYSGLYTRPARGLMETPHETRYVALGLN-VALLEULEUALAGLYLEUVALPR 189
|||||
Db 470 GTCTGTGCTGAGG-----CAGAGTCTCTCTGCTGCGCTGTGTGCTGCC 514

QY 189 OLEULEULEUGLYALATHRLEUTHTRYTHRYARRGHISCYSTRPROHISLYSPROLE 209
|||||
Db 515 CCTCTGCTTGGGGCCACCCTGACCTACACATACCGCCACTGTGGCTCACAGGCCCT 574
QY 209 VALTHRALASPLUALAGLYMETGLUALALEUTHRPROPROALATHRHISLEUSE 229
|||||
Db 575 GGTTACTGCAGATGAAGCTGGATGAGGCTGTGACCCACACCGGCCACCATCTGTC 634
QY 229 RPROLEUASPSEALAHISTHREULEUALAPROPROASPSESERGLULYSILECYSTH 249
|||||
Db 635 ACCCTTGACAGCGCCACACCCCTTACACACCTCTGACACAGCAGTAGAGATCTGCAC 694
QY 249 RVALEGLNLEUVALGLYASNSETHRTHRPROGLYTRYPROGLUTHRGLNGLUALALEUCY 269
|||||
Db 695 CGTCCAGTTGGTGGTACAGCTGAGACCCCTGGCTACCCCAAGACCCAGAGCGCTCTG 754
QY 269 SPROGLNVALTHRTPSERTRPASPGLNLEUPROSERARG--ALALEUGLYPROALAAL 288
|||||
Db 755 CCCGCAAGTAGACATGTCCTGGAGCAATTCGCCAGCAAGCTCTGCGCCCGCTGGC 814
QY 288 AALAPROTHRLEUSERPROGLUSERPROALAGLY-----SERPROALAMETME 304
|||||
Db 815 TGCGCCCAATTCCTTGCCAGAGTCCCGCAGCGCGGCTCGCCAGCCCATGTGATGCC 874
QY 304 TLEUGLNPROGLY 308
Db 875 TTGCCAACCCGGG 887

RESULT 2
AI807913
LOCUS

DEFINITION AI807913 698 bp mRNA linear EST 19-DEC-1999
IMAGE:2359204 3' similar to SW:WSL1_HUMAN Q93038 WSL-1 PROTEIN
PRECURSOR ;, mRNA sequence.

ACCESSION AI807913
VERSION AI807913.1 GI:5394479
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 698)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL COMMENT

Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1568 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 459.

FEATURES

source

1. .698
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2359204"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NbHL19W, testis NHT, and B-cell
NCI-CGAP_GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo."

```
BASE COUNT      111 a      218 c      214 g      155 t
ORIGIN
Alignment Scores:
Pred. No.:      1.22e-91      Length:      698
Score:          1211.00      Matches:      210
Percent Similarity: 95.02%      Conservative: 0
Best Local Similarity: 95.02%      Mismatches: 11
Query Match:      54.82%      Indels:      0
DB:              9      Gaps:      0

US-09-993-234-6_COPY_25_417 (1-393) x AI807913 (1-698)

QY      1  GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
Db      36  CAGGGGGGGGCTCGTATCCCGAGGTGTGACTGTGCCGGTACTTCCACAGAAGATGGT 95
QY      21  LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
Db      96  CTGTTTGTGTGACAGAGGCTGCCAGCGGGGCACTACTGAAGGCCCTTGACAGGAGCCC 155
QY      41  CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db      156  TCGGGCAACTCCACCTGCTGTGTGTCCCAAGACACCTTCTGGCCCTGGAGAACAC 215
QY      61  HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db      216  CATATACTTGATGTGCGCCGCTGCCAGGCTGTGATGAGCAGGCCCTCCAGGTGGCGCTG 275
QY      81  GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
Db      276  GAGAACTGTTCAGCAGTGGCCGACACACCCGCTGTGGCTGTAAAGCCAGGCTGTGTGAG 335
QY      101  CysGlnValSerGlnCysValSerSerSerProPheTyrCysGlnProCysLeuAspCys 120
Db      336  TGGCAGGTTCAGCCAAATGTGTGACGAGTTACACCTTCTACTGCCAACCATGCCCTAGACTGC 395
QY      121  GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db      396  GGGGCCCTGCACCGCCACACAGGGCTACTCTGTCCCGCAGAGATACTGACTGTGGGACC 455
QY      141  CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db      456  TGCCTGCCTGGCTTCTATGACATGGCGATGGCTGCGTCTGCTGCCTCAGCAGACCCCTG 515
QY      161  GlySerCysProGluArgCysAlaAlaValCysGlyTrpArgGlnMetPheTrpValGln 180
Db      516  TGGAGCTGTCCAGAGCGCTGTGCCGCTGTGTGTGGCTGGAGCAGATGTTCTGGGTGCAG 575
QY      181  ValLeuLeuAlaGlyLeuValValProLeuLeuGlyAlaThrLeuThrTyrThrTyr 200
Db      576  GTGCTCTGTGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 635
QY      201  ArgHisCysTrpProHisLysProLeuValThrAlaAspGluAlaGlyMetGluAlaLeu 220
Db      636  CTGCACTGTGGCTTCACATGCACGCTGTGACTGCAGATGAAGCTTGATGAGGCTGTG 695
QY      221  Thr 221
Db      696  ACT 698

RESULT 3
BE563566      681 bp      mRNA      linear      EST 15-AUG-2000
LOCUS      601334867F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3688721 5',
DEFINITION      mRNA sequence.
ACCESSION      BE563566
VERSION      BE563566.1 GI:9807286
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

```
REFERENCE      1 (bases 1 to 681)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cgabs-r@mail.nih.gov
              Tissue Procurement: ATCC
              cDNA Library Preparation: Ling Hong/Rubin Laboratory
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: L1CM382 row: f column: 18
              High quality sequence stop: 681.
              Location/Qualifiers
                1..681
                  /organism="Homo sapiens"
                  /db_xref="taxon:9606"
                  /clone="IMAGE:3688721"
                  /clone_11b="NIH_MGC_39"
                  /tissue_type="adenocarcinoma"
                  /lab_host="DH10B (phage-resistant)"
                  /note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
                  Site_2: EcoRI; cDNA made by oligo-dT priming.
                  directionally cloned into EcoRI/XhoI sites using the
                  following 5' adaptor: GGCACGAG(G). Library constructed
                  by Ling Hong in the laboratory of Gerald M. Rubin
                  (University of California, Berkeley) using ZAP-cDNA
                  synthesis kit (Stratagene) and Superscript II RT (Life
                  Technologies)."
```

```
BASE COUNT      110 a      236 c      220 g      115 t
ORIGIN
Alignment Scores:
Pred. No.:      5.69e-89      Length:      681
Score:          1179.00      Matches:      225
Percent Similarity: 99.12%      Conservative: 0
Best Local Similarity: 99.12%      Mismatches: 2
Query Match:      53.37%      Indels:      2
DB:              10      Gaps:      0

US-09-993-234-6_COPY_25_417 (1-393) x BE563566 (1-681)

QY      151  GlyCysValSerCysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaVal 170
Db      3  GGCTGCTGTCTGCCCCACGAGCACCCTGGGAGCTGTCCAGAGCGCTGTGCCGCTGTC 62
QY      171  CysGlyTrpArgGlnMetPheTrpValGlnValLeuLeuAlaGlyLeuValValProLeu 190
Db      63  TGTGGCTGGAGGCAGATGTTCTGGGTCCAGGTGCTCCTGGCTGGCTGTGTGTGTGTGTGT 122
QY      191  LeuLeuGlyAlaThrLeuThrTyrThrTyrArgHisCysTrpProHisLysProLeuVal 210
Db      123  CTGCTGGGGGCCACCCCTGACCTACATACCGCCACTGTGCTGCTGCACAAAGCCCTGTGTT 182
QY      211  ThrAlaAspGluAlaGlyMetGluAlaLeuThrProProProAlaThrHisLysSerPro 230
Db      183  ACTGCAGATGAAGCTGGATGGAGCTGTGACCCACACCGGCGCACCATCTGTACACC 242
QY      231  LeuAspSerAlaHisThrLeuLeuAlaProProAspSerSerGluLysIleCysThrVal 250
Db      243  TTGGACAGCGCCACACCTTCTAGACACCTCTGACAGCAGTGAAGATCTGCACCGTC 302
QY      251  GlnLeuValGlyAsnSerTrpThrProGlyTyrProGluTrpGlnGlnAlaLeuCysPro 270
Db      303  CAGTTGTGGGTAAACAGCTGACCCCTGGCTACCCCGAGAGACCAGGCGCTGTGCCCG 362
QY      271  GlnValThrTrpSerTrpAspGlnLeuProSerArgAlaLeuGlyProAlaAlaAlaPro 290
Db      363  CAGGTGACATGCTCTGGAGCACAGTTGCCACAGAGAGCTCTTGGCCCGCTGTGCGGCC 422
QY      291  ThrLeuSerProGluSerProAlaGlySerProAlaMetMetLeuGlnProGlyProGln 310
```

```
|||||
DB 423 ACACCTCGCCAGAGATCCCCAGCCGGCTCGCCAGCCATGATGCTGCAGCCGGCCCGCAG 482
QY 311 LeuTyrAspValMetAspAlaValProAlaArgArgTrpLysGluPheValArgThrLeu 330
DB 483 CTCTACGACGTGATGACGCGGCTCCAGCCGCCCTGGAAGAGATTCTGTCGACACGCTG 542
QY 331 G1yleuArgGluAgluileGluAlaValGluValGluileGlyArgPheArgAspGln 350
DB 543 GGGCTGCGGAGGAGCAGATCGAAGCCCTGAGGTGAGATCGGCCCTTCGAGACACAG 602
QY 351 GlnTyrGluMetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyr 370
DB 603 CAGTACGAGATGCTCAAGCGCTGGCGCCAGCAGACCCCGG-GGCCCTCGAGCCGTTTAC 661
QY 371 AlaAlaLeuGluArgMetGly 377
DB 662 GCGGC-CTGAGCGCATGGGG 681

RESULT 4
BI909448 767 bp mRNA linear EST 16-OCT-2001
LOCUS 603065172F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5214568 5',
DEFINITION mRNA sequence.
ACCESSION BI909448
VERSION BI909448.1 GI:16172666
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 767)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rt@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
plate: LLM11538 row: O column: 17
High quality sequence stop: 754.

FEATURES
source
1..767
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5214568"
/clone_lib="NIH_MGC_118"
/tissue_type="leukocyte"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6; site_1: NotI; site_2: EcoRV
(destroyed); RNA source leukocytes from anonymous pool of
non-activated adult donors. Library is oligo-dT primed
and directionally cloned (EcoRV site is destroyed upoh
cloning). Average insert size 1.7 kb, insert size range
1.2-3.3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(invitrogen). Research Genetics tracking code 027. Note:
this is a NIH_MGC Library."

BASE COUNT 122 a 243 c 241 g 161 t
ORIGIN

Alignment Scores: 8.32e-88 length: 767
Pred. No.: 1166.00 Matches: 213
Score: 97.71% Conservative: 0
Percent Similarity: 97.71% Mismatches: 3
Best Local Similarity: 52.78% Indels: 5
Query Match: 13 Gaps: 1
DB: 13
```

```
US-09-993-234-6_COPY_25_417 (1-393) x BI909448 (1-767)
QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
DB 109 CAGGGCGGCACTCGTAGACCCAGGTGTGACTGTGCCGGTGTGACTGTCCACAAGAATGGT 168
QY 21 LeuPheCysCysArgGlyCysProAla-GlyHisTyrLeuLysAlaProCysThrGluPr 40
DB 169 CTGTTTGTGTGAGAGAGGCTGCCAGCTGGGGCAGCTACCTGAAGGCCCTTGACGAGGCC 228
QY 40 ocysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnH 60
DB 229 CTGCGGCACTCCACCTGCTTGTGTGTCCTCCAAAGACACCTTCTTGCCCTGGGAGAACCA 288
QY 60 SHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAla 80
DB 289 CCATAAATCTGATGTGCCCCGCTGCCAGCCTGTGATGAGCAGGCCCTCCAGGTGGCGCT 348
QY 80 uGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValG 100
DB 349 GGAGAACTGTTTACGACAGTGCGCCGACACCCGCTGTGGCTGTAAAGCCAGGCTGTTTGA 408
QY 100 ucysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCy 120
DB 409 GTGCCAGGTGACGACAGTGTGTACAGACAGTTCACCTTCTACTGCCAACCATGCTAGACTG 468
QY 120 sGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyTh 140
DB 469 CGGGGCCCTGCACGCCACACACAGCGCTACTGTTCGCCGACAGAAATGACTGTGGAC 528
QY 140 rCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrle 160
DB 529 CTGCCCTCGCTGCTTATGACATGGCGATGGCTGCTGCTGCTGCCGCCACGACACCT 588
QY 160 uGlySerCysProGluArgCysAlaAlaValCysGlyTrpArgGlnMetPheTrpValG 180
DB 589 GGGGAGCTGTCCAGAGCGCTGTGCCGCTGTGTGGCTGAGGACAGATGTTCTGGTCCA 648
QY 180 nValLeuLeuAlaGlyLeuValValProLeuLeuLeuGlyAlaThrLeuThrTyrThrTy 200
DB 649 GGTGCTCTGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 707
QY 200 rArgHisCysTrpProHisLysProLeuValThrAlaAspGluAlaGlyMet 217
DB 708 CGC-CACTGCTGGCT-CACAAGCCCTGTGTTACT---GATGAAGCTGGGATG 754

RESULT 5
AW268610 632 bp mRNA linear EST 03-JAN-2000
LOCUS xv41b12.x1 Soares_NFL_T-GBC_S1 Homo sapiens cDNA clone
DEFINITION IMAGE:2815679 3' similar to SW:WSL1_HUMAN Q93038 WSL-1 PROTEIN
PRECURSOR ;, mRNA sequence.
ACCESSION AW268610
VERSION AW268610.1 GI:6655640
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 632)
AUTHORS NCI-CGAP http://www.nci.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rt@mail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Seq primer: -400P from Gibco
High quality sequence stop: 455.
```


FEATURES
source
Location/Qualifiers
1. 632
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2815679"
/lab_host="DH10B"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NBHL19W, testis NHT, and B-cell NCI-CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo."
BASE COUNT 102 a 194 c 192 g 143 t 1 others
ORIGIN
Alignment Scores:
Pred. No.: 1.49e-81 Length: 632
Score: 1090.00 Matches: 190
Percent Similarity: 94.06% Conservative: 0
Best Local Similarity: 94.06% Mismatches: 12
Query Match: 49.34% Indels: 0
DB: 10 Gaps: 0
US-09-993-234-6_COPY_25_417 (1-393) x AW268610 (1-632)
QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
Db 27 CAGGGCGGCACTCGTAGCCCGAGGTGTGACTGTGCCGTGACTTCCACAGAAGATTGCT 86
QY 21 LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
Db 87 CTGTTTGTGTGACAGAGCGTGGCCAGCGGGCACTACCTGAAGGCCCTTGCACGGAGCCC 146
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db 147 TGGGGCACTCCACCTGCTGTGTCTCCCAAGACACCTTCTGGCCCTGGAGAACAC 206
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db 207 CATTAATTCTGAATGTGCCCGCTGCCAGGCCGTGTGATGAGCAGGCCCTCCAGGTGGCGCTG 266
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
Db 267 GAGAACTGTTCAAGCAGTGGCCGACACCCGCTGTGGCTGAAGCCAGGCTGTTGTGGAG 326
QY 101 CysGlnValSerGlnCysValSerSerSerProPheTyrCysGlnProCysLeuAspCys 120
Db 327 TGGCAGGTCAAGCAATGTGTACAGCAGTACACCTTCTACTGCCAACATGACCTAGACTGC 386
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 387 GGGGCCCTGCACCGCCACACAGCGCTACTCTGTCCCGACAGATACTGACTGTGGAGCC 446
QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db 447 TGCCCTGCTGGCTTCTATGAACATGGCGATGGCTGTGTCTTCTGGCCACGAGCACACTG 506
QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArgGlnMetPheTrpValGln 180
Db 507 GGGAGCTGTGCAGAGCGCTGTGCTGTGTGGTGAGGACAGATGTTCTTGTTCAG 566
QY 181 ValLeuLeuAlaGlyLeuValValProLeuLeuGlyAlaThrLeuThrTyrThrTyr 200
Db 567 GTGCTCCCTGCTTGGCTGTGTCTCCCTACTGCTTGGAGGCATCTCTGAACATAACATAC 626
QY 201 ArgHis 202

Db 627 TGTAC 632
RESULT 6
BM009354
LOCUS
DEFINITION BM009354 651 bp mRNA linear EST 30-OCT-2001
603629813F1 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5443659 5',
mRNA sequence.
ACCESSION BM009354
VERSION BM009354.1 GI:16523708
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 651)
AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: DCTD/DTP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCM1921 row: 1 column: 04
High quality sequence stop: 649.
FEATURES
source
1. 651
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5443659"
/clone_lib="NIH_MGC_41"
/tissue_type="amelanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pOT87; Site_1: XhoI; Site_2:
/EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
BASE COUNT 107 a 224 c 204 g 116 t
ORIGIN
Alignment Scores:
Pred. No.: 7.29e-81 Length: 651
Score: 1082.00 Matches: 210
Percent Similarity: 98.14% Conservative: 1
Best Local Similarity: 97.67% Mismatches: 2
Query Match: 48.98% Indels: 4
DB: 13 Gaps: 0
US-09-993-234-6_COPY_25_417 (1-393) x BM009354 (1-651)
QY 142 LeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeuGly 161
Db 4 CTGCCCTGGCTTCTATGAACATGGCGATGGCTGCGTGTG-TGCCACAGACACCTGGGG 62
QY 162 SerCysProGluArgCysAlaAlaValCysGlyTrpArgGlnMetPheTrpValGlnVal 181
Db 63 AGCTGTCCAGAGCGCTGTGCCCTGTGTGTGGCTGAGGACAGATGTTCTGGGTCCAGGTG 122
QY 182 LeuLeuAlaGlyLeuValValProLeuLeuGlyAlaThrLeuThrTyrThrArg 201
Db 123 CTCTGGCTGGCTTGTGTGCTCCCTCTGCTTGGGGCCACCTGACCTACACATACCGC 182
QY 202 HisCysTrpProHisLysProLeuValThrAlaAspGluAlaGlyMetGluAlaLeuThr 221

Db 183 CACTGTGGCCCTACAGAGCCCTGTTACTGCAGATGAAGCTGGATGAGGCTCTGACC 242
QY 222 PROPROAlaThrHisLeuSerProLeuAspSeraIaHisThrLeuAlaProPro 241
Db 243 CCACCACCGGC - ACCCATCTGTCCACCTTGGACAGCCACACACCTTCTAGACCTCCT 301
QY 242 AspSerSerGluValIleCysThrValGlnLeuValGlyAsnSerTrpThrProGlyTyr 261
Db 302 GACAGCAGTAGAGATCTGCACCGTCCAGTTGGTGGTAACAGCTGAGCCCTGGCTAC 361
QY 262 ProGluThrGlnGluAlaLeuCysProGlnValThrTrpSerTrpAspGlnLeuProSer 281
Db 362 CCCGAGACCCAGAGGCGCTCTGCCCGCAGGTGACATGCTCCTGGAGACAGTTGCCACGC 421
QY 282 ArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGluSerProAlaGlySerPro 301
Db 422 AGAGCTCTTGGCCCCGCTGCTGCGCCACACTCTCGCCAGAGTCCCCAGCGGCTCGCCA 481
QY 302 AlaMetMetLeuGln-ProGlyProGlnLeuTyrAspValMetAspAlaValProAlaAr 321
Db 482 GCCATGATGCTGCAGCGCCCGGCGCCAGCTCTACGACGTGATGGACGCGGTCCACGCGC 541
QY 321 GArgTrpLysGluPheValArgThrLeuGlyLeuArgGluAlaGluIleGlyAlaValG1 341
Db 542 GCGCTGAAGAGATTCTGTCGCACGCTGGGGCTGCCGAGGACAGAGATCGAAGCCGTGGA 601
QY 341 uValGluIleGly-ArgPheArgAspGlnGlnTyrGluMet 354
Db 602 GGTGAGATCGGCCCTTCCGAGACAGACAGAGTACGAGATT 642

RESULT 7
BM794760 647 bp mRNA linear EST 05-MAR-2002
LOCUS K-EST0076219 S22SNU16n1 Homo sapiens cDNA clone S22SNU16n1-48-G11
DEFINITION 5', mRNA sequence.
ACCESSION BM794760
VERSION BM794760.1 GI:19142992
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 647)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 48 row: G column: 11
High quality sequence stop: 647.
Location/Qualifiers
1. 647
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="S22SNU16n1-48-G11"
/clone_lib="S22SNU16n1"
/sex="F"
/tissue_type="Ascites"
/cell_type="Lymphoblast-like"
/cell_line="SNU-16"
/lab_host="DH10B"
/note="Organ: Stomach; Vector: pT7T3-Pac; Site_1: EcoRI;
Site_2: NotI; The S22SNU16 library was contributed by the
Soares laboratory and it was constructed as described by
Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome
Research 6(9): 791-806. RNA was prepared from harvested

cells of SNU-16 culture. SNU-16 cell was obtained from
Korean Cell Line Bank (KCLB). SNU-16 was established from
ascitic fluids of Korean patients by Park J.G. et al.
(1990), Cancer Res 50: 2773-2780."

BASE COUNT 110 a 229 c 203 g 105 t
ORIGIN

Alignment Scores: 1.44e-79 Length: 647
Pred. No.: 1066.50 Matches: 201
Score: 99.51% Conservative: 1
Percent Similarity: 99.01% Mismatches: 0
Best Local Similarity: 48.28% Indels: 1
Query Match: 14 Gaps: 1
DB:

US-09-993-234-6_COPY_25_417 (1-393) x BM794760 (1-647)

QY 176 MetPheTrpValGlnValLeuLeuAlaGlyLeuValProLeuLeuGlyAlaThr 195
Db 40 GTGTTCTGGGTCAGGTGCTCTGCTGGCTGGCTGTGTCCTCTGCTGGGCGCAC 99
QY 196 LeuThrTyrThrTyrArgHisCysTrpProHisLysProLeuValThrAlaAspGluAla 215
Db 100 CTGACCTACACATACCGCCACTGCTGGCTGCACAAAGCCCTGTTACT--GATGAAGCT 156
QY 216 GlyMetGluAlaLeuThrProProProAlaThrHisLeuSerProLeuAspSeraIaHis 235
Db 157 GGGATGAGGCTCTACACCCACACACCGGCCACCATCTGTACACCTTGACAGCGCCAC 216
QY 236 ThrLeuLeuAlaProProAspSerSerGluIleCysThrValGlnLeuValGlyAsn 255
Db 217 ACCCTTCTAGCACCTCTCTGACAGCAGTGAAGATCTGCACCGCTCCAGTTGGTGGTAA 276
QY 256 SerTrpThrProGlyTyrProGluThrGlnGluAlaLeuCysProGlnValThrTrpSer 275
Db 277 AGCTGACCCCTGCTTACCCCGAGACCCAGAGCGCGCTCTGCCCGCAGTGACATGTCTC 336
QY 276 TrpAspGlnLeuProSerArgAlaLeuGlyProAlaAlaAlaProThrLeuSerProGlu 295
Db 337 TGGGACAGTTGCCAGCAGAGACTCTTGGCCCGCTGCTGCGCCACACTCTCGCCAGAG 396
QY 296 SerProAlaGlySerProAlaMetMetLeuGlnProGlyProGlnLeuTyrAspValMet 315
Db 397 TCCCACAGCCGCTCGCCAGCCATGATGTGCAGCGGGCCCGCAGCTCTACGACGTGATG 456
QY 316 AspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGluAla 335
Db 457 GACGCGGTCCACGCGCGCTGGAAGAGATTGTCGCACGCTGGGCGCTGCCGAGCA 516
QY 336 GluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGluMetLeu 355
Db 517 GAGATCGAAGCCGTGAGGTGAGATCGGCCGCTTCCGAGACAGCAGATGATGCTC 576
QY 356 LysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArg 375
Db 577 AAGCGCTGGCGCCAGCAGACAGCCCGGGGCTTGGAGAGCCGTTTACGGCGGCTGAGAGCG 636
QY 376 MetGlyLeu 378
Db 637 ATGGGGCTG 645

RESULT 8
LOCUS AI424936 688 bp mRNA linear EST 30-MAR-1999
DEFINITION tg19b08.x1 NCI_CGAP_CL11 Homo sapiens cDNA clone IMAGE:2109207 3'
similar to TR:000276 000276 LYMPHOCTE ASSOCIATED RECEPTOR OF DEATH
2.;, mRNA sequence.
ACCESSION AI424936
VERSION AI424936.1 GI:4270854
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Db 65 CAGGGCGCACTGTAGCCAGGTGTGACTGTGCCGGTGACTTCCACAGAAGATTGGT 124
QY 21 LeuphecysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
Db 125 CTGTTTGTGTCAGAGGCTGCCAGCGGGGCACTACCTGAAGCCCCCTGCACGGAGCCC 184
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
Db 185 TCGGGCAACTCCACCTGCTGTGTGTCCCAAGACACCTTCTGGCCGTGGGAGAACAC 244
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
Db 245 CATTAATTCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCTCCAGGTGGCGCTG 304
QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
Db 305 GAGAACTGTTCAAGCAGTGGCCGACACCCGCTGTGGCTGTAAGCCAGGCTGGTTTGTGAG 364
QY 101 CysGlnValSerGlnCysValSerSerSerProPheTyrCysGlnProCysLeuAspCys 120
Db 365 TGGCAGGTGACGCAATGTGTACGACAGTTCAACCTTCTACTGCCAACCATGCTTAGACTGC 424
QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
Db 425 GGGGCCCTGCACCGCACACAGGCTACTCTGTCCGACAGATACTGACTGTGGAGCC 484
QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160
Db 485 TGCCTGCTGGCTTCTATGAACATGGCGATGGCTGCTGCTGCCACAGACACCTTG 544
QY 161 GlySerCysProGluArg 166
Db 545 NGAGCTGTCCAGAGCGC 562

RESULT 10
LOCUS BF726557 539 bp mRNA linear EST 05-JAN-2001
DEFINITION by08d05.y1 Human Lens cDNA (Un-normalized, unamplified): By Homo sapiens CDNA clone by08d05 5', mRNA sequence.
ACCESSION BF726557
VERSION BF726557.1 GI:12042468
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 539)
Wistow,G.J., Bernstein,S., Behal,A. and Smith,D.
NEIBANK: EST analysis and bioinformatics for ocular genomics
Invest. Ophthalmol. Vis. Sci. 41, (2000) In press
CONTACT: Wistow G
Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
Email: graeme@helix.nih.gov
Plate: 08 row: d column: 05
Seq primer: M13RP1 reverse primer (ABI).
FEATURES
source location/Qualifiers
1..539
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="by08d05"
/clone_lib="Human Lens cDNA (Un-normalized, unamplified): By"
/tissue_type="Lens"
/dev_stage="Adult"
/lab_host="EMD10B"
/note="Organ: Eye; Vector: pCMVSPORT6; Two human lenses from different adults (both approximately 40 years old) together yielded 20ug of total RNA and 150ng mRNA for cDNA library synthesis. A directionally cloned cDNA library in

the pCMVSPORT6 vector was constructed at Life Technologies, essentially following the protocols of the Superscript plasmid system full details of which are contained in the manufacturer's instruction manual (<http://www.lifetech.com/>). First strand synthesis was carried out using a Not I primer-adaptor [5'-PGACTAGTCTAGATCGGAGCGGCGCC(T)15-3']. Not I/blunt end inserts were cloned into the Not I/EcoR V sites in the vector. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."

BASE COUNT 97 a 192 c 167 g 83 t
ORIGIN

Alignment Scores:
Pred. No.: 2.02e-71 Length: 539
Score: 968.00 Matches: 179
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 43.82% Indels: 0
DB: 12 Gaps: 0

US-09-993-234-6_COPY_25_417 (1-393) x BF726557 (1-539)

QY 192 LeuGlyAlaThrLeuThrTyrTyrThrArgHisCysTrpProHisLysProLeuValThr 211
Db 2 CTTGGGGCACCTGACCTACACATACCGCCACTGCTGGCCCTCAAGCCCTGGTACT 61
QY 212 AlaAspGluAlaGlyMetGluAlaLeuThrProProAlaThrHisLeuSerProLeu 231
Db 62 GCAGATGAAGCTGGATGAGGCTCTGACCCACACCGGCCACCATCTGTACACCTTG 121
QY 232 AspSerAlaHisThrLeuLeuAlaProProAspSerSerGluLysIleCysThrValGln 251
Db 122 GACAGCGCCACACCTTCTAGCACCTCTGACACAGCAGTGAAGAATCTGCACCGTCCAG 181
QY 252 LeuValGlyAsnSerTrpThrProGlyTyrProGluThrGlnGluAlaLeuCysProGln 271
Db 182 TTGGTGGTAAACAGCTGGAACCCCTGGCTACCCCGAAGACCAGAGGGCTCTGCCGCGAG 241
QY 272 ValThrTrpSerTrpAspGlnLeuProSerArgAlaLeuGlyProAlaAlaAlaProThr 291
Db 242 GTGACATGTTCTTGGGACCAAGTTGCCACAGCAGCTCTTGCCCCCGCTGCGCCACACA 301
QY 292 LeuSerProGluSerProAlaGlySerProAlaMetLeuGlnProGlyProGlnLeu 311
Db 302 CTCTGCCAGAGTCCCCAGCCGGCTGCGCCAGCATGATGCTGCAGCCGCGCCGACGCTC 361
QY 312 TyrAspValMetAspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGly 331
Db 362 TACGACGTGATGACGGCGTCCACAGCGCGGCTGGAAGAGTTGCTGCGCACGCTGGGG 421
QY 332 LeuArgGluAlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGln 351
Db 422 CTGCGGAGGAGAGATCGAAGCCGTGAGGTGAGATCGGCCGCTTCGAGACCAAGCAG 481
QY 352 TyrGluMetLeuLysArgTrpArgGlnGlnProAlaGlyLeuGlyAlaValTyr 370
Db 482 TACGAGATGCTCAAGCGCTGGCGCCAGCAGCAGCCCGGCGCTCGAGCGCTTAC 538

RESULT 11
LOCUS BM783972 552 bp mRNA linear EST 05-MAR-2002
DEFINITION K-EST0062019 S6SNU620 Homo sapiens CDNA clone S6SNU620-31-H06 5', mRNA sequence.
ACCESSION BM783972
VERSION BM783972.1 GI:19132204
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 552)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,

Db 65 CAGGGCGGCACTGTAGCCCCAGGTGTGACTGTGCGGTGACTTCCACAGAAGATTGGT 124

QY 21 LeuphCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40

Db 125 CTGTTTGTGTGCAGAGGCTGCCAGCGGGCAGCTTGAAGCCCCCTTGACGAGCCCC 184

QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60

Db 185 TCGGCACTCCACCTGCTGTGTGTGCCCAAGACACCTTCTTGCGCTGGAGAACCAC 244

QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80

Db 245 CATAATTCTGAATGTGCCCGCTGCCAGGCTGTGATGACAGGCTCCAGGTGGCGCTG 304

QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100

Db 305 GAGAACTGTTCAGCAGTGGCGGACACCCGCTGTGCTTAAGCCAGGCTGTTTGAGAG 364

QY 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120

Db 365 TGCAGGTCAGCCAAATGTTCAGCAGTTCACCTTCTTAAGCCATGCTTACTGCTGC 424

QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140

Db 425 GGGGCCCTGCACCGCCACACAGGCTACTCTGTTCGCCGACAGATACTGACTGTGGACC 484

QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160

Db 485 TGCCTGCGCTGGCTTCTATGACATGCGATGCGTGCCTGCTGCCGCCACGTAATTCCTA 544

QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArgGln 175

Db 545 -----GCTGTGCTGGATGGAGGGA 565

RESULT 13

BM744307 565 bp mRNA linear EST 01-MAR-2002

LOCUS R-EST0017828 S6SNU620 Homo sapiens cDNA clone S6SNU620-17-C06 5',

DEFINITION mRNA sequence.

ACCESSION BM744307

VERSION BM744307.1 GI:19065636

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 565)

AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.

TITLE 21C Frontiers Korean EST Project 2001

JOURNAL Unpublished (2002)

COMMENT Contact: Kim YS

Genome Research Center

Korea Research Institute of Bioscience & Biotechnology

52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4470

Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr

Plate: 17 row: C column: 06

High quality sequence stop: 565.

FEATURES

Location/Qualifiers

1..565

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="S6SNU620-17-C06"

/clone_lib="S6SNU620"

/sex="F"

/tissue_type="Ascites"

/cell_type="Scattering floating"

/cell_line="SNU-620"

/lab_host="Top10F"

/note="Organ: Stomach; Vector: pcNS; Site_1: EcoRI;

Site_2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

BASE COUNT 95 a 175 c 178 g 117 t

ORIGIN

Alignment Scores:

Pred. No.: 2.7e-69 Length: 565

Score: 943.00 Matches: 162

Percent Similarity: 93.14% Conservative: 1

Best Local Similarity: 92.57% Mismatches: 4

Query Match: 42.69% Indels: 8

DB: 14 Gaps: 1

US-09-993-234-6_COPY_25_417 (1-393) x BM744307 (1-565)

QY 1 GlnGlyLysThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20

Db 38 CAGTGGCGCACTGCTGACGCTGCCAGGCTGTGACTGTGCCGGTACTTCCACAGAAGATTGGT 97

QY 21 LeuphCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40

Db 98 CTGTTTGTGTGCAGAGGCTGCCAGCGGGCAGCTGAAGGCCCTTGACAGGAGGCC 157

QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60

Db 158 TCGGCACTCCACCTGCTGTGTGTGCCCAAGACACCTTCTTGCGCTGGAGAACCAC 217

QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80

Db 218 CATAATTCTGAATGTGCCGCTGCCAGGCTGTGATGACAGGCTCCACGAGTGGCGCTG 277

QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100

Db 278 GAGAACTGTTCAGCAGTGGCGGACACCCGCTGTGCTTAAGCCAGGCTGTTTGAGAG 337

QY 101 CysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAspCys 120

Db 338 TGCAGGTCAGCCAAATGTTCAGCAGTTCACCTTCTTAAGCCATGCTTACACTGC 397

QY 121 GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140

Db 398 GGGGCCCTGCACCGCCACACAGGCTACTCTGTTCGCCGACAGATACTGACTGTGGACC 457

QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThrSerThrLeu 160

Db 458 TGCCTGCGCTGCTTCTATGACATGCGATGCGTGCCTGCTGCCGCCACGTAATTCCTA 517

QY 161 GlySerCysProGluArgCysAlaAlaValCysGlyTrpArgGln 175

Db 518 -----GCTGTGCTGGATGGAGGGA 538

RESULT 14

BM756372 514 bp mRNA linear EST 04-MAR-2002

LOCUS R-EST0034666 S6SNU620 Homo sapiens cDNA clone S6SNU620-27-G03 5',

DEFINITION mRNA sequence.

ACCESSION BM756372

VERSION BM756372.1 GI:19085987

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 514)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
TITLE 21C Frontler Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 27 row: G column: 03
High quality sequence stop: 514.
FEATURES
source
1. 514
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="S6SNU620-27-G03"
/clone_lib="S6SNU620"
/sex="F"
/tissue_type="Ascites"
/cell_type="Scattering floating"
/cell_line="SNU-620"
/lab_host="Top10F"
/note="Organ: Stomach; Vector: pcNS; Site_1: EcoRI; Site_2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including Ecor I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."
BASE COUNT 86 a 166 c 153 g 109 t
ORIGIN
Alignment Scores:
Pred. No.: 7.52e-69 Length: 514
Score: 937.00 Matches: 157
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 42.42% Indels: 0
DB: 14 Gaps: 0
US-09-993-234-6_COPY_25_417 (1-393) x BM756372 (1-514)
QY 1 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly 20
|||||
Db 38 CAGGGCGGCACTGCTAGCCCCCAGGTGTGACTGTGCGGTGACTTCACAGAAGATTGGT 97
QY 21 LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 40
|||||
Db 98 CTGTTTGTGTGCAGAGGCTGCCCGGCGGCACTACCTGAAGGCCCTTGCACGAGGCC 157
QY 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 60
|||||
Db 158 TGGGGCACTCCACCTGCTGTGTGCCCAAGACACCTTCTTGCCCTGGGAGAACCCAC 217
QY 61 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 80
|||||
Db 218 CATATTTCTGAATGTGCCCGCTGCCAGGCCCTGTGATGAGCAGGCCCTCCAGGTGGCGCTG 277

QY 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100
|||||
Db 278 GAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGGCTGTAAAGCCAGGCTGTGTGAG 337
QY 101 CysGlnValSerGlnCysValSerSerSerProPheTyrCysGlnProCysLeuAspCys 120
|||||
Db 338 TGGCAGGTACCAATGTGTACAGCAGTTCACCTTCTACTGCCAACCAATGCTAGACTGC 397
QY 121 GlysAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr 140
|||||
Db 398 GGGGCCCTGCACCGCCACACAGGCTACTGTTCGCCGACAGATACTGACTGTGGACC 457
QY 141 CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThr 157
Db 458 TGCTGCTGCTGCTTCTATGAACATGGCGATGGCTGCGTGCCTGCCCCACG 508
RESULT 15
BM783979 514 bp mRNA linear EST 05-MAR-2002
LOCUS BM783979
DEFINITION K-EST0062030 S6SNU620 Homo sapiens cDNA clone S6SNU620-32-A05 5', mRNA sequence.
ACCESSION BM783979
VERSION BM783979.1 GI:19132211
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 514)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
TITLE 21C Frontler Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 32 row: A column: 05
High quality sequence stop: 514.
FEATURES
source
1. 514
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="S6SNU620-32-A05"
/clone_lib="S6SNU620"
/sex="F"
/tissue_type="Ascites"
/cell_type="Scattering floating"
/cell_line="SNU-620"
/lab_host="Top10F"
/note="Organ: Stomach; Vector: pcNS; Site_1: EcoRI; Site_2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including Ecor I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."
BASE COUNT 86 a 166 c 153 g 109 t
ORIGIN

Alignment Scores:

Pred. No.:	7.52e-69	Length:	514
Score:	937.00	Matches:	157
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	42.42%	Indels:	0
DB:	14	Gaps:	0

US-09-993-234-6_COPY_25_417 (1-393) x BM783979 (1-514)

QY	1	GLNGLYGLYThrArgSerProArgCysAspCysAlaGlyAspPheHisLysLysIleGly	20
DB	38	CAGGGCGGCACTCGTAGCCCGAGGTGTGACTGTGCCGGTACTTCCACAGAAGATGGT	97
QY	21	LeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro	40
DB	98	CTGTTTGTGTGACAGAGGCTGCCAGCGGGGCACTACTGAGAGGCCCTTGACAGGAGCC	157
QY	41	CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis	60
DB	158	TGCGGCAACTCCACCTGCTTGTGTGTCCCAAGACACCTTCTTGCGCTGGAGAACAC	217
QY	61	HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu	80
DB	218	CATAATTCTGAATGTGCCGCTGCCAGGCTGTGATGAGCAGGCCCTCCAGGTGGCGCTG	277
QY	81	GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu	100
DB	278	GAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGGCTGTAAAGCCAGGCTGTTGTGAG	337
QY	101	CysGlnValSerGlnCysValSerSerSerProPheTyrCysGlnProCysLeuAspCys	120
DB	338	TGCCAGGTCAGCCAATGTGTCAAGCAGTTCACCCCTTCTACTGCCAACCATGCTAGACTGC	397
QY	121	GlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAspCysGlyThr	140
DB	398	GGGGCCCTGCACCGCCACACAGGCTACTCTGTTCGCCGACAGATACTGACTGTGGAGCC	457
QY	141	CysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThr	157
DB	458	TGCTTGCTGTGCTTCTAATGACATGGCGATGGCTGCTGTCTGCTGCCACG	508

Search completed: April 6, 2003, 23:25:13
Job time : 2464.26 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 6, 2003, 15:33:09 ; Search time 74.489 Seconds
(without alignments)
2418.610 Million cell updates/sec

Title: US-09-993-234-6_COPY_338_417
Perfect score: 413
Sequence: 1 VMDAVPARRWKEFVRTLGRLR.....ERMGLDGCVEDLRSRLQRCGP 80

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US09993234/runat_27032003_115454_15312/app_query.fasta_1.2346
-DB=N_Geneseq_101002 -QFMT=fastcap -SUFFIX=ring -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=biosum62 -TRANS=human40.cdi
-LIST=45 -DOCCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09993234_@CGN_1_1_660_@runat_27032003_115454_15312 -NCPU=6 -ICPU=3
-NO_XLPHY -NO_MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_101002: *
1: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT: *
2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT: *
3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT: *
4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT: *
5: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT: *
6: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT: *
7: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT: *
8: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT: *
9: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT: *
10: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT: *
11: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT: *
12: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT: *
13: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT: *
14: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT: *
15: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT: *
16: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT: *
17: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT: *
18: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT: *
19: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT: *
20: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT: *
21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT: *
22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT: *
23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT: *
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	413	100.0	1250	22	AAF83770	Nucleotide sequenc
2	413	100.0	1254	18	AAT89427	Death domain conta
3	413	100.0	1254	20	AAK00925	Death domain conta
4	413	100.0	1254	21	AAC68777	Human death domain
5	413	100.0	1634	18	AAT91180	Human apoptosis pr
6	413	100.0	1634	22	AAH27782	Human genomic DNA
7	413	100.0	1634	22	AAI47186	Human rheumatoid a
8	413	100.0	1662	22	AAC91477	Human PRO779 cDNA.
9	413	100.0	1662	24	ABK40265	CDNA encoding huma
10	413	100.0	1783	18	AAT89426	Death domain conta
11	413	100.0	1783	20	AAK00924	Death domain conta
12	413	100.0	1783	21	AAC68776	Human death domain
13	413	100.0	1847	19	AAV28700	Human apoptosis in
14	413	100.0	4825	24	AAI47185	Human DR3 gene ass
15	413	100.0	10797	23	ABK42690	Genomic sequence #
16	401	97.1	1743	24	ABL64119	Breast cancer rela
17	395	95.6	1251	19	AAV28701	Mouse apoptosis in
18	307	74.3	511	24	ABQ47530	Oligonucleotide fo
19	307	74.3	511	24	ABQ47531	Oligonucleotide fo
20	240	58.1	511	24	ABQ47532	Oligonucleotide fo
21	240	58.1	511	24	ABQ47533	Oligonucleotide fo
22	171	41.4	2130	24	ABK63694	Rat sequence diffe
23	171	41.4	2173	11	AAQ06284	Rat Tumour Necrosi
24	158	38.3	1368	14	AAQ49932	Lambda-derived TNF
25	158	38.3	1368	21	AAA95105	Human TNFR1 coding
26	158	38.3	2062	13	AAQ20973	TNF-alpha binding
27	158	38.3	2062	13	AAQ24440	Encodes TNF-alpha
28	158	38.3	2088	12	AAQ10883	30KD TNF inhibitor
29	158	38.3	2088	22	AAC3946	Human 30 kDa TNF 1
30	158	38.3	2111	12	AAQ10955	Encodes human 55kD
31	158	38.3	2111	20	AAZ09170	Human tumour necro
32	158	38.3	2111	22	AAH48859	Human TNFBP-associ
33	158	38.3	2111	24	ABK4039	Human TNF gene diffe
34	158	38.3	2111	24	ABN95862	Gene #2360 used to
35	158	38.3	2141	11	AAQ06285	Human Tumour Necro
36	158	38.3	2161	21	AAZ48475	Human tumour necro
37	158	38.3	2161	24	ABK13194	Human tumour necro
38	158	38.3	2170	14	AAQ50870	p55 Tumour necrosi
39	158	38.3	2175	16	AAQ90513	p55 TNF-R gene. H
40	158	38.3	2176	12	AAQ12215	Type I TNF recepto
41	158	38.3	2254	21	AAA95104	Partial human TNFR
42	139	33.7	441	12	AAI88626	Human polynucleoti
43	96	23.2	2413	19	AAV14997	tvb polypeptide co
44	94	22.8	1062	19	AAV63095	Human TR6 partial
45	94	22.8	1062	22	AAC84744	Partial nucleotide

ALIGNMENTS

RESULT 1	
AAF83770	
ID	AAF83770 standard; DNA; 1250 BP.
XX	
AC	AAF83770;
XX	
DT	06-AUG-2001 (first entry)
XX	
DE	Nucleotide sequence of human TR3 gene.
XX	
KW	TR3; cell proliferation; leukemia; immunosuppressive; cytostatic;
KW	dermatological; antiarthritic; antidiabetic; neuroprotective; cardiant;
KW	antithyroid; antiinflammatory; antiallergic; T-cell-inhibitor; ds.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	CDS location/Qualifiers
	1..1250

```

FT FT /*tag= a
FT FT /transl_except= "(pos:481..482, aa:Asp)"
FT FT /note= "this codon has an apparent 1 nucleotide
FT FT deletion which alters the reading frame"
FT FT /transl_except= "(pos:558..559, aa:Cys)"
FT FT /note= "this codon has an apparent 1 nucleotide
FT FT deletion which alters the reading frame"
FT FT /transl_except= "(pos:638..639, aa:Leu)"
FT FT /note= "this codon has an apparent 1 nucleotide
FT FT deletion which alters the reading frame"
FT FT /transl_except= "(pos:718..719, aa:Met)"
FT FT /note= "this codon has an apparent 1 nucleotide
FT FT deletion which alters the reading frame"
FT sig_peptide 1..72
FT /*tag= b
FT mat_peptide 73..1247
FT /*tag= c
XX WO200135995-A2.
XX 25-MAY-2001.
XX 17-NOV-2000; 2000WO-US31692.
XX 19-NOV-1999; 99US-0166583.
XX (TITT/) TITTLE T V.
XX (WEGM/) WEGMANN K W.
XX Tittle TV, Wegmann KW;
XX WPI; 2001-343711/36.
XX P-PSDB; AAB84941.
XX Composition for treatment of T-cell mediated disease e.g. arthritis,
XX cancer comprises a biologically active TR3-specific binding agent
XX especially a monoclonal antibody -
XX Disclosure; Page 72; 77pp; English.
XX
XX The invention relates to a composition comprising a biologically active
XX TR3-specific binding agent (I) that binds to TR3 and inhibits the
XX proliferation of cells expressing TR3. (I) identified by the methods are
XX useful for treating a subject suspected of having a disease associated
XX with a proliferation of cells expressing TR3 especially leukemias or
XX lymphomas or a T-cell mediated disease especially autoimmune diseases
XX such as myasthenia gravis, systemic lupus erythematosis, rheumatoid
XX arthritis, diabetes, multiple sclerosis, sarcoidosis, myocarditis,
XX thyroiditis and tumours. (I) is also useful for treating a subject
XX suspected of having graft-versus-host disease, rejection of a
XX transplanted organ such as heart, liver, lung, kidney, pancreas, bowel,
XX skin or an appendage, or inflammatory diseases, allergies and contact
XX dermatitis. The present sequence represents the nucleotide sequence of
XX human TR3 gene.
XX
XX SQ Sequence 1250 BP; 201 A; 419 C; 406 G; 224 T; 0 other;
XX
XX Alignment Scores:
XX Pred. No.: 1.88e-44 Length: 1250
XX Score: 413.00 Matches: 80
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 100.00% Indels: 0
XX DB: 22 Gaps: 0
XX
XX US-09-993-234-6_COPY_338_417 (1-80) x AAF83770 (1-1250)
XX
XX QY 1 ValMetAspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX Db 1008 GTGATGGACGCGGTCCACGCCGCGCTGGAGGAGTTCGTGCCGACGCTGGCGCGC 1067
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX QY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnIntyrGlu 40
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

```

Db	1068	GAGCGACAGATCGAAGCCGTGGAGGTGAGATCGGCCCTTCGAGACACGACGATGAG	1127
QY	41	MetIeuIysArGTTPaRGInGIInGInProAlaGIleuGIyAlaValTYRaIaIeU	60
Db	1128	ATGCTCAAGCGCTGGCGCCAGACGACGCCCGGGCCCTCGAGCCGTTACGCGGCCCTG	1187
QY	61	GIuArgMetGIleuAspGIyCySValGIuAspIeuArgSerArgIeuGIuArgGIyPro	80
Db	1188	GAGCGCATGGGGCTGGACGCGCTGCGTGAAGACTTGCGCAGCCGCTGCAGCGCGGCCG	1247
RESULT 2			
AA	89427	standard; cDNA; 1254 BP.	
AC	AAT89427;		
DT	02-MAR-1998	(first entry)	
DE	Death domain containing receptor DR3 cDNA.		
KW	Death domain containing receptor; DR3; human; apoptosis;		
OS	Homo sapiens.		
FT	Key	Location/Qualifiers	
FT	sig_peptide	1..72	
FT	mat_peptide	/*tag= a	
FT		73..1251	
FT		/*tag= b	
PN	WO9733904-A1.		
PD	18-SEP-1997.		
PF	17-OCT-1996;	96WO-US16849.	
PR	12-MAR-1996;	96US-0013285.	
PA	(HUMA-) HUMAN GENOME SCI INC.		
PA	(UNMT) UNIV MICHIGAN.		
PI	Dillon PJ, Dixit VM, Gentz RL, Ni J, Yu G;		
DR	WPI, 1997-470812/43.		
DR	P-PSDB; AAW31517.		
PT	Death domain containing receptor polypeptide(s) DR3 and DR3-V1 -		
PT	for activation of apoptosis and NF-kappaB, antagonists can be used		
PT	to treat inflammatory diseases		
XX	Claim 6; Page 75-77; 108pp; English.		
XX	This cDNA clone codes for human death domain containing receptor		
CC	DR3 (see AAW31517), a novel member of the tumour necrosis factor		
CC	receptor family. It was isolated from a HUVEC cDNA library.		
CC	Related death domain containing receptor DR3-V1 cDNA (see AAT89426)		
CC	was isolated from a human testis tumour cDNA library. The genes		
CC	have also been identified in cDNA libraries of foetal liver,		
CC	foetal brain, tonsil and leukocyte. Nucleic acids encoding full-		
CC	length or mature DR3, or the extracellular, transmembrane,		
CC	intracellular or especially the death domain of DR3, can be used to		
CC	produce recombinant polypeptides in transformed host cells. These		
CC	polypeptides can be used to treat diseases and disorders associated		
CC	with the inhibition of apoptosis. Antagonists can be used to treat		
CC	diseases and disorders associated with increased apoptosis and for		
CC	treating inflammatory diseases and disorders.		
XX	Sequence 1254 BP; 201 A; 420 C; 407 G; 226 T; 0 other;		
SD			
Alignment Scores:			
Pred. No.:		1.89e-44	Length: 1254
Score:		413.00	Matches: 80

PS Example 2B; Fig 2; 273pp; English.
XX
CC The present invention provides the protein and coding sequences for two
CC death domain containing receptors, designated DR3 and DR3-V1. These
CC receptors are involved in apoptosis, and the sequences given can be used
CC in the treatment of cancers, infections, cardiovascular disorders such as
CC arrhythmias, ischaemia, aneurysms, arterial occlusive diseases, embolisms,
CC and congenital heart defects, neurodegenerative diseases including
CC Alzheimer's and Parkinson's diseases, autoimmune disease such as multiple
CC sclerosis, arthritis, diabetes, Graves' disease, asthma and psoriasis,
CC and to promote angiogenesis and wound healing.
XX
SQ Sequence 1254 BP; 201 A; 420 C; 407 G; 226 T; 0 other;

Alignment Scores:
Pred. No.: 1 89e-44 Length: 1254
Score: 413.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-09-993-234-6_COPY_338_417 (1-80) x AAC68777 (1-1254)
QY 1 ValMetAspAlaValProAlaArgArgTrpIysGluPheValArgThrLeuGlyLeuArg 20
DB 1012 GTGATGACGCGGTCCACGCGCGCGCTGGAAGAGTTCGTGCGCACCGCTGGGCTGCC 1071
QY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGlu 40
DB 1072 GAGGCAGAGATCGAAGCCGTGAGGTGAGATCGGCCCTTCCGAGACCAGCATACGAG 1131
QY 41 MetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeu 60
DB 1132 ATGCTCAAGCGCTGGCGCCACGACGAGCCCGCGGCGCTCGAGCGCTTACGCGGCCCTG 1191
QY 61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80
DB 1192 GAGCGCATGGGGCTGGACGCGCTGCGTGAAGACTTGCAGACCGCGCTGCAGCGGCCCG 1251

RESULT 5
AAT91180
ID AAT91180 standard; cDNA; 1634 BP.
XX
AC AAT91180;
DT 14-APR-1998 (first entry)
XX
DE Human apoptosis protein Apo-3 cDNA clone FH20.57.
XX
KW Apo-3; apoptosis; human; therapy; drug screening; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 89..1342
FT sig_peptide /*tag= a
FT 89..160
FT /*tag= b
FT /*note= "determined by hydrophathy analysis"
FT 161..1339
FT mat_peptide /*tag= c
XX
XX
XX WO9737020-A1.
XX
XX PD 09-OCT-1997.
XX
XX PF 31-MAR-1997; 97WO-US05230.
XX
XX OS 23-SEP-1996; 96US-0710802.
XX PR 01-APR-1996; 96US-0625328.
XX
XX PA (GETH) GENENTECH INC.

XX
PI Askenazi AJ;
XX
DR WPI; 1997-503105/46.
XX
PT Polypeptide(s) Apo-3 and Apo-2LI - useful for regulating apoptosis
PT in mammalian cells
XX
PS Example 1; Page 45-46; 70pp; English.
XX
CC cDNA clone FH20.57 (ATCC 55820) codes for a novel polypeptide (see
CC W26709), designated Apo-3, that stimulates or induces apoptotic
CC activity in mammalian cells. It was isolated from a human foetal
CC heart cDNA library by screening with probes (see T91183-84) based
CC on an EST sequence (GenBank locus W71984) that showed homology to
CC the intracellular domain of human TNFR1 and CD95. Amino acid
CC residues 1-181 of Apo-3 are identical to another novel apoptosis
CC polypeptide, Apo-2LI (see W26708). Nucleic acids encoding Apo-3
CC can be used diagnostically for tissue-specific typing and to
CC produce recombinant Apo-3 polypeptides, especially the
CC extracellular domain (amino acids 1-198) or death domain (amino
CC acids 338-417). Apo-3 can be used to induce apoptosis or
CC NF-kappa-N- or JNK-mediated gene expression for therapeutic
CC purposes. Non-human transgenic animals containing cells that
CC express Apo-3 nucleic acid, and knockout animals containing
CC cells that have an altered Apo-3 gene, can be used in drug
CC screening and development.
SQ Sequence 1634 BP; 300 A; 528 C; 519 G; 287 T; 0 other;

Alignment Scores:
Pred. No.: 2 61e-44 Length: 1634
Score: 413.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-09-993-234-6_COPY_338_417 (1-80) x AAT91180 (1-1634)
QY 1 ValMetAspAlaValProAlaArgArgTrpIysGluPheValArgThrLeuGlyLeuArg 20
DB 1100 GTGATGACGCGGTCCACGCGCGCGCTGGAAGAGTTCGTGCGCACCGCTGGGCTGCC 1159
QY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGlu 40
DB 1160 GAGGCAGAGATCGAAGCCGTGAGGTGAGATCGGCCCTTCCGAGACCAGCATACGAG 1219
QY 41 MetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeu 60
DB 1220 ATGCTCAAGCGCTGGCGCCACGACGAGCCCGCGGCGCTCGAGCGCTTACGCGGCCCTG 1279
QY 61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80
DB 1280 GAGCGCATGGGGCTGGACGCGCTGCGTGAAGACTTGCAGACCGCGCTGCAGCGGCCCG 1339

RESULT 6
AAH27782
ID AAH27782 standard; DNA; 1634 BP.
XX
AC AAH27782;
DT 15-AUG-2001 (first entry)
XX
XX
XX DE Human genomic DNA encoding a rheumatoid arthritis associated protein.
XX
XX KW Rheumatoid arthritis; transmembrane protein; human; ds.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
FT CDS 89..1342
FT /*tag= a

FT /product= "Rheumatoid arthritis associated protein"
XX
PN WO200132921-A2.
XX 10-MAY-2001.
XX
PF 01-NOV-2000; 2000WO-JP07690.
XX
PR 01-NOV-1999; 99JP-0310805.
XX
PA (SHIO/) SHIOZAWA S.
XX
PI Shiozawa S, Konishi Y;
XX
DR WPI: 2001-308750/32.
DR P-PSDB; AAB97370.
XX
PT Diagnosing rheumatoid arthritis by probing digested human genomic DNA
PT or comparing expression of mRNA or polypeptide of a region of
PT transmembrane protein
XX
PS Claim 1; Page 14-18; 21pp; Japanese.
XX
CC This invention relates to a method of diagnosing chronic rheumatoid
CC arthritis by digesting human genomic DNA with EcoRI and hybridizing it
CC with a probe containing a fragment of the present sequence which
CC represents DNA encoding a transmembrane protein. The method is used for
CC the diagnosis of chronic rheumatoid arthritis, and for developing new
CC treatments.
XX
SQ Sequence 1634 BP; 300 A; 528 C; 519 G; 287 T; 0 other;
XX
Alignment Scores:
Pred. No.: 2.61e-44 Length: 1634
Score: 413.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0
US-09-993-234-6_COPY_338_417 (1-80) x AAL47186 (1-1634)
QY 1 ValMetaspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
DB 1100 GTGATGGACGGCGCTGCCAGCGCGCGCTGGAAGAGTTCGTGCGCACGCTGGCGCTGCCG 1159
QY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrglu 40
DB 1160 GAGGCAGAGATCGAAGCCGCTGGAGATCGGCGCTTCCGAGACCAAGACAGTACGAG 1219
QY 41 MetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaLeu 60
DB 1220 ATGCTCAAGCGCTGGCGCCAGCAGACCCGCGGCGCTCGAGCCGTTACGCGGCCCTG 1279
QY 61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80
DB 1280 GAGCGCATGGGGCTGGACGGCTGCTGGAAGACTTCCGACAGCCGCTGACGGCGGCCCG 1339
RESULT 7
AAL47186
ID AAL47186 standard; cDNA; 1634 BP.
XX
AC AAL47186;
XX
DT 22-AUG-2002 (first entry)
XX
DE Human rheumatoid arthritis associated DR3 gene related cDNA #1.
XX
KW Human; DR3; rheumatoid arthritis; antirheumatic; antilarthritic;
KW gene therapy; gene; ss.
XX
OS Homo sapiens.
XX

FH Key Location/Qualifiers
FT CDS 89..1342
FT /*tag= a
FT /product= "AAO17879"
XX
PN WO200234912-A1.
XX
PD 02-MAY-2002.
XX
PF 24-OCT-2001; 2001WO-JP09313.
XX
PR 24-OCT-2000; 2000JP-0324296.
PR 27-MAR-2001; 2001JP-0090546.
PR 30-MAR-2001; 2001JP-0099990.
XX
PA (NEWI-) NEW IND RES ORG.
PA (SHIO/) SHIOZAWA S.
XX
PI Shiozawa S, Konishi Y;
XX
DR WPI: 2002-417132/44.
DR P-PSDB; AAO17879.
XX
PT Genomes, particularly DR3 genomic DNA, participating in rheumatoid
PT arthritis via mutation, useful in evaluating disease onset and its
PT possibility and providing therapy and remedies -
XX
PS Example 1; Page 66-69; 84pp; Japanese.
XX
CC The present invention relates to the human DR3 gene, which is associated
CC with rheumatoid arthritis. Certain mutations in the gene can be linked to
CC the disease. The sequences can be used to evaluate disease onset and its
CC possibility and to provide therapy and remedies. The present sequence is
CC a coding sequence described in the exemplification of the invention.
XX
SQ Sequence 1634 BP; 300 A; 528 C; 519 G; 287 T; 0 other;
XX
Alignment Scores:
Pred. No.: 2.61e-44 Length: 1634
Score: 413.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 24 Gaps: 0
US-09-993-234-6_COPY_338_417 (1-80) x AAL47186 (1-1634)
QY 1 ValMetaspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
DB 1100 GTGATGGACGGCGCTGCCAGCGCGCGCTGGAAGAGTTCGTGCGCACGCTGGCGCTGCCG 1159
QY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrglu 40
DB 1160 GAGGCAGAGATCGAAGCCGCTGGAGATCGGCGCTTCCGAGACCAAGACAGTACGAG 1219
QY 41 MetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaLeu 60
DB 1220 ATGCTCAAGCGCTGGCGCCAGCAGACCCGCGGCGCTCGAGCCGTTACGCGGCCCTG 1279
QY 61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80
DB 1280 GAGCGCATGGGGCTGGACGGCTGCTGGAAGACTTCCGACAGCCGCTGACGGCGGCCCG 1339
RESULT 8
AAC91477
ID AAC91477 standard; cDNA; 1662 BP.
XX
AC AAC91477;
XX
DT 21-MAR-2001 (first entry)
XX
DE Human PRO779 cDNA.
XX

KW Human; PRO; antiinflammatory; dermatological; antiarthritic;
KW antirheumatic; cardiac; antianaemic; immunosuppressive; antithyroid;
KW antidiabetic; nootropic; neuroprotective; hepatotropic; virucide;
KW antiallergic; antiasthmatic; immune related disorder;
KW hepatobiliary disease; autoimmune disease; allergy; ss.
OS Homo sapiens.
XX WO200073452-A2.
PN 07-DEC-2000.
XX 02-JUN-2000; 2000WO-US15264.
PF 02-JUN-1999; 99WO-US12252.
XX 20-JUL-1999; 99US-0144732.
PR 20-JUL-1999; 99US-0144758.
PR 28-JUL-1999; 99US-0146222.
PR 01-SEP-1999; 99WO-US20111.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 29-OCT-1999; 99US-0162506.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28634.
PR 09-DEC-1999; 99US-0170262.
PR 20-DEC-1999; 99WO-US30911.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
XX (GETH) GENENTECH INC.
PA Ashkenazi AJ, Baker KP, Chan B, Goddard A, Godowski PJ, Gurney AL;
PI Hebert C, Henzel W, Kabakoff RC, Shelton DL, Tumas D, Watanabe CK;
PI Wood WI;
XX WPI; 2001-025253/03.
DR P-PSDB; AAB50918.
XX Thirty three nucleic acids encoding PRO polypeptides which are useful
PT in the diagnosis and treatment of immune related disorders, e.g.
PT systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
PT thyroiditis and diabetes mellitus -
XX Claim 48; Fig 33; 218pp; English.
PS The present sequence is one of thirty three nucleic acids encoding PRO
XX polypeptides. The PRO polypeptides, anti-PRO antibodies, agonists and
CC antagonists are useful for treating and diagnosing immune related
CC disorders such as systemic lupus erythematosus, rheumatoid arthritis,
CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,
CC immune-mediated renal disease, demyelinating diseases of the central
CC and peripheral nervous systems (such as multiple sclerosis, idiopathic
CC demyelinating polynuropathy or Guillain-Barre syndrome, and chronic
CC inflammatory demyelinating polynuropathy), hepatobiliary diseases
CC (such as infectious, autoimmune chronic active hepatitis, primary
CC biliary cirrhosis, granulomatous hepatitis and sclerosing cholangitis),
CC inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's
CC disease, autoimmune or immune-mediated skin diseases (such as bullous
CC skin diseases, erythema multiforme, contact dermatitis, psoriasis),

CC allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,
CC food hypersensitivity and urticaria), immunological diseases of the
CC lung (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis
CC and hypersensitivity pneumonitis), transplantation associated diseases
CC including graft rejection and graft-versus-host diseases.
XX SQ Sequence 1662 BP; 302 A; 540 C; 531 G; 289 T; 0 other;
XX Alignment Scores:
Pred. No.: 2.67e-44 Length: 1662
Score: 413.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0
US-09-993-234-6_copy_338_417 (1-80) x AAC91477 (1-1662)
QY 1 ValMetAspAlaValProAlaArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
Db 1114 GTGATGGACGGGCTCCCAAGCGCGCGCTGGAAGAGTTCTGTCGACGCTGGGCTGCGC 1173
QY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnIleTyrGlu 40
Db 1174 GAGGCAGAGATCGAAGCCGCTGAGAGTGCAGATCGCGCTCCGACACACAGCATACGAG 1233
QY 41 MetLeuLysArgTrpArgGlnGlnProAlaGlyLeuGlyAlaValTyrAlaLeu 60
Db 1234 ATGCTCAAGCGCTGGCGCCAGCAGACGCCCGGCGCTCGAGCGCTTACGCGCCCTG 1293
QY 61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80
Db 1294 GAGCGCATGGGGCTGACGCGCTGCTGAAGACTTGCCGACGCCCTGCAAGCGGCGCCG 1353
RESULT 9
ABK40265
ID ABK40265 standard; cDNA; 1662 BP.
XX
AC ABK40265;
XX
DT 15-JUL-2002 (first entry)
XX
DE cDNA encoding human PRO779 polypeptide.
XX
KW Human; PRO; benign tumour; malignant tumour; lymphoid malignancy;
KW leukaemia; neuronal disorder; stromal disorder; blastocoele disorder;
KW inflammatory disorder; immune disorder; angiogenic disorder;
KW gene therapy; cytostatic; neuroprotective; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200153486-A1.
XX
PD 26-JUL-2001.
XX
PF 11-FEB-2000; 2000WO-US03565.
XX
XX 08-MAR-1999; 99WO-US05028.
PR 11-MAR-1999; 99US-123972P.
PR 11-MAY-1999; 99US-133459P.
PR 02-JUN-1999; 99WO-US12252.
PR 22-JUN-1999; 99US-140650P.
PR 22-JUN-1999; 99US-140653P.
PR 20-JUL-1999; 99US-144758P.
PR 26-JUL-1999; 99US-145698P.
PR 28-JUL-1999; 99US-146222P.
PR 17-AUG-1999; 99US-149395P.
PR 31-AUG-1999; 99US-151689P.
PR 01-SEP-1999; 99WO-US20111.
PR 15-SEP-1999; 99WO-US21090.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.

PR 05-JAN-2000; 2000WO-US00219.
XX (GETH) GENENTECH INC.
PA
XX Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL, Hillan KJ;
PI Marsters SA, Pan J, Pitteri RM, Roy MA, Smith V, Stone DM;
PI Watanabe CK, Wood WI;
XX
DR WPI; 2002-205567/26.
DR P-PSDB; AAU86139.
XX
XX Thirty five nucleic acids encoding PRO polypeptides, useful for
PT treating benign or malignant tumours, leukaemias and lymphoid
PT malignancies, inflammatory, angiogenic and immunologic disorders -
XX
XX Claim 50; Fig 23; 302pp; English.
XX
CC The present invention relates to the isolation of novel human PRO
CC polypeptides and the polynucleotide sequences encoding them. The
CC PRO polypeptides, agonists, antagonists or anti-PRO antibodies are
CC useful for treating benign or malignant tumours (e.g. renal, kidney,
CC bladder, breast, etc), leukaemias and lymphoid malignancies, other
CC disorders such as neuronal, glial, astrocytal, hypothalamic, glandular,
CC macrophagal, stromal and blastocoelec disorders, inflammatory, immune
CC and angiogenic disorders. The polynucleotide sequences are also
CC useful in gene therapy. ABK40254-ABK40288 encode for the human PRO
CC polypeptides of the invention.
XX
SQ Sequence 1662 BP; 302 A; 540 C; 531 G; 289 T; 0 other;

Alignment Scores:
Pred. No.: 2.67e-44 Length: 1662
Score: 413.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 24 Gaps: 0

US-09-993-234-6_COPY_338_417 (1-80) x ABK40265 (1-1662)
QY 1 ValMetAspAlaValAlProAlaArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
DB 1114 GTGATGGACGCGGTCCACGCGCGCTGGAAGAGATTCTGCGCACGCTGGGGCTGCGC 1173
QY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlyArg 40
DB 1174 GAGCGACAGATCGAAGCCGTGGAGGTGAGATCGCGCTTCCAGACACGACGATACGAG 1233
QY 41 MetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaLeu 60
DB 1234 ATGCTCAAGCGCTGGCGCCAGACAGCCCGCGGCTCGGAGCCGTTACGCGGCCCTG 1293
QY 61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80
DB 1294 GAGCGCATGGGCTGACGCGCTGCGTGAAGACTTGCAGCCGCGCTGACGCGGCCCG 1353
RESULT 10
AAT89426
ID AAT89426 standard; cDNA; 1783 BP.
XX
AC AAT89426;
XX
DT 02-MAR-1998 (first entry)
XX
DE Death domain containing receptor DR3-VI cDNA.
XX
KW Death domain containing receptor; DR3-VI; human; apoptosis;
KW inflammation; NF-kappaB; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 198..1484

FT sig_peptide /*tag= a
FT 198..302
FT /*tag= b
FT mat_peptide 304..1481
FT /*tag= c
XX
PN WO9733904-A1.
XX
PD 18-SEP-1997.
XX
PF 17-OCT-1996; 96WO-US16849.
XX
PR 12-MAR-1996; 96US-0013285.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (UNMI) UNIV MICHIGAN.
XX
PI Dillon PJ, Dixit VM, Gentz RL, Ni J, Yu G;
XX
DR WPI; 1997-470812/43.
DR P-PSDB; AAW31516.
XX
XX Death domain containing receptor polypeptide(s) DR3 and DR3-VI -
PT for activation of apoptosis and NF-kappaB, antagonists can be used
PT to treat inflammatory diseases
XX
PS Claim 2; Page 71-73; 108pp; English.
XX
XX This cDNA clone, deposited as ATCC 97456, codes for human death
CC domain containing receptor DR3-VI (see AAW31516), a novel member of
CC the tumour necrosis factor receptor family. It was isolated from a
CC cDNA library derived from cells of a human testis tumour. Related
CC death domain containing receptor DR3 cDNA (see AAT89427) was isolated
CC from a HUVEC cDNA library. The genes have also been identified in
CC cDNA libraries of foetal liver, foetal brain, tonsil and leukocyte.
CC Nucleic acids encoding full-length or mature DR3-VI can be used to
CC produce recombinant polypeptides in transformed host cells. These
CC polypeptides can be used to treat diseases and disorders associated
CC with the inhibition of apoptosis. Antagonists, such as antibodies
CC raised against DR3-VI, can be used to treat diseases and disorders
CC associated with increased apoptosis and for treating inflammatory
CC diseases and disorders.
XX
SQ Sequence 1783 BP; 330 A; 562 C; 564 G; 327 T; 0 other;

Alignment Scores:
Pred. No.: 2.91e-44 Length: 1783
Score: 413.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-09-993-234-6_COPY_338_417 (1-80) x AAT89426 (1-1783)
QY 1 ValMetAspAlaValAlProAlaArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
DB 1242 GTGATGGACGCGGTCCACGCGCGCTGGAAGAGTTCGTGCGCACGCTGGGGCTGCGC 1301
QY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlyArg 40
DB 1302 GAGCGACAGATCGAAGCCGTGGAGGTGAGATCGCGCTTCCAGACACGACGATACGAG 1361
QY 41 MetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaLeu 60
DB 1362 ATGCTCAAGCGCTGGCGCCAGACAGCCCGCGGCTCGAGCCGTTACGCGGCCCTG 1421
QY 61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80
DB 1422 GAGCGCATGGGCTGACGCGCTGCGTGAAGACTTGCAGCCGCGCTGACGCGGCCCG 1481
RESULT 11
AAK00924

ID AAX00924 standard; cDNA; 1783 BP.
XX AAX00924;
AC AAX00924;
XX 25-MAR-1999 (first entry)
DT 25-MAR-1999 (first entry)
XX Death domain containing receptor polypeptide (DR3-V1) encoding cDNA.
DE Death domain containing receptor polypeptide (DR3-V1) encoding cDNA.
XX Death domain; receptor; DR3-V1; DR3; recombinant; ds.
KM Homo sapiens.
XX Homo sapiens.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 198..1484
FT /tag= a
FT /product= "Death domain containing receptor DR3-V1"
FT sig_peptide 198..300
FT /tag= b
FT mat_peptide 301..1481
FT /tag= c
XX JP11000170-A.
PN 06-JAN-1999.
PD 06-JAN-1999.
XX 12-MAR-1997; 97JP-0057503.
PF 12-MAR-1997; 97JP-0057503.
XX 06-FEB-1997; 97US-0037341.
PR 12-MAR-1996; 96US-0013285.
PR 17-OCT-1996; 96US-0028711.
XX (HUMA-) HUMAN GENOME SCI INC.
PA (UNMT) UNIV MICHIGAN.
XX WPI; 1999-124390/11.
DR P-PSDB; AAW95537.
XX New death domain containing receptor and recombinant vector -
PT optionally comprising leader sequence
PT optionally comprising leader sequence
XX Claim 2; Fig 1, 2; 50pp; Japanese.
PS The invention provides nucleotide sequences encoding death domain
XX containing receptor polypeptides DR3-V1 and DR3. The DR3-V1 cDNA clone
CC is contained in ATCC deposition No. 97456 and the DR3 cDNA clone is
CC contained in ATCC deposition No. 97757. Recombinant vectors comprising
CC the nucleic acid sequences and optionally the leader sequences are
CC used for the recombinant production of the proteins. The present
CC sequence represents a cDNA encoding the death domain containing
CC receptor polypeptide (DR3-V1).
XX SQ Sequence 1783 BP; 330 A; 562 C; 564 G; 327 T; 0 other;
Alignment Scores:
Pred. No.: 2.91e-44 Length: 1783
Score: 413.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 20 Gaps: 0
US-09-993-234-6_COPY_338_417 (1-80) x AAX00924 (1-1783)
QY 1 ValMetAspAlaValProAlaArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
Db 1242 GTGATGGACGGCTCCAGCGCGCTGGAAGAGTTCTGCGCACCGTGGGCTGCGC 1301
QY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGlu 40
Db 1302 GAGCGAGAGATCGAAGCCGTGAGAGTGAATCGCCGCTCCGAGACACAGAGTACGAG 1361
QY 41 MetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeu 60
|||||

Db 1362 ATGCTCAAGCGCTGGCGCCAGCAGACAGCCCGCGGCTCGGAGCCGTTACGGCCCTG 1421
QY 61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80
Db 1422 GAGCGCATGGGGCTGAGAGCGCTGCGTGAAGACTTGGCCAGCCGCTGACAGCGGCCCG 1481
RESULT 12
AAC68776
ID AAC68776 standard; cDNA; 1783 BP.
XX AAC68776;
AC AAC68776;
XX 20-FEB-2001 (first entry)
DT 20-FEB-2001 (first entry)
XX Human death domain containing receptor DR3-V1 coding sequence.
DE Human death domain containing receptor; DR3-V1; cancer;
XX Human; death domain containing receptor; DR3-V1; cancer;
KW autoimmune disorder; inflammation; cardiovascular disorder; infection;
KW neurodegenerative disease; angiogenesis; ss.
XX Homo sapiens.
OS Homo sapiens.
XX WO200064465-A1.
PN 02-NOV-2000.
PD 02-NOV-2000.
XX 21-APR-2000; 2000WO-US10741.
PF 21-APR-2000; 2000WO-US10741.
XX 22-APR-1999; 99US-0130488.
PR 28-MAY-1999; 99US-0136741.
XX (HUMA-) HUMAN GENOME SCI INC.
PA (UNMT) UNIV MICHIGAN.
XX (YUGG/) YU G.
PA (NIJ/) NI J.
PA (GENT/) GENTZ R L.
PA (DILL/) DILLON P J.
PA (DIXI/) DIXIT V M.
XX Yu G, Ni J, Gentz RL, Dillon PJ, Dixit VM;
PI WPI; 2000-687263/67.
XX P-PSDB; AAB36264.
DR Treating graft-versus-host disease, cancer, immunodeficiency or an
XX autoimmune disease comprising administering an antibody to Death Domain
PT Containing Receptor proteins and a second therapeutic agent -
PT Containing Receptor proteins and a second therapeutic agent -
XX Example 1; Fig 1; 273pp; English.
PS The present invention provides the protein and coding sequences for two
XX death domain containing receptors, designated DR3 and DR3-V1. These
CC receptors are involved in apoptosis, and the sequences given can be used
CC in the treatment of cancers, infections, cardiovascular disorders such as
CC arrhythmias, ischemia, aneurysms, arterial occlusive diseases, embolisms
CC and congenital heart defects, neurodegenerative diseases including
CC Alzheimer's and Parkinson's diseases, autoimmune diseases such as multiple
CC sclerosis, arthritis, diabetes, Graves' disease, asthma and psoriasis,
CC and to promote angiogenesis and wound healing.
XX SQ Sequence 1783 BP; 330 A; 562 C; 564 G; 327 T; 0 other;
Alignment Scores:
Pred. No.: 2.91e-44 Length: 1783
Score: 413.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0
US-09-993-234-6_COPY_338_417 (1-80) x AAC68776 (1-1783)
QY 1 ValMetAspAlaValProAlaArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
|||||

|||||
Db 1242 GTGATGGACGGGTCCACGGCGGGCTGTGAAGAGTTCGTGGCACGCTGGGGCTGCC 1301
OY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnTyrGlu 40
|||||
Db 1302 GAGGCAGAGATCGAAGCCCTGAGAGTGCAGATCGGCCCTCCGAGACGACGAGTACGAG 1361
OY 41 MetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeu 60
|||||
Db 1362 ATGCTCAAGCGCTGGCGGCAGACAGCCCGGGCTCGAGCCGTTACGGGCCCTG 1421
OY 61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80
|||||
Db 1422 GAGCGCATGGGGCTGGACGGCTGCGTGAAGACTTCCGCACGCCCTGCAGCGCGGCCG 1481
RESULT 13
AAV28700
ID AAV28700 standard; cDNA; 1847 BP.
XX AAV28700;
XX 20-AUG-1998 (first entry)
DE Human apoptosis inducing receptor coding sequence.
XX
KW Apoptosis inducing receptor; AIR protein; human; cell death regulator;
KW Type I transmembrane protein; tumour cell death; autoimmune disease;
KW therapy; ss.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 236..1489
FT /*tag= a
FT /product= AIR
XX
XX W09814565-A1.
XX
XX 09-APR-1998.
XX
XX 03-OCT-1997; 97WO-US17876.
XX
XX 04-OCT-1996; 96US-0044456.
XX
XX (IMMV) IMMUNEX CORP.
XX
XX Perkins PA;
XX
XX WPI; 1998-240077/21.
XX P-PSDB; AAW57045.
XX
XX
PT DNA encoding apoptosis inducing receptor - which is Type I
PT transmembrane protein, useful for regulating cell death
XX
XX Claim 2; Page 28-30; 45pp; English.
XX
XX This sequence encodes the human apoptosis inducing receptor (AIR) of the
XX invention. AIR is a Type I transmembrane protein, soluble forms of which
XX can be used to regulate cell death in a therapeutic setting. Soluble AIR
XX can also be used in vitro to block apoptosis or AIR-expressing cells, or
XX to screen agonists or antagonists of AIR activity. The cytoplasmic domain
XX of AIR can be used to develop assays for inhibitors of AIR-induced cell
XX death, which is useful to regulate cell death in a therapeutic setting as
XX well as in vitro. Agonists of AIR activity can be used to kill tumour
XX cells that express AIR, or T cells expressing AIR in autoimmune diseases.
XX
XX Sequence 1847 BP; 316 A; 605 C; 579 G; 347 T; 0 other;

Query Match: 100.00% Indels: 0
DB: 19 Gaps: 0
US-09-993-234-6_copy_338_417 (1-80) x AAV28700 (1-1847)
OY 1 ValMetAspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
|||||
Db 1247 GTGATGAGCGCGGTCCACAGCGGGCTGGAAGAGTTCGTGGCACGCTGGGCTGCCG 1306
OY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnTyrGlu 40
|||||
Db 1307 GAGGCAGAGATCGAAGCCCTGAGGTGAGATCGGCCCTCCGAGACGACGAGTACGAG 1366
OY 41 MetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeu 60
|||||
Db 1367 ATGCTCAAGCGCTGGCGGCAGACAGCCCGGGCTCGAGCGCGCTTACGGGCCCTG 1426
OY 61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80
|||||
Db 1427 GAGCGCATGGGGCTGGACGGCTGCGTGAAGACTTCCGCACGCCCTGCAGCGCGGCCG 1486
RESULT 14
AAL47185
ID AAL47185 standard; DNA; 4825 BP.
XX AAL47185;
XX
AC AAL47185;
XX
XX 22-AUG-2002 (first entry)
DE Human DR3 gene associated with rheumatoid arthritis.
XX
XX
KW Human; DR3; rheumatoid arthritis; antirheumatic; antiarthritic;
KW gene therapy; gene; ds.
XX
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..4825
FT /*tag= a
FT /product= "DR3"
FT /note= "this sequence contains introns"
FT 1..127
FT /*tag= b
FT /number= 1
FT 128..635
FT /*tag= c
FT /number= 1
FT 636..756
FT /*tag= d
FT /number= 2
FT 757..973
FT /*tag= e
FT /number= 2
FT 974..1108
FT /*tag= f
FT /number= 3
FT 1109..1476
FT /*tag= g
FT /number= 3
FT 1477..1644
FT /*tag= h
FT /number= 4
FT 1645..1742
FT /*tag= i
FT /number= 4
FT 1743..1821
FT /*tag= j
FT /number= 5
FT 1822..3068
FT /*tag= k
FT /number= 5
FT 3069..3124
FT /*tag= l

Alignment Scores:
Pred. No.: 3.04e-44 Length: 1847
Score: 413.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

FT /number= 6
FT Intron 3125..3225
FT /*tag= m
FT exon 3226..3333
FT /*tag= n
FT Intron 3334..3529
FT /*tag= o
FT exon 3530..3577
FT /*tag= p
FT Intron 3578..4021
FT /*tag= q
FT exon 4022..4202
FT /*tag= r
FT Intron 4203..4433
FT /*tag= s
FT exon 4434..4825
FT /*tag= t
FT /number= 10

WO200234912-A1.

02-MAY-2002.

24-OCT-2001; 2001WO-JP09313.

PR 24-OCT-2000; 2000JP-0324296.

PR 27-MAR-2001; 2001JP-0090546.

PR 30-MAR-2001; 2001JP-0099990.

XX (NEWI-) NEW IND RES ORG.

XX (SHIO/) SHIOZAWA S.

XX Shiozawa S, Konishi Y;

XX WPI; 2002-417132/44.

XX Genomes, particularly DR3 genomic DNA, participating in rheumatoid

XX arthritis via mutation, useful in evaluating disease onset and its

XX possibility and providing therapy and remedies -

XX Claim 1; Page 64-66; 84pp; Japanese.

XX The present invention relates to the human DR3 gene, which is associated

XX with rheumatoid arthritis. Certain mutations in the gene can be linked to

XX the disease. The sequences can be used to evaluate disease onset and its

XX possibility and to provide therapy and remedies. The present sequence is

XX the gene of the invention.

XX Sequence 4825 BP; 921 A; 1378 C; 1521 G; 1005 T; 0 other;

XX Alignment Scores:

XX Pred. No.: 9.92e-44

XX Score: 413.00

XX Percent Similarity: 100.00%

XX Best Local Similarity: 100.00%

XX Query Match: 100.00%

XX DB: 24

US-09-993-234-6_COPY_338_417 (1-80) x AAL47185 (1-4825)

OY 1 ValmetaspalaValProAlaArgTrpLysGluPheValArgThrLeuGlyLeuArg 20

Db 4520 GTGATGGACGGCGTCCAGCGCGGCTGGAGAGAGTTCGTGCGCACGCTGGGGCTGCGC 4579

OY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGlu 40

|||||

Db 4580 GAGCAGAGATCGAAGCCGTGGAGGTGAGATCGGCCGCTTCCGAGACGACGATACGAG 4639

OY 41 MetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaLeu 60

Db 4640 ATGCTCAAGCGCTGGCGCCAGCAGCAGACCCGCGGCTCGGAGCCGTTACGCGGCCCTG 4699

OY 61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80

Db 4700 GAGCGCATGGGGCTGGACGCGCTGCTGGAAGACTTGGCAGCCGCTGCAAGCGGCCCG 4759

RESULT 15

ABK42690

ID ABK42690 standard; DNA; 10797 BP.

XX ABK42690;

DE 21-MAY-2002 (first entry)

DE Genomic sequence #589 encoding novel human connective tissue polypeptide.

KW Human; connective tissue related disorder; cancer; gene therapy;

OS cytosstatic; gene; ds.

OS Homo sapiens.

PN WO200155343-A1.

PD 02-AUG-2001.

PF 17-JAN-2001; 2001WO-US01322.

XX 31-JAN-2000; 2000US-0179065.

PR 04-FEB-2000; 2000US-0180628.

PR 24-FEB-2000; 2000US-0184664.

PR 02-MAR-2000; 2000US-0186350.

PR 16-MAR-2000; 2000US-0189874.

PR 17-MAR-2000; 2000US-0190076.

PR 18-APR-2000; 2000US-0198123.

PR 19-MAY-2000; 2000US-0205515.

PR 07-JUN-2000; 2000US-0209467.

PR 28-JUN-2000; 2000US-0214886.

PR 30-JUN-2000; 2000US-0215135.

PR 07-JUL-2000; 2000US-0216647.

PR 11-JUL-2000; 2000US-0217487.

PR 11-JUL-2000; 2000US-0217496.

PR 14-JUL-2000; 2000US-0218290.

PR 26-JUL-2000; 2000US-0220963.

PR 26-JUL-2000; 2000US-0220964.

PR 14-AUG-2000; 2000US-0224518.

PR 14-AUG-2000; 2000US-0224519.

PR 14-AUG-2000; 2000US-0225213.

PR 14-AUG-2000; 2000US-0225214.

PR 14-AUG-2000; 2000US-0225266.

PR 14-AUG-2000; 2000US-0225267.

PR 14-AUG-2000; 2000US-0225268.

PR 14-AUG-2000; 2000US-0225270.

PR 14-AUG-2000; 2000US-0225447.

PR 14-AUG-2000; 2000US-0225757.

PR 14-AUG-2000; 2000US-0225758.

PR 14-AUG-2000; 2000US-0225759.

PR 18-AUG-2000; 2000US-0226279.

PR 22-AUG-2000; 2000US-0226681.

PR 22-AUG-2000; 2000US-0226868.

PR 22-AUG-2000; 2000US-0227182.

PR 23-AUG-2000; 2000US-0227009.

PR 30-AUG-2000; 2000US-0228924.

PR 01-SEP-2000; 2000US-0229287.

PR 01-SEP-2000; 2000US-0229343.

PR 01-SEP-2000; 2000US-0229344.

PR 01-SEP-2000; 2000US-0229345.

PR 05-SEP-2000; 2000US-0229509.

PR 05-SEP-2000; 2000US-0229513.

PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.

PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-565190/63.
DR
XX
XX
PT Nucleic acid encoding novel connective tissue associated polypeptides,
PT used in diagnosing, preventing, treating or ameliorating a disorder
PT such as cancer or rheumatoid arthritis -
XX
XX
PS Disclosure; SEQ ID No 1577; 673pp; English.
XX
XX
CC The present invention relates to the isolation of novel human connective
CC tissue related polypeptides (AAU86435-AAU86923) and the polynucleotide
CC (cDNA and genomic) sequences encoding them. The sequences of the
CC invention are useful in the diagnosis, treatment, prevention and/or
CC prognosis of diseases associated with connective tissue(s), including
CC cancer. The polynucleotide sequences of the invention are also useful
CC in gene therapy. ABK42102-ABK43116 represent genomic sequences encoding
CC the novel human connective tissue related polypeptides.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 10797 BP; 2003 A; 3215 C; 3378 G; 2201 T; 0 other;

Alignment Scores:
Pred. No.: 2.67e-43 Length: 10797
Score: 413.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 23 Gaps: 0

US-09-993-234-6_COPY_338_417 (1-80) x ABK42690 (1-10797)
QY 1 ValMetAspAlaValProAlaArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
DB 9119 GTGATGGAGCGGGTCCAGCGCGGCGTGAAGAGTTCTGCGCAGCTGGGGCTGCGC 9178
QY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGlu 40
DB 9179 GAGCGACAGATCGAAGCCGTGAGGTGAGATCGGCCGCTTCCGAGACCACTACGAG 9238
QY 41 MetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaLeu 60
DB 9239 ATGCTCAAGCGCTGGCGCCACGACGACGCCGGGCTCGAGACCGTTTACGGCGCCCTG 9298
QY 61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80
DB 9299 GAGCGCATGGGGCTGGACGGCTGCTGAGAGACTTGGCGACGCCGCTGACGGCGCCG 9358

Mon Apr 7 09:25:00 2003

us-09-993-234-6_copy_338_417.rng

Page 12

Search completed: April 6, 2003, 16:52:44
Job time : 81.489 secs

GenCore version 5.1.4-p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 6, 2003, 15:35:34 ; Search time 929.72 Seconds
(without alignments)
2504.221 Million cell updates/sec

Title: US-09-993-234-6_COPY_338_417
Perfect score: 413
Sequence: 1 VMDAVPARRMKEFVRTLGRL.....ERMGLDGCVEDLRSLQRCR 80

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US0993234/runat_27032003_115455_15349/app_query.fasta_1.2346
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS-human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US0993234@CGN_1_1_8534@runat_27032003_115455_15349 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*

29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	413	100.0	705	9 HSU94508	U94508 Human lymph
2	413	100.0	838	9 HSU94507	U94507 Human lymph
3	413	100.0	952	9 HSU94506	U94506 Human lymph
4	413	100.0	1087	9 HSU94505	U94505 Human lymph
5	413	100.0	1119	9 HSU94509	U94509 Human lymph
6	413	100.0	1143	9 HSU94510	U94510 Human lymph
7	413	100.0	1198	9 HSU94504	U94504 Human lymph
8	413	100.0	1250	6 AX150176	AX150176 Sequence
9	413	100.0	1254	6 ARI19657	ARI19657 Sequence
10	413	100.0	1254	9 HSU72763	U72763 Human death
11	413	100.0	1254	9 HSU78029	U78029 Human apopto
12	413	100.0	1254	9 HSU94501	U94501 Human lymph
13	413	100.0	1257	9 HSU94502	U94502 Human lymph
14	413	100.0	1355	9 HSU94503	U94503 Human lymph
15	413	100.0	1528	9 HSU83597	U83597 Human death
16	413	100.0	1557	9 HSU75463	U75380 Human apopt
17	413	100.0	1581	9 AK094488	AK094488 Human apopt
18	413	100.0	1634	9 HSU74611	U74611 Human Apo-3
19	413	100.0	1662	6 AX055442	AX055442 Sequence
20	413	100.0	1662	6 AX201344	AX201344 Sequence
21	413	100.0	1783	6 ARI19656	ARI19656 Sequence
22	413	100.0	2053	9 AK094488	AK094488 Homo sapi
23	413	100.0	4811	9 AB051851	AB051851 Homo sapi
24	413	100.0	4825	9 AB051850	AB051850 Homo sapi
25	413	100.0	53982	9 AL158217	AL158217 Human DNA
26	401	97.1	1669	9 AF026070	AF026070 Homo sapi
27	401	97.1	1743	6 AX331947	AX331947 Sequence
28	401	97.1	1743	9 HSN5L1	Y09392 H.sapiens m
29	401	97.1	1763	9 AF026071	AF026071 Homo sapi
30	395	95.6	1619	10 BC017526	BC017526 Mus muscu
31	395	95.6	97483	2 AC118359	AC118359 Rattus no
32	395	95.6	196368	2 AL772240	AL772240 Mus muscu
33	389	94.2	1665	10 AF329969	AF329969 Mus muscu
34	354	85.7	18015	10 AF134858	AF134858 Mus muscu
35	300	72.6	523	11 G37503	G37503 SHGC-57889
36	175.5	42.5	2004	4 SSU19994	U19994 Sus scrofa
37	171	41.4	2115	10 AF329976	AF329976 Rattus no
38	171	41.4	2115	10 AF329977	AF329977 Rattus no
39	171	41.4	2115	10 AF329978	AF329978 Rattus no
40	171	41.4	2115	10 AF329979	AF329979 Rattus no
41	171	41.4	2115	10 AF329980	AF329980 Rattus no
42	171	41.4	2115	10 AF329981	AF329981 Rattus no
43	171	41.4	2130	6 AX401925	AX401925 Sequence
44	171	41.4	2130	10 RAT1NER	M63122 Rat tumor n
45	171	41.4	187998	2 AC125909	AC125909 Rattus no

RESULT 1

ALIGNMENTS

HSU94508
LOCUS HSU94508 705 bp mRNA linear PRI 15-MAY-1997
DEFINITION Human lymphocyte associated receptor of death 7 mRNA, alternatively
spliced, complete cds.
ACCESSION U94508
VERSION U94508.1 GI:2071962
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Screation,G.R., Xu,X.N., Olsen,A.L., Cowper,A.E., Tan,R.,
McMichael,A.J. and Bell,J.I.
1 (bases 1 to 705)
LARD: a new lymphoid-specific death domain containing receptor
regulated by alternative pre-mRNA splicing
Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)
JOURNAL MEDLINE 97272273
PUBMED 9114039
REFERENCE 2 (bases 1 to 705)
AUTHORS Screation,G.R.
TITLE Direct Submission
JOURNAL Submitted (19-MAR-1997) Molecular Immunology Group, Institute of
Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3
9DU, UK
FEATURES
source location/Qualifiers
1. 705
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Hela"
/cell_type="lymphocyte"
1. 705
/function="mediates apoptosis"
/note="similar to Fas and TNF-R1; lacks transmembrane
domain; possibly soluble; LARD-6; LARD-7; NGFR family
member"
/codon_start=1
/product="lymphocyte associated receptor of death 7"
/protein_id="AAC51313.1"
/db_xref="GI:2071963"
/translation="MEQRPRGCAVAALLLVILGARAQGTRSPRCDACGDFHKKIG
LFCCRGCPADAGMEALPPATHTLSPIDSAHTLAPDSEKICTVOLVGNSTPGY
PETQALCPQVWTMSDOLPSRALGPAAPTLSPSPAGSPAMMLQPGPOLYDVMDAVP
ARRWKEFVRTGLREAEIEAVEVEIGFRDQYEMLRKRWQQPAGLGAVVALEMG
LDGVEDLRSRLQRP"
misc_feature 160..161
/note="deletion compared to LARD 1a, deposited in GenBank
Accession Number U94501, probable skipping of putative
exons 3, 4, 5, 6 and 7"
BASE COUNT 112 a 236 c 248 g 109 t
ORIGIN
Alignment Scores:
Pred. No.: 1.3e-35 Length: 705
Score: 413.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-09-993-234-6_COPY_338_417 (1-80) x HSU94508 (1-705)
QY 1 ValMetaspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
Db 463 GTGATGACGCGGTCCAGCGCGCGCTGGAAGAGATTGTCGCGACGCTGGGGCTGC 522
QY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGlu 40
Db 523 GAGCGAGAGATCGAAGCGCTGAGAGATCGCGCGCTCCGACAGACAGAGTACGAG 582
QY 41 MetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeu 60
Db 583 ATGCTCAAGCGCTGGCGCCAGACAGACCCCGCGGCTCGGAGCCGTTTACGGCGCCCTG 642

QY 61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80
Db 643 GAGCGCATGGGGCTGGACGCGCTGCTGGAAGACTTGGCGACGCCGCTGCAGCGCGGCCG 702
RESULT 2
LOCUS HSU94507
DEFINITION HSU94507 838 bp mRNA linear PRI 15-MAY-1997
Human lymphocyte associated receptor of death 6 mRNA, alternatively
spliced, complete cds.
ACCESSION U94507
VERSION U94507.1 GI:2071960
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Screation,G.R., Xu,X.N., Olsen,A.L., Cowper,A.E., Tan,R.,
McMichael,A.J. and Bell,J.I.
1 (bases 1 to 838)
LARD: a new lymphoid-specific death domain containing receptor
regulated by alternative pre-mRNA splicing
Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)
JOURNAL MEDLINE 97272273
PUBMED 9114039
REFERENCE 2 (bases 1 to 838)
AUTHORS Screation,G.R.
TITLE Direct Submission
JOURNAL Submitted (19-MAR-1997) Molecular Immunology Group, Institute of
Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3
9DU, UK
FEATURES
source location/Qualifiers
1. 838
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Hela"
/cell_type="lymphocyte"
1. 381
/function="mediates apoptosis"
/note="similar to Fas and TNF-R1; truncated before the
transmembrane domain; possibly soluble; LARD-6"
/codon_start=1
/product="lymphocyte associated receptor of death 6"
/protein_id="AAC51312.1"
/db_xref="GI:2071961"
/translation="MEQRPRGCAVAALLLVILGARAQGTRSPRCDACGDFHKKIG
LFCCRGCPAASQVALENCASAVADTRCGCKPGWFEQVSCVSSSPFYCQPCLDGAL
HRHTRLCHPSVTTLGQRPHPSSSTS"
misc_feature 160..161
/note="deletion compared to LARD 1a, deposited in GenBank
Accession Number U94501, probable skipping of putative
exon 3"
misc_feature 328..329
/note="deletion compared to LARD-1a, deposited in GenBank
Accession Number U94501, probably due to skipping of
putative exons 5, 6 and 7, leading to premature
transcriptional termination"
BASE COUNT 134 a 281 c 285 g 138 t
ORIGIN
Alignment Scores:
Pred. No.: 1.56e-35 Length: 838
Score: 413.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-09-993-234-6_COPY_338_417 (1-80) x HSU94507 (1-838)
QY 1 ValMetaspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
Db 596 GTGATGACGCGGTCCAGCGCGCGCTGGAAGAGATTGTCGCGACGCTGGGGCTGC 655

QY 21 GUAAGLUILEGLUALAVALGUAIGLUILEGLYARGPHEARGSPGLNGINTYRGU 40
DB 656 GAGGCAGAGATCGAAGCCGTGGAGGTGAGATCGGCCCTTCGAGACCAGCAGTACGAG 715
QY 41 MetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeu 60
DB 716 ATGCTCAAGCGCTGGCGCCAGCAGACCCGGCGCTCGAGCCGTTTACGGGCCCTG 775
QY 61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80
DB 776 GAGCGCATGGGGCTGGACGGCTGGGAAGACTTGGCGCAGCCGCTGCAGCGCGCCCG 835
RESULT 3
HSU94506 952 bp mRNA linear PRI 15-MAY-1997
LOCUS Human lymphocyte associated receptor of death 5 mRNA, alternatively
DEFINITION spliced, complete cds.
ACCESSION U94506
VERSION U94506.1 GI:2071958
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 952)
AUTHORS Screaton,G.R., Xu,X.N., Olsen,A.L., Cowper,A.E., Tan,R.,
McMichael,A.J. and Bell,J.I.
TITLE LARD: a new lymphoid-specific death domain containing receptor
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)
MEDLINE 97272273
PUBMED 9114039
REFERENCE 2 (bases 1 to 952)
AUTHORS Screaton,G.R.
TITLE Direct Submission
JOURNAL Submitted (19-MAR-1997) Molecular Immunology Group, Institute of
Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3
9DU, UK
FEATURES
source Location/Qualifiers
1..952
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Hela"
/cell_type="lymphocyte"
1..411
/function="mediates apoptosis"
/note="LARD-5; similar to Fas and TNF-R1; possibly
soluble; truncated before the transmembrane domain"
/codon_start=1
/product="lymphocyte associated receptor of death 5"
/protein_id="AAC51311.1"
/db_xref="GI:2071959"
/translation="MEQRPFGCAVAALLLVLLGARAQGGTRSPRCDCAGDFHKKIG
LFCRCGPASQVALENCASAVADTRCGCRPGWFEVCQVSQVSSSPFYCQPLDCGAL
HRHRLICSRDITDCGTCLPGFYEHDGCVSCP"
160..161
/note="deletion compared to LARD 1a, deposited in GenBank
Accession Number U94501, probable skipping of putative
exon 3"
misc_feature
407..408
/note="deletion compared to LARD 1a, deposited in GenBank
Accession Number U94501, probably due to skipping of
putative exons 6 and 7, leading to premature
transcriptional termination"
BASE COUNT 154 a 317 c 319 g 162 t
ORIGIN
Alignment Scores:
Pred. No.: 1.79e-35 Length: 952
Score: 413.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-09-993-234-6_copy_338_417 (1-80) x HSU94506 (1-952)
QY 1 ValMetAspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
DB 710 GTGATGAGCGGGTCCACGCGCGCGGTGAAGAGATTGTCGGCACGCTGGGGCTGCC 769
QY 21 GUAAGLUILEGLUALAVALGUAIGLUILEGLYARGPHEARGSPGLNGINTYRGU 40
DB 770 GAGCGAGAGATCGAAGCCGTGGAGGTGAGATCGGCCCTTCGAGACCAGCAGTACGAG 829
QY 41 MetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeu 60
DB 830 ATGCTCAAGCGCTGGCGCCAGCAGACCCGGCGCTCGAGCCGTTTACGGGCCCTG 889
QY 61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80
DB 890 GAGCGCATGGGGCTGGACGGCTGGGAAGACTTGGCGCAGCCGCTGCAGCGCGCCCG 949

RESULT 4
HSU94505 1087 bp mRNA linear PRI 15-MAY-1997
LOCUS Human lymphocyte associated receptor of death 4 mRNA, alternatively
DEFINITION spliced, complete cds.
ACCESSION U94505
VERSION U94505.1 GI:2071956
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1087)
AUTHORS Screaton,G.R., Xu,X.N., Olsen,A.L., Cowper,A.E., Tan,R.,
McMichael,A.J. and Bell,J.I.
TITLE LARD: a new lymphoid-specific death domain containing receptor
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)
MEDLINE 97272273
PUBMED 9114039
REFERENCE 2 (bases 1 to 1087)
AUTHORS Screaton,G.R.
TITLE Direct Submission
JOURNAL Submitted (19-MAR-1997) Molecular Immunology Group, Institute of
Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3
9DU, UK
FEATURES
source Location/Qualifiers
1..1087
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Hela"
/cell_type="lymphocyte"
1..546
/function="mediates apoptosis"
/note="LARD-4; similar to Fas and TNF-R1; possibly
soluble; truncated before the transmembrane domain"
/codon_start=1
/product="lymphocyte associated receptor of death 4"
/protein_id="AAC51310.1"
/db_xref="GI:2071957"
/translation="MEQRPFGCAVAALLLVLLGARAQGGTRSPRCDCAGDFHKKIG
LFCRCGPAGHYLKAPCTEPCGNSSTLCVCPDPTFLAMENHNSCARCOACDQASQV
ALENCASAVADTRCGCRPGWFEVCQVSQVSSSPFYCQPLDCGALHRHRLICSRDIT
DCGTCLPGFYEHDGCVSCP"
542..543
/note="deletion compared to LARD 1a, deposited in GenBank
Accession Number U94501, probable skipping of putative
exons 6 and 7 leading to premature transcriptional
termination"
BASE COUNT 180 a 363 c 355 g 189 t
ORIGIN
misc_feature

Alignment Scores:

Pred. No.: 2.06e-35 Length: 1087
Score: 413.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-993-234-6_COPY_338_417 (1-80) x HSU94505 (1-1087)

QY 1 ValMetAspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
|||||
Db 845 GTGATGAGCGCGTCCACGCCGCCGCTGGAGAGATTCTGCGCACGCTGGGGCTGCC 904
QY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGlu 40
|||||
Db 905 GAGGCAGAGATCGAAGCCGTGAGGTGAGATCGGCCCTTCCGAGACCAGCAGTAGCAG 964
QY 41 MetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeu 60
|||||
Db 965 ATGCTCAAGCGCTGCGCCAGCAGACGCCGCCGCTCGAGCCGTTACGGCGCCCTG 1024
QY 61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80
|||||
Db 1025 GAGCGCATGGGGCTGACGGCTGCGTGAAGACTTGGCAGACGCCCTGACAGCGGCCCG 1084

RESULT 5
HSU94509 1119 bp mRNA linear PRI 15-MAY-1997
LOCUS Human lymphocyte associated receptor of death 8 mRNA, alternatively
spliced, complete cds.
ACCESSION U94509
VERSION U94509.1 GI:2071964

KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens.

REFERENCE
AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
1 (bases 1 to 1119) Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

TITLE
JOURNAL Sreaton,G.R., Xu,X.N., Olsen,A.L., Cowper,A.E., Tan,R.,
MEDLINE LARD: a new lymphoid-specific death domain containing receptor
PUBMED regulated by alternative pre-mRNA splicing
97272273 Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)
9114039

REFERENCE
AUTHORS 2 (bases 1 to 1119)
TITLE Sreaton,G.R.
JOURNAL Direct Submission
MEDLINE Submitted (19-MAR-1997) Molecular Immunology Group, Institute of
PUBMED Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3
9DU, UK

FEATURES
source Location/Qualifiers

1..1119
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Hela"
/cell_type="lymphocyte"
1..1119
/function="mediates apoptosis"
/note="LARD-8; NGFR family member; similar to Fas and
TNF-R1"

/codon_start=1
/product="lymphocyte associated receptor of death 8"
/protein_id="AAC51314.1"
/db_xref="GI:2071965"

/translation="MEQRPRGCAVAALLLVLGARAQGTRSPRCDCAGDFHKIG
LFCCRGCPAASQVALENSAVADTRCGCKPGWFEVCOYSCVSSPFYCOPCLDCGAL
HRRTRLICSRDITDCGTCILPGFYEHGDCVSCPTSLGSCPERCAAVCGWRQMFVYQV
LAGLVPLILGATLTYTRHCPHKLPLVTADAGMALTPPAPATHLSPLDSAHHTLLA
PPDSSEKICTVOLVGNWSMTGYPETOALCPQVYWSMDQLPSRALGPAAPTLSPESP
AGSPAMLIQPGPOLVDVADAVPARMKEFVRTLGLREAEIEAVEVEIGRFDDQYEML
KRWKQQQPAGLGAVYAAIERMGLDGCVEDLRSRLQKGP"

misc_feature

160..161
/note="deletion compared to LARD 1a, deposited in GenBank
Accession Number U94501, probable skipping of putative
exon 3"
BASE COUNT 175 a 374 c 371 g 199 t
ORIGIN

Alignment Scores:

Pred. No.: 2.13e-35 Length: 1119
Score: 413.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-993-234-6_COPY_338_417 (1-80) x HSU94509 (1-1119)

QY 1 ValMetAspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
|||||
Db 877 GTGATGAGCGCGTCCACGCCGCCGCTGGAGAGATTCTGCGCACGCTGGGGCTGCC 936
QY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGlu 40
|||||
Db 937 GAGGCAGAGATCGAAGCCGTGAGGTGAGATCGGCCCTTCCGAGACCAGCAGTAGCAG 996
QY 41 MetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeu 60
|||||
Db 997 ATGCTCAAGCGCTGCGCCACAGCAGACGCCGCCGCTCGAGCCGTTACGGCGCCCTG 1056
QY 61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80
|||||
Db 1057 GAGCGCATGGGGCTGACGGCTGCGTGAAGACTTGGCAGACGCCCTGACAGCGGCCCG 1116

RESULT 6
HSU94510 1143 bp mRNA linear PRI 15-MAY-1997
LOCUS Human lymphocyte associated receptor of death 9 mRNA, alternatively
spliced, complete cds.
ACCESSION U94510
VERSION U94510.1 GI:2071966

KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens.

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
1 (bases 1 to 1143) Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

TITLE
JOURNAL Sreaton,G.R., Xu,X.N., Olsen,A.L., Cowper,A.E., Tan,R.,
MEDLINE LARD: a new lymphoid-specific death domain containing receptor
PUBMED regulated by alternative pre-mRNA splicing
97272273 Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)
9114039

REFERENCE
AUTHORS 2 (bases 1 to 1143)
TITLE Sreaton,G.R.
JOURNAL Direct Submission
MEDLINE Submitted (19-MAR-1997) Molecular Immunology Group, Institute of
PUBMED Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3
9DU, UK

FEATURES
source Location/Qualifiers

1..1143
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Hela"
/cell_type="lymphocyte"
1..1143
/function="mediates apoptosis"
/note="LARD-9; NGFR family member; similar to Fas and
TNF-R1"

/codon_start=1
/product="lymphocyte associated receptor of death 9"
/protein_id="AAC51315.1"
/db_xref="GI:2071967"


```

/translation="MEORPRGCAVAALLLVLGARAQGGTRSPRCDACGDFHKKIG
LFCCRGPAGHYLKAPCTEPCGNSTCLVCPDFTFLAMENHNHSEACARCADEQASOV
ALENCSAVADTRCGCKPGWFEVCQSVSSPFYCGPCLDCGALHHRHRLCSRDT
DCGTCLPGFYEHDGCVSPTSLGSCPERCAVCGWRONAGMEALTPPATHLSP
LSAHTLAPDSSERICTVQVLGNWSWTPGTPETQALCPQVTWSMDQLPSRALGPAA
PTLSPSPAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTGLREAETEAWEVEIGRF
RDQYEMLMKRWROQQPAGLGAVALALERMGLDGCVEDLRSLRQRP"
598.599
/misc_feature
/note="deletion compared to LARD 1a, deposited in GenBank
Accession Number U94501, probable skipping of putative
exon 7 encoding the transmembrane domain"
BASE COUNT      188 a      378 g      378 g      199 t
ORIGIN

Alignment Scores:
Pred. No.:      2.18e-35      Length:      1143
Score:          413.00      Matches:      80
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:             9      Gaps:      0

US-09-993-234-6_COPY_338_417 (1-80) x HSU94510 (1-1143)
QY      1 ValMetaspAlaValProAlaArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
Db      901 GTGATGGACGGCGTCCAGCGCGCGCTGGAAAGAGTTCTGTCGCACGCTGGGGCTGCGC 960
QY      21 GluAlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGlu 40
Db      961 GAGGCAGAGATCGAAGCCGCTGGAGTGGAGATCGGCCCTTCGAGACACAGCAGTACAGAG 1020
QY      41 MetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeu 60
Db      1021 ATGCTCAAGCGCTGGCGCCAGCAGACCCCGCGGCTCGAGCCGTTTACGCGGCCCTG 1080
QY      61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80
Db      1081 GAGCGCATGGGGCTGGACGGCTGCTGGAAGACTTGCGCAGCCGCTGCAGCGCGGCCCG 1140

RESULT 7
LOCUS      HSU94504      1198 bp      mRNA      linear      PRI 15-MAY-1997
DEFINITION Human lymphocyte associated receptor of death 3 mRNA, alternatively
spliced, complete cds.
ACCESSION      U94504
VERSION      U94504.1 GI:2071954
KEYWORDS
SOURCE      Homo sapiens.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 1198)
AUTHORS      Screation,G.R., Xu,X.N., Olsen,A.L., Cowper,A.E., Tan,R.,
McMichael,A.J. and Bell,J.I.
TITLE      LARD: a new lymphoid-specific death domain containing receptor
regulated by alternative pre-mRNA splicing
JOURNAL      Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)
MEDLINE      97272273
PUBMED      9114039
REFERENCE      2 (bases 1 to 1198)
AUTHORS      Screation,G.R.
TITLE      Direct Submission
JOURNAL      Submitted (19-MAR-1997) Molecular Immunology Group, Institute of
Molecular Medicine, John Radcliffe Hospital, Headington, Oxford, OX3
9DU, UK

FEATURES
source      1..1198
location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Hela"
/cell_type="lymphocyte"
1..657
CDS
```

```

/function="mediates apoptosis"
/note="LARD-3; similar to Fas and TNF-R1; possibly
soluble; truncated before the transmembrane domain"
/codon_start=1
/product="lymphocyte associated receptor of death 3"
/protein_id="AAC51309.1"
/db_xref="GI:2071955"
/translation="MEORPRGCAVAALLLVLGARAQGGTRSPRCDACGDFHKKIG
LFCCRGPAGHYLKAPCTEPCGNSTCLVCPDFTFLAMENHNHSEACARCADEQASOV
ALENCSAVADTRCGCKPGWFEVCQSVSSPFYCGPCLDCGALHHRHRLCSRDT
DCGTCLPGFYEHDGCVSPTSLGSCPERCAVCGWRONAGMEALTPPATHLSP
LSAHTLAPDSSERICTVQVLGNWSWTPGTPETQALCPQVTWSMDQLPSRALGPAA
PTLSPSPAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTGLREAETEAWEVEIGRF
RDQYEMLMKRWROQQPAGLGAVALALERMGLDGCVEDLRSLRQRP"
542.543
/misc_feature
/note="deletion compared to LARD 1a, deposited in GenBank
Accession Number U94501, probable skipping of putative
exon 6 leading to premature transcriptional termination"
BASE COUNT      193 a      405 c      384 g      216 t
ORIGIN

Alignment Scores:
Pred. No.:      2.29e-35      Length:      1198
Score:          413.00      Matches:      80
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:             9      Gaps:      0

US-09-993-234-6_COPY_338_417 (1-80) x HSU94504 (1-1198)
QY      1 ValMetaspAlaValProAlaArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
Db      956 GTGATGGACGGCGTCCAGCGCGCGCTGGAAAGAGTTCTGTCGCACGCTGGGGCTGCGC 1015
QY      21 GluAlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGlu 40
Db      1016 GAGGCAGAGATCGAAGCCGCTGGAGTGGAGATCGGCCCTTCGAGACACAGCAGTACAGAG 1075
QY      41 MetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeu 60
Db      1076 ATGCTCAAGCGCTGGCGCCAGCAGACCCCGCGGCTCGAGCCGTTTACGCGGCCCTG 1135
QY      61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80
Db      1136 GAGCGCATGGGGCTGGACGGCTGCTGGAAGACTTGCGCAGCCGCTGCAGCGGCCCGC 1195

RESULT 8
LOCUS      AX150176      1250 bp      DNA      linear      PAT 08-JUN-2001
DEFINITION      Sequence 1 from Patent WO0135995.
ACCESSION      AX150176
VERSION      AX150176.1 GI:14348204
KEYWORDS
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 1250)
AUTHORS      Tittle,T.V. and Wegmann,K.W.
TITLE      Tr3-specific binding agents and methods for their use
JOURNAL      Patent: WO 0135995-A 1 25-MAY-2001;
Tittle, Thomas V. (US) ; Wegmann, Keith W. (US)

FEATURES
source      1..1250
location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT      201 a      420 c      406 g      223 t
ORIGIN

Alignment Scores:
Pred. No.:      2.4e-35      Length:      1250
Score:          413.00      Matches:      80
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
```

Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-993-234-6_COPY_338_417 (1-80) x AX150176 (1-1250)
QY 1 ValMetaspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
DB 1008 GTGATGACGCGGCTCCACGCGCGGCTGGAAGAGTTCGTGCGCAGCGCTGGGCTGCC 1067
QY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnIntYrglu 40
DB 1068 GAGCAGAGATCGAAGCCGTGGAGGTGAGATCGCCGCTTCGAGACGACGAGTACGAG 1127
QY 41 MetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeu 60
DB 1128 ATGCTCAAGCGCTGGCGCCAGCAGACGCCGCGGCTCGGAGCCGTTACGGCGCCCTG 1187
QY 61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80
DB 1188 GAGCGCATGGGGCTGGACGCGCTGCGTGGAGAGACTTCCGACGCCGCTGCAGCGCGCCCG 1247
RESULT 9
AR119657 1254 bp DNA linear PAT 16-MAY-2001
LOCUS AR119657 Sequence 3 from patent US 6153402.
DEFINITION AR119657
ACCESSION AR119657
VERSION AR119657.1 GI:14102356
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1254)
AUTHORS Yu,G.-L., Ni,J., Gentz,R.L. and Dillon,P.J.
TITLE Death domain containing receptors
JOURNAL Patent: US 6153402-A 3 28-NOV-2000;
FEATURES location/Qualifiers
source 1..1254
BASE COUNT 201 a 420 c 407 g 226 t
ORIGIN
Alignment Scores:
Pred. No.: 2.4e-35 Length: 1254
Score: 413.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-993-234-6_COPY_338_417 (1-80) x AR119657 (1-1254)
QY 1 ValMetaspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
DB 1012 GTGATGACGCGGCTCCACGCGCGGCTGGAAGAGTTCGTGCGCAGCGCTGGGCTGCC 1071
QY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnIntYrglu 40
DB 1072 GAGCAGAGATCGAAGCCGTGGAGGTGAGATCGCCGCTTCGAGACGACGAGTACGAG 1131
QY 41 MetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeu 60
DB 1132 ATGCTCAAGCGCTGGCGCCAGCAGACGCCGCGGCTCGGAGCCGTTACGGCGCCCTG 1191
QY 61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80
DB 1192 GAGCGCATGGGGCTGGACGCGCTGCGTGGAGAGACTTGGCAGCGCGCTGCAGCGCGCCCG 1251
RESULT 10
HSU72763 1254 bp mRNA linear PRI 15-NOV-1996
LOCUS HSU72763 Human death receptor 3 (DR3) mRNA, complete cds.
DEFINITION U72763
ACCESSION U72763.1 GI:1669511
VERSION

KEYWORDS Homo sapiens.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 1254)
AUTHORS Chinnaiyan,A.M., O'Rourke,K., Yu,G.-L., Lyons,R.H., Garg,M., Duan,D.R., Xing,L., Gentz,R., Ni,J. and Dixit,V.M.
TITLE Signal transduction by DR3, a death domain-containing receptor related to TNFR-1 and CD95
JOURNAL Science 274 (5289), 990-992 (1996)
MEDLINE 97081063
PUBMED 8875942
REFERENCE 2 (bases 1 to 1254)
AUTHORS Chinnaiyan,A.M., O'Rourke,K., Yu,G.-L., Lyons,R.H., Garg,M., Duan,R., Xing,L., Gentz,R., Ni,J. and Dixit,V.M.
TITLE Direct Submission
JOURNAL Submitted (29-SEP-1996) Pathology, University of Michigan Medical School, 1301 Catherine St., Box 0602, Ann Arbor, MI 48109, USA
FEATURES location/Qualifiers
source 1..1254
gene /organism="Homo sapiens"
CDS /db_xref="taxon:9606"
1..1254
/gene="DR3"
1..1254
/gene="DR3"
/codon_start=1
/product="death receptor 3"
/protein_id="AAC50819.1"
/db_xref="GI:1669512"
/translation="MEQPRGCAVAALLLVILGARAQGTSPRCDCAGDFHKIG
LFCRCGPAGHYLKAPCTEPCGNSCLVCPQDTFLAWENHNSECARCQACDEQASQV
ALENCSAVADTRCGCKPGWFEVCQVSCVSSPFYCQPCIDCGALHRTRLCSRRDT
DCGTCLPGEYEHGDGCVSPTSLGSCBERCAAVCGRWQVYLLAGLVPLLGA
TLTYTYRHQWPKPLVTADAEAMEALTTPPATHLSPLDASHLLAPPDSEKICTVOL
VGNSTWTPGYPETQEALCPQVYWSMDQLPSRALGPAAPLTISPSPAGSPAMMLOPQP
LYDVMDAVPARWKEFVRTGLREAEIEAVEVEIGRFDDQYEMLKRWRQQPAGLGA
VYALERMGLDGVEDLRSRLQRP"
BASE COUNT 201 a 420 c 407 g 226 t
ORIGIN
Alignment Scores:
Pred. No.: 2.4e-35 Length: 1254
Score: 413.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-09-993-234-6_COPY_338_417 (1-80) x HSU72763 (1-1254)
QY 1 ValMetaspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
DB 1012 GTGATGACGCGGCTCCACGCGCGGCTGGAAGAGTTCGTGCGCAGCGCTGGGCTGCC 1071
QY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnIntYrglu 40
DB 1072 GAGCAGAGATCGAAGCCGTGGAGGTGAGATCGCCGCTTCGAGACGACGAGTACGAG 1131
QY 41 MetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeu 60
DB 1132 ATGCTCAAGCGCTGGCGCCAGCAGACGCCGCGGCTCGGAGCCGTTACGGCGCCCTG 1191
QY 61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80
DB 1192 GAGCGCATGGGGCTGGACGCGCTGCGTGGAGAGACTTGGCAGCGCGCTGCAGCGCGCCCG 1251
RESULT 11
HSU78029 1254 bp mRNA linear PRI 15-JAN-1997
LOCUS HSU78029 Human apoptosis inducing receptor AIR mRNA, complete cds.
DEFINITION U78029
ACCESSION

VERSION U78029.1 GI:1778763
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS 1 (bases 1 to 1254)
Degli-Esposti,M.A., Din,W.S., Cosman,D., Smith,C.A. and Goodwin,R.G.
TITLE AIR, A Novel Member of the TNF Receptor Family, Is a Strong Inducer of Apoptosis
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1254)
AUTHORS Degli-Esposti,M.A. and Goodwin,R.G.
TITLE Direct Submission
JOURNAL Submitted (12-NOV-1996) Biochemistry, Immunex Corporation, 51 University St., Seattle, WA 98101, USA
FEATURES
source
1.1254
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/map="1pter"
/cell_type="peripheral blood T-cells"
1.1254
/codon_start=1
/product="apoptosis inducing receptor AIR"
/protein_id="AAB40918.1"
/db_xref="GI:1778764"
/translation="MEORPRGCAAVAAALLVLGARAQGGTRSPRCDCAGDFHKKIG LFCCRGCPAGHYLKAPCTEPCGNSTCLVCPDFTLAWENHNHNSCARCQACDEQASQY ALENCASAVADTRCGCKPGWFEVCQVSSSPFYCQPLDCGALHRTLRILCSRRDT DCGTCLPGFYEHDGCVSPTSTIGSCPCCAAYCGWRQMFVQVLLAGLVVPLLGA TLTYTYRHCMWPKPLVTADAGMEALTPPATHTLSPDASHLTLAPDSSSEKICTYQL VGNSTPGYPETOALCPQVWMSMDQLPSRALGPAAPTLSPESPAGSPAMMLOPQPO LYDMDAVPARRWKEFVRTLGLREAIEAVEVEIGFRFDQOYEMLKRWROQOPAGLGA VYALERMGLDGCVEDLRSLRQGP"

CDS

BASE COUNT 201 a 420 c 407 g 226 t
ORIGIN

Alignment Scores:
Pred. No.: 2.4e-35 Length: 1254
Score: 413.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-993-234-6_COPY_338_417 (1-80) x HSU78029 (1-1254)

QY 1 ValMetaspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
Db 1012 GTGATGACGCGGTCCAGCGCGGCTGGAAGAGTTCGTGGCAGCGCTGGGGCTCGGC 1071
QY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGlu 40
Db 1072 GAGGCAGAGATCGAAGCCGTGAGGTGGAGATCGCCGCTTCCGAGACCAGCAGTACGAG 1131
QY 41 MetLeuLysArgTrpArgGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeu 60
Db 1132 ATGCTCAAGCGCTGGCGCCAGCAGACCCCGGGGCTCGAGCGCTTACGCGGCCCTG 1191
QY 61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80
Db 1192 GAGCGCATGGGGCTGGACGGCTGCGAAGACTTGGCGCAGCGCGCTGCAGCGCGGCCG 1251

RESULT 12
LOCUS HSU94501 1254 bp mRNA linear PRI 15-MAY-1997
DEFINITION Human lymphocyte associated receptor of death 1a mRNA, complete cds.
ACCESSION U94501
VERSION U94501.1 GI:2071948

KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS 1 (bases 1 to 1254)
Screaton,G.R., Xu,X.N., Olsen,A.L., Cowper,A.E., Tan,R., McMichael,A.J. and Bell,J.I.
TITLE LARD: a new lymphoid-specific death domain containing receptor regulated by alternative pre-mRNA splicing
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)
REFERENCE 97272273
PUBMED 9114039
AUTHORS 2 (bases 1 to 1254)
Screaton,G.R.
TITLE Direct Submission
JOURNAL Submitted (19-MAR-1997) Molecular Immunology Group, Institute of Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3 9DU, UK
FEATURES
source
1.1254
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Hela"
/cell_type="lymphocyte"
1.1254
/function="mediates apoptosis"
/note="LARD-1a; membrane protein; similar to Fas and TNF-R1; contains a death domain"
/codon_start=1
/product="lymphocyte associated receptor of death 1a"
/protein_id="AAC51306.1"
/db_xref="GI:2071949"
/translation="MEORPRGCAAVAAALLVLGARAQGGTRSPRCDCAGDFHKKIG LFCCRGCPAGHYLKAPCTEPCGNSTCLVCPDFTLAWENHNHNSCARCQACDEQASQY ALENCASAVADTRCGCKPGWFEVCQVSSSPFYCQPLDCGALHRTLRILCSRRDT DCGTCLPGFYEHDGCVSPTSTIGSCPCCAAYCGWRQMFVQVLLAGLVVPLLGA TLTYTYRHCMWPKPLVTADAGMEALTPPATHTLSPDASHLTLAPDSSSEKICTYQL VGNSTPGYPETOALCPQVWMSMDQLPSRALGPAAPTLSPESPAGSPAMMLOPQPO LYDMDAVPARRWKEFVRTLGLREAIEAVEVEIGFRFDQOYEMLKRWROQOPAGLGA VYALERMGLDGCVEDLRSLRQGP"

CDS

BASE COUNT 201 a 420 c 407 g 226 t
ORIGIN

Alignment Scores:
Pred. No.: 2.4e-35 Length: 1254
Score: 413.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-993-234-6_COPY_338_417 (1-80) x HSU94501 (1-1254)

QY 1 ValMetaspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
Db 1012 GTGATGACGCGGTCCAGCGCGGCTGGAAGAGTTCGTGGCAGCGCTGGGGCTCGGC 1071
QY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGlu 40
Db 1072 GAGGCAGAGATCGAAGCCGTGAGGTGGAGATCGCCGCTTCCGAGACCAGCAGTACGAG 1131
QY 41 MetLeuLysArgTrpArgGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeu 60
Db 1132 ATGCTCAAGCGCTGGCGCCAGCAGACCCCGGGGCTCGAGCGCGCTTACGCGGCCCTG 1191
QY 61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80
Db 1192 GAGCGCATGGGGCTGGACGGCTGCGAAGACTTGGCGCAGCGCGCGCTGCAGCGGCCG 1251

RESULT 13
LOCUS HSU94502 1257 bp mRNA linear PRI 15-MAY-1997
DEFINITION Human lymphocyte associated receptor of death 1a mRNA, complete cds.
ACCESSION U94502
VERSION U94502.1 GI:2071948

DEFINITION Human lymphocyte associated receptor of death 1b mRNA, alternatively spliced, complete cds.

ACCESSION U94502

VERSION U94502.1 GI:2071950

KEYWORDS

SOURCE Homo sapiens.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1257)
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
Screation,G.R., Xu,X.N., Olsen,A.L., Cowper,A.E., Tan,R., McMichael,A.J. and Bell,J.I.
LARD: a new lymphoid-specific death domain containing receptor regulated by alternative pre-mRNA splicing
Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)

TITLE LARD: a new lymphoid-specific death domain containing receptor regulated by alternative pre-mRNA splicing

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)

MEDLINE 97272273

PUBMED 9114039

REFERENCE 2 (bases 1 to 1257)
Screation,G.R.
Direct Submission
Submitted (19-MAR-1997) Molecular Immunology Group, Institute of Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3 9DU, UK

AUTHORS

JOURNAL

FEATURES

source

1. .1257
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Hela"
/cell_type="lymphocyte"
1. .1257
/function="mediates apoptosis"
/note="LARD-1b; membrane protein; similar to Fas and TNF-R1; contains a death domain"
/codon_start=1
/product="lymphocyte associated receptor of death 1b"
/protein_id="AAC51307.1"
/db_xref="GI:2071951"
/translation="MEQRPKCAVAALLLVLLGARAQGGTRSPKDCAGDFHKKIG LFCRCGPAGHYLKAPCTEPCGNSCLVCPDPTFLAWENHNSCARCQACDEQASQV ALENCASAVADTRCGCKPGWFEVCOVSSSPFYCQPCIDCGALHRTLRILCSRDIT DCGTCLPGFEYEHGDGCVSPTSLGSCPERCAVCGWRQMWQVLLAGLVPLLLGA TLTYYTRHCWPHKPLVTAADGEMALTPPATHLSPDLSAHTLLAPDSEKICTVQ LVGNSWTPRGYPETQELCPQVYMSMDQLPSRALGPAAPTLSPSPAGSPAMMLQPGP QLYDVMDAVPARWKEFVRTGLREAEIEAVEVEIGRFRDQYEMLRWRQOOPAGLG AVYALERMGLDGCVEDLRSLQKGP"

CDS

misc_feature

708. .711
/note="insertion compared to LARD-1a, deposited in GenBank Accession Number U94501, probably represents alternative 3' splice site"

BASE COUNT 202 a 421 c 408 g 226 t

ORIGIN

Alignment Scores:

Pred. No.: 2.41e-35 Length: 1257

Score: 413.00 Matches: 80

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 9 Gaps: 0

US-09-993-234-6_COPY_338_417 (1-80) x HSU94502 (1-1257)

OY 1 ValMetAspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArg 20

Db 1015 GTGATGGACGGCGTCCACAGCGCGCGCTGGAAGAGTTCGTGCGCACGCTGGGGCTGCCG 1074

OY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGlu 40

Db 1075 GAGGCAGAGATCGAAGCCGTGAGGTGAGATCGCGCTTCGAGACAGCAGTACGAG 1134

OY 41 MetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeu 60

Db 1135 ATGCTCAAGCGCTGGCGCAGCAGCAGCGCGCGCTCGAGACCGCTTACGCGGCCCTG 1194

OY 61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80

Db 1195 GAGCGCATGGGGCTGAGCGCTGCGTGAAGACTTGGCGACGCCCTGACAGCGGCCCG 1254

RESULT 14

HSU94503

LOCUS

DEFINITION 1355 bp mRNA linear PRI 15-MAY-1997

Human lymphocyte associated receptor of death 2 mRNA, alternatively spliced, complete cds.

ACCESSION U94503

VERSION U94503.1 GI:2071952

KEYWORDS

SOURCE Homo sapiens.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1355)
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
Screation,G.R., Xu,X.N., Olsen,A.L., Cowper,A.E., Tan,R., McMichael,A.J. and Bell,J.I.
LARD: a new lymphoid-specific death domain containing receptor regulated by alternative pre-mRNA splicing
Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)

TITLE LARD: a new lymphoid-specific death domain containing receptor regulated by alternative pre-mRNA splicing

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)

MEDLINE 97272273

PUBMED 9114039

REFERENCE 2 (bases 1 to 1355)
Screation,G.R.
Direct Submission
Submitted (19-MAR-1997) Molecular Immunology Group, Institute of Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3 9DU, UK

AUTHORS

JOURNAL

FEATURES

source

1. .1355
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Hela"
/cell_type="lymphocyte"
1. .762
/function="mediates apoptosis"
/note="LARD-2; similar to Fas and TNF-R1; possibly soluble; truncated before the transmembrane domain"
/codon_start=1
/product="lymphocyte associated receptor of death 2"
/protein_id="AAC51308.1"
/db_xref="GI:2071953"
/translation="MEQRPKCAVAALLLVLLGARAQGGTRSPKDCAGDFHKKIG LFCRCGPAGHYLKAPCTEPCGNSCLVCPDPTFLAWENHNSCARCQACDEQASQV ALENCASAVADTRCGCKPGWFEVCOVSSSPFYCQPCIDCGALHRTLRILCSRDIT DCGTCLPGFEYEHGDGCVSPTSLGSCPERCAVCGWRQMWQVLLAGLVPLLLGA TLTYYTRHCWPHKPLVTAADGEMALTPPATHLSPDLSAHTLLAPDSEKICTVQ LVGNSWTPRGYPETQELCPQVYMSMDQLPSRALGPAAPTLSPSPAGSPAMMLQPGP QLYDVMDAVPARWKEFVRTGLREAEIEAVEVEIGRFRDQYEMLRWRQOOPAGLG AVYALERMGLDGCVEDLRSLQKGP"

CDS

misc_feature

599. .700
/note="insertion compared to LARD 1a, deposited in GenBank Accession Number U94501, probable retained intron leading to premature transcriptional termination"

BASE COUNT 223 a 441 c 451 g 240 t

ORIGIN

Alignment Scores:

Pred. No.: 2.61e-35 Length: 1355

Score: 413.00 Matches: 80

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 9 Gaps: 0

US-09-993-234-6_COPY_338_417 (1-80) x HSU94503 (1-1355)

OY 1 ValMetAspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArg 20

Db 1113 GTGATGGACGGGTCCACAGCGCGCGCTGGAAGAGTTCGTGCGCACGCTGGGGCTGCCG 1172

OY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGlu 40

Db 1173 GAGGCAGAGATCGAAGCCGTGGAGGTGAGATCGGCCCTTCGAGACCAAGCAGTACGAG 1232

OY 41 MetLeuLysArgTrpArgGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeu 60

Db 1233 ATGCTCAAGCGCTGGCGCCAGCAGACGCCGGGCGCTCGAGCGCGTTTACGGCGCCCTG 1292

OY 61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80

Db 1293 GAGCGCATGGGGCTGGACGGCTCGGTGGAAGACTTGCGCAGCGCCCTGCAGCGCGGCCCG 1352

RESULT 15

LOCUS HSU83597 1528 bp mRNA linear PRI 27-JAN-1997

DEFINITION Human death domain receptor 3 (DDR3) mRNA, partial cds.

ACCESSION U83597

VERSION U83597.1 GI:1800292

KEYWORDS

SOURCE Homo sapiens.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1528)

AUTHORS Chaudhary, P.M. and Hood, L.E.

TITLE Direct Submission

JOURNAL Submitted (03-JAN-1997) Molecular Biotechnology, University of Washington, 1705 NE Pacific Street, HSB-K360, Seattle, WA 98195, USA

FEATURES

source location/Qualifiers

1..1528

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="1"

/map="1p36"

1..1528

/gene="DDR3"

<1..1238

/gene="DDR3"

/function="mediates apoptosis when cross-linked"

/note="A TNFR1-related death-domain containing receptor; DR3, WSL-IR, Apo-3, TRAMP; transmembrane form; similar to human EST clone 298913, GenBank Accession Number N71143"

/codon_start=3

/product="death domain receptor 3"

/protein_id="AAB41432.1"

/db_xref="GI:1800293"

/translation="GCAAVAALLLVLGARAQGGTRSPRCDCAGDFHKKIGLEFCRGCPAGHYLKAPCTEPCGNSCTCLVCPQDTFLAWENHNSCARQACDEQASQVALENCSAVADTRCGCKPGWFEVCOVSQCVSSPFYCPCLDCGALHRTLRLLCSRRDTDCETCLGFEYEHGDCVSCPTSLGSCPERCAVCGWRQMFVQVLLAGLVPLLGATLTYTYRHCPHPKPLVTADAEAGMEALTPTPATLHSLPLDSAHTLAPPDSEKICTVQLVGNSTPGYPETOEALCPQVTSWMDQLPSRALGPAAPTLSPSPAGSPAMLQPGPOLYDAMDAPPARWKEFVRTLGLEAEIEAVEVEIGRFDDQYEMLKRWROQOPAGLGAVYAALERMGLDGCVEDLRSRLQRP"

gene

CDS

BASE COUNT 280 a 496 c 470 g 282 t

ORIGIN

Alignment Scores:

Pred. No.: 2.97e-35 Length: 1528

Score: 413.00 Matches: 80

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 9 Gaps: 0

US-09-993-234-6_copy_338_417 (1-80) x HSU83597 (1-1528)

OY 1 ValMetAspAlaValProAlaArgTrpLysGluPheValArgThrLeuGlyLeuArg 20

Db 996 GTGATGAGCGCGTCCAGCGCGCGTGAAGAGTTCGTGCGCAGCGTGGCGCTGCC 1055

OY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGlu 40

Db 1056 GAGCGAGAGATCGAAGCGCGTGGAGGTGAGATCGGCCGCTTCGAGACCAAGCAGTACGAG 1115

OY 41 MetLeuLysArgTrpArgGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeu 60

Db 1116 ATGCTCAAGCGCTGGCGCCAGCAGCAACCGCGGCGCTCGAGCGCGTTTACGGCGCCCTG 1175

OY 61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80

Db 1176 GAGCGCATGGGGCTGGACGGCTCGGTGGAAGACTTGCGCAGCGCCCTGCAGCGCGGCCCG 1235

Search completed: April 6, 2003, 21:08:02

Job time : 933.72 secs

181

THIS PAGE BLANK (USPTO)

GenCore version 5.1.4-p5-4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 6, 2003, 16:28:24 ; Search time 13.5049 Seconds
(without alignments)
1816.682 Million cell updates/sec

Title: US-09-993-234-6_COPY_338_417

Perfect score: 413
Sequence: 1 VMDAVPARRWKEFVRTIGLR.....ERMGLDGCVEDLRSRLQRRP 80

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-O=/cgn2_1/USPTO_spool/US09993234/runat_27032003_115457_15378/app_query.fasta_1.2346
-DB-Issued_Patents_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09993234 @CGN_1_1_116 @runat_27032003_115457_15378 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	413	100.0	1254	3	US-08-815-469-3	Sequence 3, Appl1
2	413	100.0	1634	4	US-08-928-069-11	Sequence 11, Appl1
3	413	100.0	1634	4	US-08-828-683A-9	Sequence 9, Appl1
4	413	100.0	1783	3	US-08-815-469-1	Sequence 1, Appl1
5	167.5	40.6	1956	2	US-08-762-308-10	Sequence 10, Appl1
6	163	39.5	2440	4	US-09-513-007-1	Sequence 1, Appl1
7	158	38.3	427	4	US-09-397-787-236	Sequence 236, App
8	158	38.3	2062	1	US-08-050-319B-24	Sequence 24, Appl
9	158	38.3	2062	2	US-08-465-982-24	Sequence 24, Appl
10	158	38.3	2161	3	US-09-106-038A-1	Sequence 1, Appl1
11	158	38.3	2161	4	US-09-505-250-3	Sequence 3, Appl1
12	158	38.3	2175	1	US-08-321-668-1	Sequence 1, Appl1

13	158	38.3	2175	1	US-08-837-941-1	Sequence 1, Appl1
14	158	38.3	2175	1	US-08-126-016-1	Sequence 1, Appl1
15	158	38.3	2175	4	US-08-054-970-1	Sequence 1, Appl1
16	96	23.2	2413	2	US-08-651-579-1	Sequence 1, Appl1
17	94	22.8	1062	4	US-09-333-593A-3	Sequence 3, Appl1
18	94	22.8	1236	4	US-09-134-618-1	Sequence 1, Appl1
19	94	22.8	1323	3	US-08-883-036A-1	Sequence 1, Appl1
20	94	22.8	1799	4	US-09-329-633A-1	Sequence 1, Appl1
21	94	22.8	1799	4	US-09-079-029-2	Sequence 2, Appl1
22	94	22.8	3881	4	US-09-333-593A-1	Sequence 1, Appl1
23	83.5	20.2	2268	1	US-08-444-005-14	Sequence 14, Appl
24	77	18.6	2040	2	US-08-533-669A-5	Sequence 5, Appl1
25	77	18.6	2040	4	US-09-183-861-5	Sequence 5, Appl1
26	77	18.6	2040	4	US-09-022-765-5	Sequence 5, Appl1
27	74	17.9	1407	4	US-09-505-250-2	Sequence 2, Appl1
28	74	17.9	2152	4	US-09-013-895A-1	Sequence 1, Appl1
29	74	17.9	2152	4	US-09-565-918-1	Sequence 1, Appl1
30	74	17.9	2152	4	US-09-448-868-1	Sequence 1, Appl1
31	70.5	17.1	606	4	US-09-328-111-495	Sequence 495, App
32	70.5	17.1	2016	4	US-09-132-118-1	Sequence 1, Appl1
33	70.5	17.1	2137	1	US-08-444-005-16	Sequence 16, Appl
34	70.5	17.1	2617	3	US-09-161-443-1	Sequence 1, Appl1
35	70.5	17.1	9687	4	US-09-133-944-2	Sequence 2, Appl1
36	70.5	17.1	9687	4	US-09-208-827-2	Sequence 2, Appl1
37	67	16.2	157	3	US-08-883-036A-3	Sequence 7, Appl1
38	65	15.7	2808	3	US-08-870-126-7	Sequence 7, Appl1
39	65	15.7	2808	4	US-09-445-247-7	Sequence 18, Appl
40	64	15.5	5288	2	US-08-540-406-18	Sequence 18, Appl
41	64	15.5	5288	3	US-08-656-055-18	Sequence 18, Appl
42	64	15.5	5288	4	US-08-954-668-18	Sequence 18, Appl
43	64	15.5	5288	4	US-08-918-658-18	Sequence 18, Appl
44	64	15.5	5288	5	PCT-US95-13233-18	Sequence 18, Appl
45	64	15.5	11443	4	US-08-961-527-49	Sequence 49, Appl

ALIGNMENTS

RESULT 1
US-08-815-469-3
; Sequence 3, Application US/08815469
; Patent No. 6153402
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Dixit, Vishva
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dillon, Patrick J.
; TITLE OF INVENTION: Death Domain Containing Receptors
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/815,469
; FILING DATE: HERewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: No. 6153402 Yet Assigned
; FILING DATE: 06-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,711
; FILING DATE: 17-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,285

FILING DATE: 12-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1254 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1251
US-08-815-469-3

Alignment Scores:
Pred. No.: 6,63e-47 Length: 1254
Score: 413.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-993-234-6_COPY_338_417 (1-80) x US-08-815-469-3 (1-1254)

QY 1 ValMetAspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
DB 1012 GTGATGACCGCGGTCCACGCGCGCGCTGGAAGAGTTCTGTCGCGACGCTGGGCTGCGC 1071
QY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGlu 40
DB 1072 GAGGACAGATCGAAGCCGTGAGGTGAGATCGGCCCTTCGAGACACAGCAGTACGAG 1131
QY 41 MetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeu 60
DB 1132 ATGCTCAAGCGCTGGCGCCACGACGACGCCCGCGCTCGAGCCGCTTACCGCGCCCTG 1191
QY 61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80
DB 1192 GAGCGCATGGGCTGACGCGCTGCTGGAAGACTTGCACACCGCCCTGCAGCGCGGCCCG 1251

RESULT 2

US-08-928-069-11
Sequence 11, Application US/08928069
Patent No. 6462176
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-3 POLYPEPTIDE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,069
FILING DATE: 11-Sep-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/026943
FILING DATE: 09/23/1996

ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1052R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1634 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-928-069-11

Alignment Scores:
Pred. No.: 9,35e-47 Length: 1634
Score: 413.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-993-234-6_COPY_338_417 (1-80) x US-08-928-069-11 (1-1634)

QY 1 ValMetAspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
DB 1100 GTGATGACCGCGGTCCACGCGCGCGCTGGAAGAGTTCTGTCGCGACCGCTGGGCTGCGC 1159
QY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGlu 40
DB 1160 GAGGACAGATCGAAGCCGTGAGGTGAGATCGGCCCTTCGAGACACAGCAGTACGAG 1219
QY 41 MetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeu 60
DB 1220 ATGCTCAAGCGCTGGCGCCACGACGACGCCCGCGCTCGAGCCGCTTACCGCGGCCCTG 1279
QY 61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80
DB 1280 GAGCGCATGGGCTGACGCGCTGCTGGAAGACTTGCACACCGCCCTGCAGCGCGGCCCG 1339

RESULT 3

US-08-828-683A-9
Sequence 9, Application US/08828683A
Patent No. 6469144
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,683A
FILING DATE: 31-Mar-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/625328
FILING DATE: 1-Apr-1996
APPLICATION NUMBER: 08/710802
FILING DATE: 23-Sep-1996
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600

REFERENCE/DOCKET NUMBER: P1007P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1634 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-08-828-683A-9

Alignment Scores:
Pred. No.: 9.35e-47 Length: 1634
Score: 413.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-993-234-6_COPY_338_417 (1-80) x US-08-828-683A-9 (1-1634)

QY 1 ValMetAspAlaValProAlaArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
|||||
DB 1100 GTGATGACGCGGTCCAGCGCGCGCTGGAAGAGTTCGTGCGCAGCGCTGGGGCTGCC 1159
QY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnIntyrGlu 40
|||||
DB 1160 GAGGCAGAGATCGAAGCCGTGAGGTGAGATCGGCCCTTCGAGACGACGACTAGCAG 1219
QY 41 MetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeu 60
|||||
DB 1220 ATGCTCAAGCGCTGGCGCCAGCAGCAGCCCGCGGCGCTCGGAGCCGTTTACGCGCCCTG 1279
QY 61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80
|||||
DB 1280 GAGCGCATGGGCTGACGCGCTGCGTGAAGACTTGCAGACCGCGCTGACGCGCGCCG 1339

RESULT 4
US-08-815-469-1
Sequence 1, Application US/08815469
Patent No. 6153402
GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang
APPLICANT: Ni, Jian
APPLICANT: Dixit, Vishva
APPLICANT: Gentz, Reiner L.
APPLICANT: Dillon, Patrick J.
TITLE OF INVENTION: Death Domain Containing Receptors
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/815,469
FILING DATE: HERewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: No. 6153402 yet Assigned
FILING DATE: 06-FEB-1997
APPLICATION NUMBER: US 60/028,711
FILING DATE: 17-OCT-1996

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,285
FILING DATE: 12-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1783 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 198..1481
US-08-815-469-1

Alignment Scores:
Pred. No.: 1.05e-46 Length: 1783
Score: 413.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-993-234-6_COPY_338_417 (1-80) x US-08-815-469-1 (1-1783)

QY 1 ValMetAspAlaValProAlaArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
|||||
DB 1242 GTGATGACGCGGTCCAGCGCGCGCTGGAAGAGTTCGTGCGCAGCGCTGGGGCTGCC 1301
QY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnIntyrGlu 40
|||||
DB 1302 GAGGCAGAGATCGAAGCCGTGAGGTGAGATCGGCCCTTCGAGACGACGACTAGCAG 1361

QY 41 MetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeu 60
|||||
DB 1362 ATGCTCAAGCGCTGGCGCCAGCAGCAGCCCGCGGCGCTCGGAGCCGTTTACGCGCCCTG 1421

QY 61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80
|||||
DB 1422 GAGCGCATGGGCTGACGCGCTGCGTGAAGACTTGCAGACCGCGCTGACGCGCGCCG 1481

RESULT 5
US-08-762-308-10
Sequence 10, Application US/08762308
Patent No. 5925548
GENERAL INFORMATION:
APPLICANT: Beutler, Bruce A.
APPLICANT: Bazzoni, Flavia M.
TITLE OF INVENTION: MODIFIED RECEPTORS THAT CONTINUOUSLY
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/762,308
FILING DATE: 09-DEC-1996

```
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/224,593
FILING DATE: 05-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: UTSD:335--1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 418-3000
TELEFAX: 474-7577
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1956 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-762-308-10
```

```
Alignment Scores:
Pred. No.: 2,23e-13 Length: 1956
Score: 167.50 Matches: 38
Percent Similarity: 61.90% Conservative: 14
Best Local Similarity: 45.24% Mismatches: 27
Query Match: 40.56% Indels: 5
DB: 2 Gaps: 3
```

US-09-993-234-6_COPY_338_417 (1-80) x US-08-762-308-10 (1-1956)

```
OY 1 ValMetAspAlaValProAlaArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
    |||::||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1179 GTGTGATGGCGCTGCTCCAGCGCGCTGAGAGATTGCGTTTCATGGGGCTGAGC 1238

OY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArg---PheArgAspGlnGlnTyr 39
    ||| ||||| ||||| ::|||::||| ||||| ||||| ||||| |||||
Db 1239 GAGCAGAGATCGAGAGCGCTGAGATGACAGAACGGCGCGCTGCGCGCAGCGCTCAGTAC 1298

OY 40 GluMetLeuLysArgTrpArgGlnGlnGlnProAla-----GlyLeuGlyAlaVal 56
    |||||::||| |||||::||| |||||::||| |||||::||| |||||::|||
Db 1299 AGCATGCTGGAACCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGGAAGTAGTG 1358

OY 57 TyrAlaAlaLeuGluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeu 76
    |||::||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1359 GGCCTGCTGCTTCCAGATGAACCTGGCTGGGTGCTGAGAAATATCTCGAGGCTCTG 1418

OY 77 GlnArgGlyPro 80
    ||| ||||
Db 1419 ---AGAAATCCC 1427
```

RESULT 6

US-09-513-007-1

```
; Sequence 1, Application US/09513007
; Patent No. 6406907
; GENERAL INFORMATION:
; APPLICANT: Taylor, J. Michael
; APPLICANT: Kehrl, Jr., Marcus
; APPLICANT: Lee, Eun-Kyung
; APPLICANT: Mwangi, Simon
; TITLE OF INVENTION: BOVINE TUMOR NECROSIS FACTOR RECEPTOR-1
; FILE REFERENCE: 08411-018001
; CURRENT APPLICATION NUMBER: US/09/513,007
; CURRENT FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 60/122,156
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2440
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: CDS
```

LOCATION: (294)...(1706)
US-09-513-007-1

```
Alignment Scores:
Pred. No.: 1.21e-12 Length: 2440
Score: 163.00 Matches: 38
Percent Similarity: 60.00% Conservative: 10
Best Local Similarity: 47.50% Mismatches: 28
Query Match: 39.47% Indels: 4
DB: 4 Gaps: 2
```

US-09-993-234-6_COPY_338_417 (1-80) x US-09-513-007-1 (1-2440)

```
OY 1 ValMetAspAlaValProAlaArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
    |||::||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1425 GTGTGACGGCGCTGCCCGCTGCGCTGAGAGATTGTCGCGCGCGCTGAGACTGAGC 1484

OY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArg---PheArgAspGlnGlnTyr 39
    ||| ||||| ||||| ::|||::||| ||||| ||||| ||||| |||||
Db 1485 GAGCAGAGATCGAGCGCGCTGAGCTGAGAACGGCGCGCGCGCGCGCGCGCGCGCGCTGAGCTGAGC 1544

OY 40 GluMetLeuLysArgTrpArgGlnGlnGlnPro-----AlaGlyLeuGlyAlaVal 56
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1545 AGCATGCTGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTG 1604

OY 57 TyrAlaAlaLeuGluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeu 76
    ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1605 GGCGCGCTGCTCAGGACATGACCTGCTGGGTGCTGCTGAAACATAGAGAGCGGCTG 1664
```

RESULT 7

US-09-397-787-236

```
; Sequence 236, Application US/09397787
; Patent No. 6468758
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mitcham, Jennifer L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR OVARIAN
; FILE REFERENCE: 210121.466C2
; CURRENT APPLICATION NUMBER: US/09/397,787
; CURRENT FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 236
; LENGTH: 427
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-397-787-236
```

```
Alignment Scores:
Pred. No.: 5.97e-13 Length: 427
Score: 158.00 Matches: 36
Percent Similarity: 61.25% Conservative: 13
Best Local Similarity: 45.00% Mismatches: 27
Query Match: 38.26% Indels: 4
DB: 4 Gaps: 2
```

US-09-993-234-6_COPY_338_417 (1-80) x US-09-397-787-236 (1-427)

```
OY 1 ValMetAspAlaValProAlaArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
    |||::||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 53 GTGTGAGAGACGTGCCCGCTGCGCTGGAAGGAATTCGTGCGCGCGCTAGGGCTGAGC 112

OY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArg---PheArgAspGlnGlnTyr 39
    ::||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 113 GACCACGAGATCGATCGCTGAGCTGCAAGACGGCGCTGCTGCGCGAGCGCAATAC 172

OY 40 GluMetLeuLysArgTrpArgGlnGlnGlnPro-----AlaGlyLeuGlyAlaVal 56
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 173 AGCATGCTGCGACCTGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGAGCTGCTG 232
```

OY 57 TyraAlaAlaLeuGluaRgmctgIleuAspgIcysValGluAspLeuArgSerArgLeu 76
Db 233 GGACGGCTGCTCCGGACATGACCTGCTGGGCTGCCCTGAGACATCGAGAGCGCCTT 292

RESULT 8

US-08-050-319B-24

; Sequence 24, Application US/08050319B

; Patent No. 5633145

; GENERAL INFORMATION:

; APPLICANT: M.Feldmann, P.W. Gray,

; APPLICANT: M.J.C. Turner, F.M. Brennan

; TITLE OF INVENTION: Modified human TNFalpha (Tumor

; TITLE OF INVENTION: Necrosis Factor alpha) Receptor

; NUMBER OF SEQUENCES: 57

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Reed & Robbins

; STREET: 635 Bryant Street

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94301

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/050,319B

; FILING DATE: 10-May-1993

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Robbins, Roberta L.

; REGISTRATION NUMBER: 33,208

; REFERENCE/DOCKET NUMBER: 5150-0030

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 617-8999

; TELEFAX: (415) 327-3231

; INFORMATION FOR SEQ ID NO: 24:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2062 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA to mRNA

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 155..1519

; US-08-050-319B-24

Alignment Scores:

Pred. No.:	4.62e-12	Length:	2062
Score:	158.00	Matches:	36
Percent Similarity:	61.25%	Conservative:	13
Best Local Similarity:	45.00%	Mismatches:	27
Query Match:	38.26%	Indels:	4
DB:	1	Gaps:	2

US-09-993-234-6_COPY_338_417 (1-80) x US-08-050-319B-24 (1-2062)

OY 1 ValMetAspAlaValProAlaArgTrpIysGluPheValArgThrLeuGlyLeuArg 20
Db 1238 GTGGTGAGAACGTGCCCGCTGCGCTGGAAGAAATCGCGCGCTAGAGCTGAGC 1297
OY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArg---PheArgAspGlnGlnTyr 39
Db 1298 GACCACGAGATCGATCGGCTGAGCTGCAGAACGGCGCTGCCCTGCGGAGGCCAATAC 1357
OY 40 GluMetLeuLysArgTrpArgGlnGlnGlnPro-----AlaGlyLeuGlyAlaVal 56
Db 1358 ACCATGCTGGCGACCTGGAGCGCGCCGCGCGGAGGCCACGCTGAGAGCTGCTG 1417
OY 57 TyraAlaAlaLeuGluaRgmctgIleuAspgIcysValGluAspLeuArgSerArgLeu 76

Db 1418 GGACGGCTGCTCCGGACATGACCTGCTGGGCTGCCCTGAGGACATCGAGAGCGCCTT 1477

RESULT 9

US-08-465-982-24

; Sequence 24, Application US/08465982

; Patent No. 5863786

; GENERAL INFORMATION:

; APPLICANT: M.Feldmann, P.W. Gray,

; APPLICANT: M.J.C. Turner, F.M. Brennan

; TITLE OF INVENTION: Modified human TNFalpha (Tumor

; TITLE OF INVENTION: Necrosis Factor alpha) Receptor

; NUMBER OF SEQUENCES: 57

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Reed & Robbins

; STREET: 635 Bryant Street

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94301

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/465,982

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/050,319

; FILING DATE: 10-May-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Robbins, Roberta L.

; REGISTRATION NUMBER: 33,208

; REFERENCE/DOCKET NUMBER: 5150-0030

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 617-8999

; TELEFAX: (415) 327-3231

; INFORMATION FOR SEQ ID NO: 24:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2062 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA to mRNA

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 155..1519

; US-08-465-982-24

Alignment Scores:

Pred. No.:	4.62e-12	Length:	2062
Score:	158.00	Matches:	36
Percent Similarity:	61.25%	Conservative:	13
Best Local Similarity:	45.00%	Mismatches:	27
Query Match:	38.26%	Indels:	4
DB:	2	Gaps:	2

US-09-993-234-6_COPY_338_417 (1-80) x US-08-465-982-24 (1-2062)

OY 1 ValMetAspAlaValProAlaArgTrpIysGluPheValArgThrLeuGlyLeuArg 20
Db 1238 GTGGTGAGAACGTGCCCGCTGCGCTGGAAGAAATCGTGGCGCGCTAGAGCTGAGC 1297
OY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArg---PheArgAspGlnGlnTyr 39
Db 1298 GACCACGAGATCGATCGGCTGAGCTGCAGAACGGCGCTGCCCTGCGGAGGCCAATAC 1357
OY 40 GluMetLeuLysArgTrpArgGlnGlnGlnPro-----AlaGlyLeuGlyAlaVal 56
Db 1358 ACCATGCTGGCGACCTGGAGCGCGCCGCGCGGAGGCCACGCTGAGAGCTGCTG 1417
OY 57 TyraAlaAlaLeuGluaRgmctgIleuAspgIcysValGluAspLeuArgSerArgLeu 76

```
Db      1418 GGACGCGTGTCTCCGCAGCATATGGACCCTGCTGGGCTGCCCTGGAGGACATCGAGAGCGCCTT    1477
RESULT 10
US-09-106-038A-1
; Sequence 1, Application US/09106038A
; Patent No. 6007995
; GENERAL INFORMATION:
; APPLICANT: Brenda F. Baker and Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF TNFR1
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Isis Pharmaceuticals, Inc.
; STREET: 2292 Faraday Avenue
; CITY: Carlsbad
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92008
COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows NT
; SOFTWARE: Microsoft Word 97
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/106,038A
; FILING DATE: June 26, 1998
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
; NAME: Laurel Spear Bernstein
; REGISTRATION NUMBER: 37,280
REFERENCE/DOCKET NUMBER: RTS-0004
TELECOMMUNICATION INFORMATION:
; TELEPHONE: (760) 931-9200
; TELEFAX: (760) 603-3820
INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2161
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-106-038A-1

Alignment Scores:
Pred. No.:          4,91e-12           Length:        2161
Score:              158.00             Matches:         36
Percent Similarity: 61.25%            Conservative:   13
Best Local Similarity: 45.00%          Mismatches:     27
Query Match:        38.26%            Indels:         4
DB:                  3                 Gaps:           2

US-09-993-234-6_COPY_338_417 (1-80) x US-09-106-038A-1 (1-2161)
QY       1 ValmetaspAlaValProAlaargArgrTrplysgluPhevalArgThrleuglyLeuArg    20
|||:::||||| |
Dg      1339 GTGGTGGAAGAAGTCGCCCGCTTGCGCTGGAAGAAATTCGTGCGCGCCTAGGGCTGAGC    1398
|||:::||||| ::|||::: ||| |
QY      21 GluAlagluIlegluaLaValgluValgluileglyArg---PheargAspgIngtyr    39
::: |||||::: ::|||::: ||| |
Db      1399 GAACACGAGATCGATCGCGCTGGAGCTGCAGAACGGCGCTGCCCTGCGCGCAATAC    1458
||| | |||||::: ||| |
QY      40 GlumetleuLysArgTrparGlnglInglnPro-----AlaglyleuglyAlaVal    56
||| | |||||::: ||| |
Db      1459 AGCATGCTGGCGACTGGAGGGCGGCGCACGCGCGCGAGGCGCAGCTGAGCTGCTG    1518
||| | ||||| ||| |
QY      57 TyrAlalaLeuGlualArgMetglyLeuaspglyCysValgluaspleuarGserArgLeu    76
||| | ||| | ||| |
Db      1519 GGACGCGTGTCTCCGCAGCATATGGACCCTGCTGGGCTGCCCTGGAGGACATCGAGAGCGCCTT    1578
||| | ||| | ||| |

RESULT 11
US-09-505-250-3
; Sequence 3, Application US/09505250A
; Patent No. 6329148
```

```

: GENERAL INFORMATION:
: APPLICANT: Rosen, Glenn
: APPLICANT: Kao, Peter
: TITLE OF INVENTION: Synergistic Anti-Cancer Therapy with
: TITLE OF INVENTION: Triptolides and Death Domain Ligands
: FILE REFERENCE: SUN-109PRV2
: CURRENT APPLICATION NUMBER: US/09/505,250A
: CURRENT FILING DATE: 2000-02-15
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 3
: LENGTH: 2161
: TYPE: DNA
: ORGANISM: H. sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (256)...(1623)
US-09-505-250-3

Alignment Scores:
Pred. No.: 4.91e-12 Length: 2161
Score: 158.00 Matches: 36
Percent Similarity: 61.25% Conservative: 13
Best Local Similarity: 45.00% Mismatches: 27
Query Match: 38.26% Indels: 4
DB: 4 Gaps: 2

US-09-993-234-6_COPY_338_417 (1-80) x US-09-505-250-3 (1-2161)
QY 1 Valmetaspalalavalproalaargargtrplysgluphevalargthrleuglyleuarg 20
|||:::||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1339 GTGGTGAGAGACGTGCCCGCGTGGCTGCGTGAAGAAATTCGTGCGGCGCTAGGGCTGAGC 1398
QY 21 Glualaglurleglualalavalgluvalglurlegllyarg---PheargAspGlnIntyr 39
::: |||||::: ::|||::: ||||| ||||| ||||| |||||
Db 1399 GACCACGAGATCGATCGCTGCGCTGAGAGCTGCAGACGGCGCTGCCCTGCCGAGCGCATAC 1458
QY 40 GlumetleulysargtrparGlnGlnGlnPro-----AlaGlyLeuGlyalaval 56
||||| |||||::: ||| ||| ||| ||| |||
Db 1459 AGCATGCTGGCGACCTGGAGGGCGCGCACGCCGCGCGGCGGAGGCCACGCTGAGCTGCTG 1518
QY 57 TyrAlaAlaLeuGlUaRgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeu 76
||| ||| ||| |||||::: |||||::: |||||::: |||
Db 1519 GGACGCGTGTCTCGCGACATGACCTGCTGGGGCTGCCCTGAGAGACATCGAGAGCGCCTT 1578

RESULT 12
US-08-321-668-1
: Sequence 1, Application US/08321668
: Patent No. 5665859
: GENERAL INFORMATION:
: APPLICANT: WALLACH, David
: APPLICANT: BRAKEBUSCH, Cord
: APPLICANT: VARFOLOMEEV, Eugene
: APPLICANT: BATKIN, Michael
: TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF
: TITLE OF INVENTION: THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE
: NUMBER OF SEQUENCES: 42
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: BROWDY AND NEIMARK
: STREET: 419 Seventh Street, N.W., Suite 300
: CITY: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20004
: COMPUTER READABLE FORM:
: MEDIUM TYPE: floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/321,668
: FILING DATE: 12-OCT-1994
: CLASSIFICATION: 435

```


Mon Apr 7 09:25:02 2003

us-09-993-234-6_copy_338_417.rni

Page 8

```

STATE: DC
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/126, 016
FILING DATE: 24-SEP-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/625668
FILING DATE: 13-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGER L
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2175 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 256..1620
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 319..1620
US-08-126-016-1

Alignment Scores:
Pred. No.: 4.95e-12 Length: 2175
Score: 158.00 Matches: 36
Percent Similarity: 61.25% Conservative: 13
Best Local Similarity: 45.00% Mismatches: 27
Query Match: 38.26% Indels: 4
DB: 1 Gaps: 2

US-09-993-234-6_COPY_338_417 (1-80) x US-08-126-016-1 (1-2175)
QY 1 ValMetAspAlaValProAlaArgArgTrpIysGluPheValArgThrLeuGlyLeuArg 20
|||::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1339 GTGGTGAGAACGCTGCCCCCGCTGGCGCTGGAAGGAATTCGTGGCGCGCTAGGCGTGA 1398
QY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArg---PheArgAspGlnGlnTyr 39
::: |||||::: ::|||::: ||||| ||||| ||||| ||||| ||||| |||||
Db 1399 GACCACGAGATCGATCGGCTGTGAGCTGCAGAACGGGCGCTGCGCGGAGGCGCATAC 1458
QY 40 GluMetLeuIysArgTrpArgGlnGlnGlnPro-----AlaGlyLeuGlyAlaVal 56
||||| ||||| |||||::: ||| ||| ||| ||| ||| ||| ||| |||
Db 1459 AGCATGCTGGCGACCTGGAGGGCGCGCACCGCGCGCGAGGCGCACCGCTGAGCTGCTG 1518
QY 57 TyrAlaAlaLeuGluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeu 76
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1519 GGACGCGTGTCCGCGACATGACCTGCTGGCTGCTGAGGAGCATCGAGGAGCGCTT 1578

RESULT 15
US-08-054-970-1
; Sequence 1, Application US/08054970
; Patent No. 6395267
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: BRAKEBUSCH, Cord
; TITLE OF INVENTION: TNF RECEPTOR ACTION MODULATION
; NUMBER OF SEQUENCES: 8

```

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/054,970
FILING DATE: 03-MAY-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: WALLACH=9
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2175 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 256..1620
US-08-054-970-1

Alignment Scores:
Pred. No.: 4.95e-12 Length: 2175
Score: 158.00 Matches: 36
Percent Similarity: 61.25% Conservative: 13
Best Local Similarity: 45.00% Mismatches: 27
Query Match: 38.26% Indels: 4
DB: Gaps: 2

US-09-993-234-6_COPY_338_417 (1-80) x US-08-054-970-1 (1-2175)
QY 1 ValMetaspAlaValProAlaArgArGTTrpLysGluPheValArgThrLeuGlyLeuArg 20
|||::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1339 GTGGTGGAGAACGTGCCCGCGTGTGCGCTGGAAGGAATTCTGCGGCGCTAGGGCTGAGC 1398
QY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArg---PheArgAspGlnGlnTyr 39
::: |||||::: ::|||::: ||||| ||||| ||||| ||||| ||||| |||||
Db 1399 GACCACGAGATCGATCGCGCTGGAGAGCTGCAGAACGGGCGCTGCCCTGCGGAGCGGCAATAC 1458
QY 40 GluMetLeuLysArgTrpArgGlnGlnGlnPro-----AlaGlyLeuGlyAlaVal 56
||||| |||||::: ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1459 AGCATGCTGGCGACCTGGAGGGCGGCACGCGCGCGCGAGGCCACGCTGGAGCTGCTG 1518
QY 57 TyrAlaAlaLeuGluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeu 76
||| ||| ||| ||| |||||::: |||||::: |||||::: |||||::: |||||
Db 1519 GGACGCGTCTCCGCGACATGAGACCTGCTGGGCTGCTGGAGAGACATCGAGAGGCGCTT 1578

Search completed: April 6, 2003, 23:29:52
Job time : 19.5049 secs

```

GenCore version 5.1.4-p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 6, 2003, 21:08:18 ; Search time 30.4618 Seconds

(without alignments)
2303.655 Million cell updates/sec

Title: US-09-993-234-6_COPY_338_417

Perfect score: 413

Sequence: 1 VMDAVPARRWKEFVRTGLR.....ERMGLDGCVEDLRSRLQRP 80

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 593429 seqs, 438583890 residues

Total number of hits satisfying chosen parameters: 1186858

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO.spool/US09993234/runat_27032003_115459_15466/app_query.fasta_1.2346
-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=trnpb -MINMATCH=0.1
-LOOPL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09993234@cgn_1_1_249@runat_27032003_115459_15466
-NCPU=6 -ICPU=3 -NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	413	100.0	1254	10	US-09-333-966-3
2	413	100.0	1634	9	US-10-081-280-9
3	413	100.0	1634	9	US-10-112-793-9
4	413	100.0	1634	9	US-10-112-193-11

5	413	100.0	1634	10	US-09-993-234-9	Sequence 9, Appl1
6	413	100.0	1783	10	US-09-333-966-1	Sequence 1, Appl1
7	413	100.0	10797	9	US-10-092-154-1577	Sequence 1577, Ap
8	413	100.0	10797	10	US-09-764-847-1577	Sequence 1577, Ap
9	401	97.1	1743	9	US-09-954-531-1389	Sequence 1389, Ap
10	171	41.4	2130	10	US-09-917-800A-1601	Sequence 1601, Ap
11	171	41.4	2173	9	US-09-898-234-14	Sequence 14, Appl
12	171	41.4	2173	9	US-09-899-429A-24	Sequence 24, Appl
13	171	41.4	2173	9	US-09-792-356-14	Sequence 14, Appl
14	171	41.4	2173	10	US-09-899-422-14	Sequence 14, Appl
15	163	39.5	2440	10	US-09-970-532-1	Sequence 1, Appl1
16	158	38.3	427	10	US-09-876-889-236	Sequence 236, App
17	158	38.3	479	9	US-10-043-487-100	Sequence 100, App
18	158	38.3	1368	9	US-09-898-234-1	Sequence 1, Appl1
19	158	38.3	1368	9	US-09-899-429A-1	Sequence 1, Appl1
20	158	38.3	1368	9	US-09-792-356-1	Sequence 1, Appl1
21	158	38.3	1368	10	US-09-899-422-1	Sequence 1, Appl1
22	158	38.3	2111	10	US-09-880-107-2360	Sequence 2360, Ap
23	158	38.3	2141	9	US-09-898-234-16	Sequence 16, Appl
24	158	38.3	2141	9	US-09-899-429A-26	Sequence 26, Appl
25	158	38.3	2141	9	US-09-792-356-16	Sequence 16, Appl
26	158	38.3	2141	10	US-09-899-422-16	Sequence 16, Appl
27	158	38.3	2175	12	US-10-120-397-1	Sequence 1, Appl1
28	94	22.8	1062	8	US-08-916-625B-3	Sequence 3, Appl1
29	94	22.8	1236	9	US-10-076-754-1	Sequence 1, Appl1
30	94	22.8	1236	9	US-10-076-754-1	Sequence 1, Appl1
31	94	22.8	1236	12	US-10-067-615-1	Sequence 1, Appl1
32	94	22.8	1600	10	US-09-874-138-1	Sequence 1, Appl1
33	94	22.8	1600	12	US-10-005-842-1	Sequence 1, Appl1
34	94	22.8	1799	9	US-09-992-964-10	Sequence 10, Appl
35	94	22.8	1799	10	US-09-828-739-10	Sequence 1, Appl1
36	94	22.8	1799	10	US-09-887-879-10	Sequence 10, Appl
37	94	22.8	1799	12	US-10-052-798-2	Sequence 2, Appl1
38	94	22.8	3881	8	US-08-916-625B-1	Sequence 1, Appl1
39	94	22.8	3964	9	US-09-811-088-5	Sequence 5, Appl1
40	94	22.8	3964	10	US-09-757-421-3	Sequence 3, Appl1
41	94	22.8	4051	9	US-09-811-088-3	Sequence 3, Appl1
42	94	22.8	4051	10	US-09-757-421-1	Sequence 1, Appl1
43	77	18.6	2040	9	US-09-971-496-5	Sequence 5, Appl1
44	77	18.6	2040	10	US-09-874-923-5	Sequence 5, Appl1
45	77	18.6	4233	9	US-09-991-496-99	Sequence 99, Appl

ALIGNMENTS

RESULT 1
US-09-333-966-3
Sequence 3, Application US/09333966

Patent No. US20020009773A1

GENERAL INFORMATION:

APPLICANT: Yu, Guo-Liang
APPLICANT: Ni, Jian
APPLICANT: Dixit, Vishva
APPLICANT: Gentz, Reiner L.
APPLICANT: Dillon, Patrick J.
TITLE OF INVENTION: Death Domain Containing Receptors
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/333,966
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/815,469
FILING DATE:
APPLICATION NUMBER: No. US2002009773A1 Yet Assigned
FILING DATE: 06-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,711
FILING DATE: 17-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,285
FILING DATE: 12-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1254 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1251
US-09-333-966-3

Alignment Scores:
Pred. No.: 7.46e-50 Length: 1254
Score: 413.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-993-234-6_COPY_338_417 (1-80) x US-09-333-966-3 (1-1254)

QY 1 ValMetAspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
|||||
Db 1012 GTGATGACGCGGTCCAGCGCGCGCTGGAAGAGTTCGTGCGCACCGCTGGCGCTGCC 1071
QY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGlu 40
|||||
Db 1072 GAGGACAGATCGAAGCCGTGAGGTGAGATCGGCCCTTCCGAGACCAAGTACGAG 1131
QY 41 MetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeu 60
|||||
Db 1132 ATGCTCAAGCGCTGGCGCCAGCAGCAGCCCGCGGCTCGAGACCGCTTACGCGGCCCTG 1191
QY 61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80
|||||
Db 1192 GAGCGCATGGGCTGGACGCGCTGCTGGAAGACTTGGCAGCCGCGCTGACGCGGCCCG 1251

RESULT 2
US-10-081-280-9
Sequence 9, Application US/10081280
Patent No. US20020165157A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/081,280
FILING DATE: 21-Feb-2002
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/829,270
FILING DATE: 31-Mar-1997
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5416
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1634 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-081-280-9

Alignment Scores:
Pred. No.: 1.02e-49 Length: 1634
Score: 413.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-993-234-6_COPY_338_417 (1-80) x US-10-081-280-9 (1-1634)

QY 1 ValMetAspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
|||||
Db 1100 GTGATGACGCGGTCCAGCGCGCGCTGGAAGAGTTCGTGCGCACCGCTGGCGCTGCC 1159
QY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGlu 40
|||||
Db 1160 GAGCAGAGATCGAAGCCGTGAGGTGAGATCGGCCCTTCCGAGACCAAGTACGAG 1219
QY 41 MetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeu 60
|||||
Db 1220 ATGCTCAAGCGCTGGCGCCAGCAGCAGCCCGCGGCTCGAGACCGCTTACGCGGCCCTG 1279
QY 61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80
|||||
Db 1280 GAGCGCATGGGCTGGACGCGCTGCTGGAAGACTTGGCAGCCGCGCTGACGCGGCCCG 1339

RESULT 3
US-10-112-793-9
Sequence 9, Application US/10112793
Publication No. US20020192729A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)


```

:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/10/112,793
: FILING DATE: 28-Mar-2002
: CLASSIFICATION: <Unknown>
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/828,683A
: FILING DATE: 31-Mar-1997
: APPLICATION NUMBER: 08/625328
: FILING DATE: 1-Apr-1996
: APPLICATION NUMBER: 08/710802
: FILING DATE: 23-Sep-1996
:
: ATTORNEY/AGENT INFORMATION:
: NAME: Marschang, Diane L.
: REGISTRATION NUMBER: 35,600
: REFERENCE/DOCKET NUMBER: P1007P1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650/225-5416
: TELEFAX: 650/952-9881
:
: INFORMATION FOR SEQ ID NO: 9:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1634 base pairs
: TYPE: Nucleic Acid
: STRANDEDNESS: Single
: TOPOLOGY: Linear
:
: SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-112-793-9

Alignment Scores:
Pred. No.: 1.02e-49 Length: 1634
Score: 413.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-993-234-6_COPY_338_417 (1-80) x US-10-112-793-9 (1-1634)
QY 1 ValMetaspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
Db 1100 GTGATGACGCGGTCCACGCGCGCTGGAAGAGTTCTGCGCACGCTGGGCTGCGC 1159
QY 21 GluAlaGluIleGluAlaValGluValGluLeuGlyArgPheArgAspGlnGlnTyrGlu 40
Db 1160 GAGCAGAGATCGAAGCCGTGGAGTGGAGATCGGCCGCTCCAGACAGCAGTACGAG 1219
QY 41 MetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeu 60
Db 1220 ATGCTCAAGCGCTGGCGCCAGCAGACCCCGGGCGCTCGAGCCGTTTACGCGCCCTG 1279
QY 61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80
Db 1280 GAGCGCATGGGGCTGGACGCGCTGCGTGAAGACTTGCGCAGCCGCTGCAGCGGCGCCG 1339

RESULT 4
US-10-112-193-11
: Sequence 11, Application US/10112193
: Publication No. US20030004313A1
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi J.
: TITLE OF INVENTION: Apo-3 POLYPEPTIDE
: NUMBER OF SEQUENCES: 15
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 1 DNA Way
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Winpatin (Genentech)
: APPLICATION NUMBER: US/09/993,234
```

```

:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/10/112,193
: FILING DATE: 28-Mar-2002
: CLASSIFICATION: <Unknown>
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/928,069
: FILING DATE: 11-Sep-1997
: APPLICATION NUMBER: 60/026943
: FILING DATE: 23-Sep-1996
:
: ATTORNEY/AGENT INFORMATION:
: NAME: Marschang, Diane L.
: REGISTRATION NUMBER: 35,600
: REFERENCE/DOCKET NUMBER: P1052R1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650/225-5416
: TELEFAX: 650/952-9881
:
: INFORMATION FOR SEQ ID NO: 11:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1634 base pairs
: TYPE: Nucleic Acid
: STRANDEDNESS: Single
: TOPOLOGY: Linear
:
: SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-112-193-11

Alignment Scores:
Pred. No.: 1.02e-49 Length: 1634
Score: 413.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-993-234-6_COPY_338_417 (1-80) x US-10-112-193-11 (1-1634)
QY 1 ValMetaspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
Db 1100 GTGATGACGCGGTCCACGCGCGCTGGAAGAGTTCTGCGCACGCTGGGCTGCGC 1159
QY 21 GluAlaGluIleGluAlaValGluValGluLeuGlyArgPheArgAspGlnGlnTyrGlu 40
Db 1160 GAGCAGAGATCGAAGCCGTGGAGTGGAGATCGGCCGCTCCAGACAGCAGTACGAG 1219
QY 41 MetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeu 60
Db 1220 ATGCTCAAGCGCTGGCGCCAGCAGACCCCGGGCGCTCGAGCCGTTTACGCGCCCTG 1279
QY 61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80
Db 1280 GAGCGCATGGGGCTGGACGCGCTGCGTGAAGACTTGCGCAGCCGCTGCAGCGGCGCCG 1339

RESULT 5
US-09-993-234-9
: Sequence 9, Application US/09993234
: Patent No. US20020146768A1
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi J.
: TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
: NUMBER OF SEQUENCES: 11
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 460 Point San Bruno Blvd
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Winpatin (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/993,234
```


LENGTH: 10797
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-092-154-1577

Alignment Scores:
Pred. No.: 9.88e-49 Length: 10797
Score: 413.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-993-234-6_COPY_338_417 (1-80) x US-10-092-154-1577 (1-10797)

OY 1 ValMetaspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
DB 9119 GTGATGACGCGGCTCCACGCGCGCGCTGGAAGAGATTCTGCGCACGCTGGGCTGCGC 9178
OY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGlu 40
DB 9179 GAGCGAGAGATCGAAGCGCTGGAGGTGAGATCGCGCTTCCGAGACGACGATAGCAG 9238
OY 41 MetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaLeu 60
DB 9239 ATGCTCAAGCGCTGGCGCACGACGCGCGCGCTCGAGCCGTTACGCGGCCCTG 9298
OY 61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80
DB 9299 GAGCGCATGGGGCTGGACGCGCTGCGTGAAGACTTGGCGACGCGCTGCAGCGCGCCCG 9358

RESULT 8

US-09-764-847-1577
; Sequence 1577, Application US/09764847
; Patent No. US20020132767A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009
; CURRENT APPLICATION NUMBER: US/09/764,847
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2003
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1577
; LENGTH: 10797
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-847-1577

Alignment Scores:
Pred. No.: 9.88e-49 Length: 10797
Score: 413.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-993-234-6_COPY_338_417 (1-80) x US-09-764-847-1577 (1-10797)

OY 1 ValMetaspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
DB 9119 GTGATGACGCGGCTCCACGCGCGCGCTGGAAGAGATTCTGCGCACGCTGGGCTGCGC 9178
OY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGlu 40
DB 9179 GAGCGAGAGATCGAAGCGCTGGAGGTGAGATCGCGCTTCCGAGACGACGATAGCAG 9238
OY 41 MetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaLeu 60
DB 9239 ATGCTCAAGCGCTGGCGCACGACGCGCGCGCTCGAGCCGTTACGCGGCCCTG 9298
OY 61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80

DB 9299 GAGCGCATGGGGCTGGACGCGCTGCGTGAAGACTTGGCGACGCGCTGCAGCGCGCCCG 9358

RESULT 9

US-09-954-531-1389
; Sequence 1389, Application US/09954531
; Patent No. US20020165180A1
; GENERAL INFORMATION:
; APPLICANT: Weaver, Zoe
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C
; FILE REFERENCE: 689290-77
; CURRENT APPLICATION NUMBER: US/09/954,531
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: US/60/233,133
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,009
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,034
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,509
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US/60/234,567
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 1392
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1389
; LENGTH: 1743
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-531-1389

Alignment Scores:
Pred. No.: 5.72e-48 Length: 1743
Score: 401.00 Matches: 78
Percent Similarity: 97.50% Conservative: 0
Best Local Similarity: 97.50% Mismatches: 2
Query Match: 97.09% Indels: 0
DB: 9 Gaps: 0

US-09-993-234-6_COPY_338_417 (1-80) x US-09-954-531-1389 (1-1743)

OY 1 ValMetaspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
DB 1181 GTGATGACGCGGCTCCACGCGCGCGCTGGAAGAGATTCTGCGCACGCTGGGCTGCGC 1240
OY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGlu 40
DB 1241 GAGCGAGAGATCGAAGCGCGCTGGAGGTGAGATCGGTCTTCCGAGACGACGATAGCAG 1300
OY 41 MetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaLeu 60
DB 1301 ATGCTCAAGCACTGGCGCACGACGCGCGCGCTCGAGCCGTTTACGCGGCCCTG 1360
OY 61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80
DB 1361 GAGCGCATGGGGCTGGACGCGCTGCGTGAAGACTTGGCGACGCGCTGCAGCGTGCCCG 1420

RESULT 10

US-09-917-800A-1601
; Sequence 1601, Application US/09917800A
; Patent No. US20020119462A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5038-US
; CURRENT APPLICATION NUMBER: US/09/917,800A
; CURRENT FILING DATE: 2001-07-31

```
; PRIOR APPLICATION NUMBER: US 60/222,040
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 60/222,880
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/290,029
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/290,645
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 60/292,336
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/295,798
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/297,457
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,884
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,459
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 1740
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1601
; LENGTH: 2130
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020119462A1 NM_013091
US-09-917-800A-1601
```

```
Alignment Scores:
Pred. No.: 5.02e-15 Length: 2130
Score: 171.00 Matches: 38
Percent Similarity: 62.96% Conservative: 13
Best Local Similarity: 46.91% Mismatches: 26
Query Match: 41.40% Indels: 4
DB: 10 Gaps: 2
```

US-09-993-234-6_COPY_338_417 (1-80) x US-09-917-800A-1601 (1-2130)

```
OY 1 ValMetAspAlaValProAlaArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
    |||::||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1342 GTGTGTGATGGCGTGCCTCCGACACGCTGGAAGAGTTCATGCGGCTCGGCTGAGC 1401
OY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArg---PheArgAspGlnGlnTyr 39
    ||| ||||| ||||| ::|||::||| ||||| ||||| ||||| ||||| |||||
Db 1402 GAGCAGCAGATCGAGCGGCTGAGGCTGCAGAACGGCGCTGCCCTCCGAGGCTCATTTAC 1461
OY 40 GluMetLeuYsArgTrpArgGlnGlnGlnPro-----AlaGlyLeuGlyAlaVal 56
    |||||::||| |||||::||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1462 AGCATGCTGGAAGCCTGGCGCGCGCCGACACCGCAGACGAGGCCACGCTGAGCTAGTG 1521
OY 57 TyrAlaAlaLeuGluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeu 76
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1522 GGGCGGCTGCTTTCGACATGAACCTGCGTGGCTGCTGAGAACATCCGCGAGACTCTTA 1581
OY 77 Gln 77
    ::
Db 1582 GAA 1584
```

```
RESULT 11
US-09-898-234-14
; Sequence 14, Application US/09898234
; Patent No. US2002015112A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmeler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stratowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; FILE REFERENCE: 98,385-I
; CURRENT APPLICATION NUMBER: US/09/898,234
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/525,998
```

```
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 2173
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (245)..(1630)
; OTHER INFORMATION: Description of Artificial Sequence: ratTNF-R8
US-09-898-234-14
```

```
Alignment Scores:
Pred. No.: 5.14e-15 Length: 2173
Score: 171.00 Matches: 38
Percent Similarity: 62.96% Conservative: 13
Best Local Similarity: 46.91% Mismatches: 26
Query Match: 41.40% Indels: 4
DB: 9 Gaps: 2
```

US-09-993-234-6_COPY_338_417 (1-80) x US-09-898-234-14 (1-2173)

```
OY 1 ValMetAspAlaValProAlaArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
    |||::||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1349 GTGTGTGATGGCGTGCCTCCGACACGCTGGAAGAGTTCATGCGGCTCGGCTGAGC 1408
OY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArg---PheArgAspGlnGlnTyr 39
    ||| ||||| ||||| ::|||::||| ||||| ||||| ||||| ||||| |||||
Db 1409 GAGCAGCAGATCGAGCGGCTTGGAGCTGCAGAACGGCGCTTGCTCCGAGGCTCATTTAC 1468
OY 40 GluMetLeuYsArgTrpArgGlnGlnGlnPro-----AlaGlyLeuGlyAlaVal 56
    |||||::||| |||||::||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1469 AGCATGCTGGAAGCCTGGCGCGCGCCGACACCGCAGACGAGGCCACGCTGAGCTAGTG 1528
OY 57 TyrAlaAlaLeuGluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeu 76
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1529 GGGCGGCTGCTTTCGACATGAACCTGCGTGGCTGCTGAGAACATCCGCGAGACTCTTA 1588
OY 77 Gln 77
    ::
Db 1589 GAA 1591
```

```
RESULT 12
US-09-899-429A-24
; Sequence 24, Application US/09899429A
; Patent No. US20020169118A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmeler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stratowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; FILE REFERENCE: 98-385-J
; CURRENT APPLICATION NUMBER: US/09/899,429A
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/792,356
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 08/477,639
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
```



```

; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 24
; LENGTH: 2173
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ratNF-R8
; NAME/KEY: CDS
; LOCATION: (245)..(1627)
US-09-899-429A-24

Alignment Scores:
Pred. No.: 5.14e-15 Length: 2173
Score: 171.00 Matches: 38
Percent Similarity: 62.96% Conservative: 13
Best Local Similarity: 46.91% Mismatches: 26
Query Match: 41.40% Indels: 4
DB: 9 Gaps: 2

US-09-993-234-6_COPY_338_417 (1-80) x US-09-899-429A-24 (1-2173)
QY 1 ValMetaspAlaValProAlaArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
    |||::||| ||||| ::|||::||| |||||::||| |||||::|||
Db 1349 GTGTGGATGGCGTTCCTCCGACACCGCTGGAAGAGTTCAATCGCGCTGAGC 1408
QY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArg---PheArgAspGlnGlnTyr 39
    ||| |||||::||| ::|||::||| ||||| |||::|||
Db 1409 GAGCAGCAGATCGAGCGGTGGAGCTGCAGAACGGCGGTGCTCCGCGAGGCTCATTTAC 1468
QY 40 GluMetLeuLysArgTrpArgGlnGlnGlnPro-----AlaGlyLeuGlyAlaVal 56
    |||||::||| |||||::||| ||| ||| ||| |||
Db 1469 AGCATGCTGGAAGCCTGGCGCGCGCACACCGCACAGAGGCCACGCTGAGCTAGTGC 1528
QY 57 TyrAlaAlaLeuGluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeu 76
Db 1529 GGCCGCGTGTTCGACATGAACCTGCGTGGCTGCGAGAACATCCGCGAGACTCTTA 1588
QY 77 Gln 77
Db 1589 GAA 1591

RESULT 13
US-09-792-356-14
; Sequence 14, Application US/09792356
; Publication NO. US20020183485A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Hummler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stratowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; FILE REFERENCE: 98,385-G
; CURRENT APPLICATION NUMBER: US/09/792,356
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 08/477,639
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 14
```

```

; LENGTH: 2173
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (245)..(1630)
US-09-792-356-14

Alignment Scores:
Pred. No.: 5.14e-15 Length: 2173
Score: 171.00 Matches: 38
Percent Similarity: 62.96% Conservative: 13
Best Local Similarity: 46.91% Mismatches: 26
Query Match: 41.40% Indels: 4
DB: 9 Gaps: 2

US-09-993-234-6_COPY_338_417 (1-80) x US-09-792-356-14 (1-2173)
QY 1 ValMetaspAlaValProAlaArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
    |||::||| ||||| ::|||::||| |||||::||| |||||::|||
Db 1349 GTGTGGATGGCGTTCCTCCGACACCGCTGGAAGAGTTCAATCGCGCTGAGC 1408
QY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArg---PheArgAspGlnGlnTyr 39
    ||| |||||::||| ::|||::||| ||||| |||::|||
Db 1409 GAGCAGCAGATCGAGCGGTGGAGCTGCAGAACGGCGGTGCTCCGCGAGGCTCATTTAC 1468
QY 40 GluMetLeuLysArgTrpArgGlnGlnGlnPro-----AlaGlyLeuGlyAlaVal 56
    |||||::||| |||||::||| ||| ||| ||| |||
Db 1469 AGCATGCTGGAAGCCTGGCGCGCGCACACCGCACAGAGGCCACGCTGAGCTAGTGC 1528
QY 57 TyrAlaAlaLeuGluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeu 76
Db 1529 GGCCGCGTGTTCGACATGAACCTGCGTGGCTGCGAGAACATCCGCGAGACTCTTA 1588
QY 77 Gln 77
Db 1589 GAA 1591

RESULT 14
US-09-899-422-14
; Sequence 14, Application US/09899422
; Patent NO. US2002090676A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Hummler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stratowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; FILE REFERENCE: 98,385-H
; CURRENT APPLICATION NUMBER: US/09/899,422
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 09/525,998
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 14
; LENGTH: 2173
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (245)..(1630)
; OTHER INFORMATION: Description of Artificial Sequence: ratNF-R8
```


GenCore version 5.1.4.p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 6, 2003, 16:19:54 ; Search time 500.409 Seconds

(without alignments)
2589.161 Million cell updates/sec

Title: US-09-993-234-6_COPY_338_417

Perfect score: 413

Sequence: 1 VMDAVPARRWKEFVFTLGLR.....ERNGLDGCVEDLRSRLQKGP 80

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US09993234/runat_27032003_115456_15362/app-query.fasta_1.2346
-DB=EST -QFMT=fastap -SUFFIX=st -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09993234@cgn2_1.1.4749 @runat_27032003_115456_15362 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estln:*
4: em_estlm:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_estl:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	413	100.0	510	14	BM695193	BM695193 UI-E-CQ1-
2	413	100.0	550	13	BM666370	BM666370 UI-E-CQ1-
3	413	100.0	687	10	BE670189	BE670189 7e31c12.x
4	406	98.3	618	10	AM074008	AM074008 xb06c09.x
5	399	96.6	587	9	AI380959	AI380959 tg18c01.x
6	399	96.6	623	9	AI811528	AI811528 tw43h06.x
7	396	95.9	289	12	BF655336	BF655336 279811 MA
8	390	94.4	582	10	AM182875	AM182875 xp99a04.x
9	370	89.6	544	9	AI380900	AI380900 tg17f01.x
10	365	88.4	439	14	BM824360	BM824360 R-EST0095
11	346	83.8	499	14	BQ027499	BQ027499 UI-H-CO0-
12	345	83.5	507	10	AM964958	AM964958 EST376926
13	333	80.6	537	9	AI266746	AI266746 qg11c06.x
14	332	80.4	647	14	BM794760	BM794760 K-EST0076
15	328	79.4	633	10	BB212432	BB212432 BB212432
16	320	77.5	274	12	BF552058	BF552058 UI-R-C2p-
17	300	72.6	523	14	W71984	W71984 zd66a06.sl
18	295	71.4	539	12	BF726557	BF726557 by08d05.y
19	276	66.8	681	10	BE563566	BE563566 601334867
20	259.5	62.8	739	9	AA524052	AA524052 ng33b06.s
21	254	61.5	433	10	AW134494	AW134494 UI-H-B11-
22	246.5	59.7	605	9	AI913906	AI913906 wd03f01.x
23	242	58.6	292	9	AA088350	AA088350 z182d08.f
24	232	56.2	437	10	AW492480	AW492480 UI-M-BH3-
25	210	50.8	348	9	AI703436	AI703436 we24c02.x
26	191	46.2	651	13	BM009354	BM009354 603629813
27	175.5	42.5	530	10	BE014705	BE014705 126529 MA
28	175	42.4	596	9	AA887388	AA887388 o337a02.s
29	167.5	40.6	619	10	BE334962	BE334962 us91b07.y
30	167.5	40.6	789	12	BF138948	BF138948 601783079
31	167.5	40.6	853	13	BI525375	BI525375 602924303
32	160.5	38.9	506	12	BF118096	BF118096 u211g10.y
33	160	38.7	378	9	AA631757	AA631757 np76f04.s
34	160	38.7	582	10	AW355430	AW355430 pnf-b.pk0
35	159	38.5	414	9	AA088232	AA088232 z182d08.s
36	158	38.3	504	13	BI468367	BI468367 id87f12.y
37	158	38.3	591	14	BM694442	BM694442 UI-E-C11-
38	158	38.3	620	14	BM767536	BM767536 K-EST0050
39	158	38.3	636	12	BG035257	BG035257 602324771
40	158	38.3	669	14	BM742388	BM742388 R-EST0015
41	158	38.3	889	9	AU117362	AU117362 AU117362
42	158	38.3	894	14	BQ880824	BQ880824 AGENCOURT
43	158	38.3	923	14	BQ228387	BQ228387 AGENCOURT
44	158	38.3	1055	13	BM555065	BM555065 AGENCOURT
45	158	38.3	1076	14	BM923204	BM923204 AGENCOURT

ALIGNMENTS

RESULT 1	BM695193	510 bp	mRNA	linear	EST 28-FEB-2002
LOCUS	BM695193				
DEFINITION	UI-E-CQ1-aev-1-03-0-UI-r1		UI-E-CQ1	Homo sapiens	CDNA clone
ACCESSION	BM695193				
VERSION	BM695193.1	GI:19008451			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
TITLE	1 (bases 1 to 510)				
	Bonaldo,M.F., Lennon,G. and Soares,M.B.				
	Normalization and subtraction: two approaches to facilitate gene				

QY 1 ValMetaspalaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
|||||
Db 539 GTGATGACGCGGTGCCAGCGCGCGCTTGGAAGAGTTCGTGGCCACGCTGGGGCTGCC 480

QY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlyTrpGlu 40
|||||
Db 479 GAGCGAGAGATCGAAGCCGTGGAGGTGAGATCGCCGCTTCGAGACAGCAGCAGTACGAG 420

QY 41 MetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeu 60
|||||
Db 419 ATGCTCAAGCGCTGGCGCCAGCAGACCGCGGCGCTCGAGCCGTTACGGCGCCCTG 360

QY 61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80
|||||
Db 359 GAGCGCATGGGGCTGGACGCGCTGCGTGAAGACTTGCAGCCGCGCTGCAGCGCGGCCG 300

RESULT 3
BE670189/c 687 bp mRNA linear EST 08-SEP-2000
LOCUS 7e31c12.x1 NCI_CGAP_Lu24 Homo sapiens CDNA clone IMAGE:3284086 3'
DEFINITION similar to SW:WSL1_HUMAN Q93038 WSL-1 PROTEIN PRECURSOR ;, mRNA
sequence.
ACCESSION BE670189
VERSION BE670189 GI:10030730
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 687)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Seq primer: -40UP from glbco
High quality sequence stop: 466.

FEATURES
source
1. 687
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3284086"
/clone_1lb="NCI_CGAP_Lu24"
/tissue_type="carcinoid"
/lab_host="DH10B"
/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; Plasmid DNA from the normalized
library NCI_CGAP_Lu5 was prepared, and ss circles were
made in vitro. Following HAP purification, this DNA was
used as tracer in a subtractive hybridization reaction.
The driver was PCR-amplified cDNAs from a pool of 5,000
clones made from the same library (cloneIDs
1414920-1417991 and 1520904-1522439). Subtraction by Bento
Soares and M. Fatima Bonaldo."

BASE COUNT 111 a 215 c 225 g 134 t 2 others
ORIGIN

Alignment Scores:
Pred. No.: 7.36e-43 length: 687
Score: 413.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

DB: 10 Gaps: 0
US-09-993-234-6_COPY_338_417 (1-80) x BE670189 (1-687)

QY 1 ValMetaspalaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
|||||
Db 519 GTGATGACGCGGTGCCAGCGCGCGCTTGGAAGAGTTCGTGGCCACGCTGGGGCTGCC 460

QY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlyTrpGlu 40
|||||
Db 459 GAGCGAGAGATCGAAGCCGTGGAGGTGAGATCGCCGCTTCGAGACAGCAGTACGAG 400

QY 41 MetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeu 60
|||||
Db 399 ATGCTCAAGCGCTGGCGCCAGCAGACCGCGGCGCTCGAGCCGTTACGGCGCCCTG 340

QY 61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80
|||||
Db 339 GAGCGCATGGGGCTGGACGCGCTGCGTGAAGACTTGCAGCCGCGCTGCAGCGCGGCCG 280

RESULT 4
AW074008/c 618 bp mRNA linear EST 13-OCT-1999
LOCUS xb06c09.x1 NCI_CGAP_GUI Homo sapiens CDNA clone IMAGE:2575504 3'
DEFINITION similar to TR:000278 000278 LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH
7. [2] TR:000279 ;, mRNA sequence.
ACCESSION AW074008
VERSION AW074008 GI:6029006
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 618)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: Life
Technologies, Inc. CDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from glbco
High quality sequence stop: 383.

FEATURES
source
1. 618
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2575504"
/clone_1lb="NCI_CGAP_GUI"
/tissue_type="2 pooled high-grade transitional cell
tumors"
/lab_host="DH10B"
/note="Organ: gentourinary tract; Vector: pCMV-SPORT6;
Site_1: SalI; Site_2: NotI; Cloned unidirectionally.
Primer: Oligo dT. Library constructed by Life
Technologies."

BASE COUNT 110 a 204 c 182 g 120 t 2 others
ORIGIN

Alignment Scores:
Pred. No.: 4.99e-42 length: 618
Score: 406.00 Matches: 79
Percent Similarity: 98.75% Conservative: 0
Best Local Similarity: 98.75% Mismatches: 1
Query Match: 98.31% Indels: 0
DB: 10 Gaps: 0

US-09-993-234-6_COPY_338_417 (1-80) x AW074008 (1-618)

QY 1 ValMetaspAlaValProAlaArgArgTrpIysGluPheValArgThrLeuGlyLeuArg 20
|||||
Db 516 GTGATGNACGGCGGTCCAGCGCGCGCTGGAGAGAGTTCGTCCGACAGCGCTGGCGCC 457

QY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGlu 40
|||||
Db 456 GAGGACAGAGATCGAAGCCGTGGAGATCGCCGCTCCGAGACCAAGTACGAG 397

QY 41 MetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeu 60
|||||
Db 396 ATGCTCAAGCGCTGGCGCCAGCAGCAGCCCGCGCTCGAGACCGCTTACGCGGCCCTG 337

QY 61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80
|||||
Db 336 GAGCGCATGGGCTGGACGGCTGCTGGAAGACTTGGCAGCGCGCTGACGCGGCCCG 277

RESULT 5
AI380959/c 587 bp mRNA linear EST 30-MAR-1999
LOCUS tg18c01.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2109120 3'
DEFINITION similar to TR:000278 000278 LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH
7. [2] TR:000279 ;, mRNA sequence.

AI380959
AI380959.1 GI:4190801
EST.
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE 1 (bases 1 to 587)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
COMMENT Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
M.D., Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1237 Std Error: 0.00
Seq primer: -40UP from G1bco
High quality sequence stop: 325.

FEATURES
source
1. 587
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2109120"
/clone_lib="NCI_CGAP_CLL1"
/tissue_type="B-cell, chronic lymphocytic leukemia"
/lab_host="DH10B"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTTCACCAATCTGAGTGGAGCGCGCATTTGCTTTTCTTTTCTTTTCTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT7T3 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."

BASE COUNT 99 a 192 c 176 g 120 t
ORIGIN

Alignment Scores:
Pred. No.: 3.67e-41 Length: 587
Score: 399.00 Matches: 78

Percent Similarity: 97.50% Conservative: 0
Best Local Similarity: 97.50% Mismatches: 2
Query Match: 96.61% Indels: 0
DB: 9 Gaps: 0

US-09-993-234-6_COPY_338_417 (1-80) x AI380959 (1-587)

QY 1 ValMetaspAlaValProAlaArgArgTrpIysGluPheValArgThrLeuGlyLeuArg 20
|||||
Db 518 GTGATGACCGCTGCCAAGCCGCGCGCTGGAGAGAGTTCGTCCGACCAAGTACGAG 459

QY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGlu 40
|||||
Db 458 GAGGACAGATCGAAGCCGTGGAGGTGGAGATCGCCGCTCCGAGACCAAGTACGAG 399

QY 41 MetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeu 60
|||||
Db 398 ATGCTCAAGCGCTGGCGCCAGCAGCAGCCCGCGCTCGAGACCGCTTACGCGGCCCTG 339

QY 61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80
|||||
Db 338 GAGCGCATGGGCTGGACGGCTGCTGGAAGACTTGGCAGCGCGCTGACGCGGCCCG 279

RESULT 6
AI811528/c 623 bp mRNA linear EST 15-DEC-1999
LOCUS tw43h06.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2262491 3'
DEFINITION similar to TR:000278 000278 LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH
7. [2] TR:000279 ;, mRNA sequence.

AI811528
AI811528.1 GI:5398094
EST.
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE 1 (bases 1 to 623)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
COMMENT Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 2337 Std Error: 0.00
Seq primer: -40UP from G1bco
High quality sequence stop: 392.

FEATURES
source
1. 623
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2262491"
/clone_lib="NCI_CGAP_Ut1"
/tissue_type="well-differentiated endometrial
adenocarcinoma, 7 pooled tumors"
/lab_host="DH10B"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Life Technologies catalog #:
11538-014"

BASE COUNT 105 a 188 c 199 g 128 t 3 others
ORIGIN

Alignment Scores:
Pred. No.: 4e-41 Length: 623
Score: 399.00 Matches: 78

Percent Similarity: 97.50% Conservative: 0
Best Local Similarity: 97.50% Mismatches: 2
Query Match: 96.61% Indels: 0
DB: 9 Gaps: 0

US-09-993-234-6_COPY_338_417 (1-80) x AI811528 (1-623)

QY 1 ValMetAspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
||||| ||||||||||||||||||||||||||||||| |||||
Db 518 GTGATGNACGCGGTCCAGCGCGCGCTGGAAGAGATTCTGCGACAGCTGNGCGTCCG 459
QY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGlu 40
||||| ||||||||||||||||||||||||||||||| |||||
Db 458 GAGCAGAGATCGAAGCCGTGAGGTGAGATCGGCCCTTCGAGACCAGCAGTACGAG 399
QY 41 MetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeu 60
||||| ||||||||||||||||||||||||||||||| |||||
Db 398 ATGCTCAAGCGCTGGCGCCAGCAGCAGCCCGCGGCTCGGAGCCGTTACGGCGCCCTG 339
QY 61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80
||||| ||||||||||||||||||||||||||||||| |||||
Db 338 GAGCGCATGGGGCTGGACGGCTGCGTGGAAAGACTTCGCGACGCCCTGACAGCGCGCCG 279

RESULT 7
BF655336 289 bp mRNA linear EST 25-APR-2001
LOCUS 279811 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
DEFINITION BF655336
ACCESSION BF655336
VERSION BF655336.1 GI:11920468
KEYWORDS EST.
SOURCE COW.
ORGANISM Bos taurus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
Bovidae; Bovinae; Bos.
1 (bases 1 to 289)

REFERENCE
AUTHORS Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett
,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G.,
Perteau,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
Keele,J.W.

TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle

JOURNAL MEDLINE

21180013
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390

Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.

PCR Primers

FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCAGTCACGACG
Plate: 76 row: G column: 4
Seq primer: ATTTAGGTGACACTATAG.

FEATURES

source

1. .289
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 3BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: PCMV SPORT6; Site_1: NotI; Site_2: SalI;
Library made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendinosus muscle, and fetal
longissimus muscle."

BASE COUNT 41 a 90 c 116 g 42 t
ORIGIN

Alignment Scores:
Pred. No.: 3.14e-41 Length: 289
Score: 396.00 Matches: 76
Percent Similarity: 97.50% Conservative: 2
Best Local Similarity: 95.00% Mismatches: 2
Query Match: 95.88% Indels: 0
DB: 12 Gaps: 0

US-09-993-234-6_COPY_338_417 (1-80) x BF655336 (1-289)

QY 1 ValMetAspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
||||| ||||||||||||||||||||||||||||||| |||||
Db 3 GTGATGACGCGGTGCCCGCGCGCTTGAAGAGATTCTACGACAGCTAGGTTGCCG 62
QY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGlu 40
||||| ||||||||||||||||||||||||||||||| |||||
Db 63 GAGCGGAGATCGAGCGGTGAGGTGAGTCTGCCGCTCCGCGACAGCAGTACGAG 122
QY 41 MetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeu 60
||||| ||||||||||||||||||||||||||||||| |||||
Db 123 ATGCTCAAGCGCTGGCGCCAGCAGCAGCGCGGCTTGCGGCCCTCTACGCGGCCCTG 182
QY 61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80
||||| ||||||||||||||||||||||||||||||| |||||
Db 183 GAGCGCATGGGGCTGGACGGCTGCGCGAGAGACTTGGAGCCGCTTACAGCGCGGCCG 242

RESULT 8
AW182875 582 bp mRNA linear EST 18-NOV-1999
LOCUS AW182875/c
DEFINITION xp99a04.x1 Soares_NHCEC_cervical_tumor Homo sapiens cDNA clone
IMAGE:2748462 3' similar to TR:000278 000278 LYMPHOCYTE ASSOCIATED
RECEPTOR OF DEATH 7. [2] TR:000279 ;, mRNA sequence.

ACCESSION AW182875
VERSION AW182875.1 GI:6451335
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 582)

TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov

This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Glibco
High quality sequence stop: 461.

FEATURES

source

1. .582
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2748462"
/clone_lib="Soares_NHCEC_cervical_tumor"
/tissue_type="tumor"
/lab_host="DH10B (phage-resistant)"
/note="Organ: cervix; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dt) primer [5'
TGTACCAATCTGAAGTGGAGGCGGCCGCGAAGATTTTCTTTTCTTTTCTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT7T3 vector.
Library is normalized; constructed by Bento Soares and
M.Fatima Bonaldo."

BASE COUNT 99 a 189 c 178 g 115 t 1 others
ORIGIN

Alignment Scores:
Pred. No.: 5.18e-40 Length: 582
Score: 390.00 Matches: 76

Percent Similarity: 96.25% Conservative: 1
Best Local Similarity: 95.00% Mismatches: 3
Query Match: 94.43% Indels: 0
DB: 10 Gaps: 0

US-09-993-234-6_COPY_338_417 (1-80) x AW182875 (1-582)

QY 1 ValMetAspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
|||||
DB 510 GTGATGACCGGTCCCAAGCGCGCGTGAAGAGATTCTGCGCACGCTGGGGCTGCCG 451

QY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGlu 40
|||||
DB 450 GAGCAGAGATCGAAGCCGTGAGGTGAGATCGCCGCTTCCGAGACCAGAAATACGAG 391

QY 41 MetLeuLysArgTrpArgGlnGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeu 60
|||||
DB 390 ATGCTCAAGCGCTGGCGCCAGCAGACGCCGCGGCTCGAGCCGTTTACGCGGCCCTG 331

QY 61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80
|||||
DB 330 GAGCGCATGGGCTGGACGGCTGCTGAGACTTGCGCAGCCGCTGCAGCGGCCCG 271

RESULT 9
AI380900/c 544 bp mRNA linear EST 30-MAR-1999
LOCUS tg17f01.x1 NCI_CGAP_CL11 Homo sapiens cDNA clone IMAGE:2109049 3'
DEFINITION similar to TR:000278 000278 LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH
7. [2] TR:000279 ;, mRNA sequence.

ACCESSION AI380900 GI:4190753
VERSION AI380900.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 544)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
M.D., Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert length: 1246 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 348.
Location/Qualifiers
1. 544
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2109049"
/clone_lib="NCI_CGAP_CL11"
/tissue_type="B-cell, chronic lymphocytic leukemia"
/lab_host="DH10B"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTTACCAATCTGAAGTGGAGGAGCGCCGATGCTTTTCTTTTCTTTTCTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT7T3 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."

BASE COUNT 92 a 174 c 168 g 108 t 2 others
ORIGIN

Alignment Scores:
Pred. No.: 1,74e-37 Length: 544
Score: 370.00 Matches: 74
Percent Similarity: 92.50% Conservative: 0
Best Local Similarity: 92.50% Mismatches: 6
Query Match: 89.59% Indels: 0
DB: 9 Gaps: 0

US-09-993-234-6_COPY_338_417 (1-80) x AI380900 (1-544)

QY 1 ValMetAspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
|||||
DB 518 GTGATGNACCGCTCCCAAGCGCGCGTGNAAAGAGTTCTGTCGACACGCTGGGGCTGCCG 459

QY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGlu 40
|||||
DB 458 GAGCAGAGATCGAAGCCCGTGGAGGTGAGATCGCCGCTTCCGAGACCAGCAGTACGAG 399

QY 41 MetLeuLysArgTrpArgGlnGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeu 60
|||||
DB 398 ATGCTCAAGCGCTGGCGCCAGCAGACGCCGCGGCTCGAGCCGTTTACGCGGCCCTG 339

QY 61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80
|||||
DB 338 GAGCGCATGGGCTGGACGGCTGCTGAGACTTGCGCAGCCGCTGCAGCGGCCCG 279

RESULT 10
BM824360 439 bp mRNA linear EST 06-MAR-2002
LOCUS K-EST0095844 S22SNU16n1 Homo sapiens cDNA clone S22SNU16n1-85-D08
DEFINITION 5', mRNA sequence.
BM824360
ACCESSION BM824360.1 GI:19180773
VERSION BM824360
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 439)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 85 row: D column: 08
High quality sequence stop: 439.
Location/Qualifiers
1. 439
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="S22SNU16n1-85-D08"
/clone_lib="S22SNU16n1"
/sex="F"
/tissue_type="Ascites"
/cell_type="Lymphoblast-like"
/lab_host="DH10B"
/note="Organ: Stomach; Vector: pT7T3-Pac; Site_1: EcoRI;
Site_2: NotI; The S22SNU16 library was contributed by the
Soares laboratory and it was constructed as described by
Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome
Research 6(9): 791-806. RNA was prepared from harvested
cells of SNU-16 culture. SNU-16 cell was obtained from
Korean Cell Line Bank (KCLB). SNU-16 was established from
ascitic fluids of Korean patients by Park J.G. et al.

BASE COUNT 76 a 148 c 150 g 65 t
ORIGIN (1990), Cancer Res 50: 2773-2780."

Alignment Scores:
Pred. No.: 5.56e-37 Length: 439
Score: 365.00 Matches: 70
Percent Similarity: 91.25% Conservative: 3
Best Local Similarity: 87.50% Mismatches: 7
Query Match: 88.38% Indels: 0
DB: 14 Gaps: 0

US-09-993-234-6_COPY_338_417 (1-80) x BM824360 (1-439)

QY 1 ValMetAspAlaValProAlaArgTrpLysGluPheValArgThrLeuGlyLeuArg 20
Db 191 GTGATGGACGGGTCCCAACGGCGCGCTGGAAGAGATTATTCGCCACGCTGGGGCTGCC 250
QY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrglu 40
Db 251 GAGGCATTAATCGAAGCCCGGAGGTGATATCGGCCCTTACGAGACAGCAGTACGAG 310
QY 41 MetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyraAlaLeu 60
Db 311 ATGCTCAAGCGCTGGCGCAGACATCCCGCGGCTCGAGCCGTTTACGCGCGCTG 370
QY 61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80
Db 371 GAGCGCATGGGCTGACGCGCTGCGTGAAGACTTGCGCAACCGTCTGCAACGCGGACCG 430

RESULT 11

BQ027499/c 499 bp mRNA linear EST 27-MAR-2002
LOCUS UI-H-CO0-aqg-a-09-0-UI.s1 NCI_CGAP_Sub9 Homo sapiens cDNA clone
DEFINITION IMAGE:3104895 3', mRNA sequence.

ACCESSION BQ027499
VERSION BQ027499.1 GI:19762778
KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 499)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Jose Mercuende

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>

Seq primer: M13 FORWARD
POLYA-Yes.

FEATURES

source

1.499 location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3104895"
/clone_lib="NCI_CGAP_Sub9"
/tissue_type="mixed"
/dev_stage="mixed"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT7T3-Pac (Pharmacia) with a modified
polylinker; Site_1: Ecor I; Site_2: Not I; tissues:
Cholonic mucosa with Crohns disease, Cholonic mucosa with
ulcerative colitis, Fetal thymus, Cervix, Cervical
adenosquamous carcinoma, Ligament cells, Prostate
carcinoma, Bladder carcinoma, Brain oligodendroga;
NCI_CGAP_Sub9 is a subtracted cDNA library constructed

BASE COUNT 85 a 155 c 145 g 113 t 1 others
ORIGIN TAG_LIB-UI-H-CO0
TAG_TISSUE-Bladder Carcinoma
TAG_SEQ=AGACA"

Alignment Scores:
Pred. No.: 1.85e-34 Length: 499
Score: 346.00 Matches: 68
Percent Similarity: 97.14% Conservative: 0
Best Local Similarity: 97.14% Mismatches: 2
Query Match: 83.78% Indels: 0
DB: 14 Gaps: 0

US-09-993-234-6_COPY_338_417 (1-80) x BQ027499 (1-499)

QY 11 LysGluPheValArgThrLeuGlyLeuArgGluAlaGluIleGluAlaValGlu 30
Db 499 AAGGAGTTCTGTCGCGACGCTGGGCTGCGCGAGGACAGAGATCAACCCGTGAGGTGAG 440

QY 31 IleGlyArgPheArgAspGlnGlnTyrgluMetLeuLysArgTrpArgGlnGlnPro 50
Db 439 ATGNCGCCGCTTCGAGACACGAGATGCTCAAGCGCTGCGCCAGCAGACGCC 380

QY 51 AlaGlyLeuGlyAlaValTyraAlaLeuGluArgMetGlyLeuAspGlyCysValGlu 70
Db 379 GCGGGCTCGGAGCGCGTTTACGCGCGCTGAGCGCATGGGCTGACGCGCTGGAA 320

QY 71 AspleuArgSerArgLeuGlnArgGlyPro 80
Db 319 GACTTGGCAGCGCGCTGACGCGCGCCG 290

QY 71 AspleuArgSerArgLeuGlnArgGlyPro 80
Db 319 GACTTGGCAGCGCGCTGACGCGCGCCG 290

QY 71 AspleuArgSerArgLeuGlnArgGlyPro 80
Db 319 GACTTGGCAGCGCGCTGACGCGCGCCG 290

QY 71 AspleuArgSerArgLeuGlnArgGlyPro 80
Db 319 GACTTGGCAGCGCGCTGACGCGCGCCG 290

QY 71 AspleuArgSerArgLeuGlnArgGlyPro 80
Db 319 GACTTGGCAGCGCGCTGACGCGCGCCG 290

QY 71 AspleuArgSerArgLeuGlnArgGlyPro 80
Db 319 GACTTGGCAGCGCGCTGACGCGCGCCG 290

QY 71 AspleuArgSerArgLeuGlnArgGlyPro 80
Db 319 GACTTGGCAGCGCGCTGACGCGCGCCG 290

QY 71 AspleuArgSerArgLeuGlnArgGlyPro 80
Db 319 GACTTGGCAGCGCGCTGACGCGCGCCG 290

QY 71 AspleuArgSerArgLeuGlnArgGlyPro 80
Db 319 GACTTGGCAGCGCGCTGACGCGCGCCG 290

QY 71 AspleuArgSerArgLeuGlnArgGlyPro 80
Db 319 GACTTGGCAGCGCGCTGACGCGCGCCG 290

QY 71 AspleuArgSerArgLeuGlnArgGlyPro 80
Db 319 GACTTGGCAGCGCGCTGACGCGCGCCG 290

QY 71 AspleuArgSerArgLeuGlnArgGlyPro 80
Db 319 GACTTGGCAGCGCGCTGACGCGCGCCG 290

QY 71 AspleuArgSerArgLeuGlnArgGlyPro 80
Db 319 GACTTGGCAGCGCGCTGACGCGCGCCG 290

QY 71 AspleuArgSerArgLeuGlnArgGlyPro 80
Db 319 GACTTGGCAGCGCGCTGACGCGCGCCG 290

QY 71 AspleuArgSerArgLeuGlnArgGlyPro 80
Db 319 GACTTGGCAGCGCGCTGACGCGCGCCG 290

QY 71 AspleuArgSerArgLeuGlnArgGlyPro 80
Db 319 GACTTGGCAGCGCGCTGACGCGCGCCG 290

QY 71 AspleuArgSerArgLeuGlnArgGlyPro 80
Db 319 GACTTGGCAGCGCGCTGACGCGCGCCG 290

QY 71 AspleuArgSerArgLeuGlnArgGlyPro 80
Db 319 GACTTGGCAGCGCGCTGACGCGCGCCG 290

QY 71 AspleuArgSerArgLeuGlnArgGlyPro 80
Db 319 GACTTGGCAGCGCGCTGACGCGCGCCG 290

QY 71 AspleuArgSerArgLeuGlnArgGlyPro 80
Db 319 GACTTGGCAGCGCGCTGACGCGCGCCG 290

QY 71 AspleuArgSerArgLeuGlnArgGlyPro 80
Db 319 GACTTGGCAGCGCGCTGACGCGCGCCG 290

QY 71 AspleuArgSerArgLeuGlnArgGlyPro 80
Db 319 GACTTGGCAGCGCGCTGACGCGCGCCG 290

/clone_lib="MAGE resequences, MAGH"
/note="Vector: PBluescriptSKm"
BASE COUNT 85 a 155 c 156 g 111 t
ORIGIN

Alignment Scores:

Pred. No.:	2.54e-34	Length:	507
Score:	345.00	Matches:	68
Percent Similarity:	94.67%	Conservative:	3
Best Local Similarity:	90.67%	Mismatches:	4
Query Match:	83.54%	Indels:	0
DB:	10	Gaps:	0

US-09-993-234-6_COPY_338_417 (1-80) x AW964958 (1-507)

QY 6 ProAlaArgArgTrrPlysgluPheValArgThrLeuglyLeuArggluAlaGluileglu 25
|||||
DB 505 CCAGCCCGGGCGATGAAGAAGTTCGTGCGCACGCTGGGCGCGGAGCAAGAGATCAAA 446
QY 26 AlavaGluValGluileglyArgPheArgAspginglnTyrGluMetLeuysArgTrr 45
|||||
DB 445 CCGGTGAAGGTGGAGATCGCGCGCTCCCGAGACCAAGTACAGATGCTCAAGCGCTGG 386
QY 46 ArgGlnGlnInProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMetGlyLeu 65
|||||
DB 385 CGCCAGCAGCAGCCCGGGGCTCGAGCCGCTTACGGCGGCCCTGGAGCGCATGGGGCTG 326
QY 66 AspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80
|||||
DB 325 GACGGCTGCGTGAAGACTTGGCAGCCGCGCTGACGGCGGCCG 281

RESULT 13

AI266746/c 537 bp mRNA linear EST 03-FEB-1999
LOCUS qg11c06.x1 Soares_NhMPu_S1 Homo sapiens cDNA clone IMAGE:1932202
DEFINITION 3', similar to TR:000278 000278 LYMPHOCTE ASSOCIATED RECEPTOR OF
DEATH 7. [2] TR:000280 ; mRNA sequence.

AI266746
AI266746.1 GI:3884904
EST.

VERSION
KEYWORDS
SOURCE
ORGANISM

human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)

COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov

This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 837 Std Error: 0.00
Seq primer: -40UP from GIBCO

High quality sequence stop: 351.
Location/Qualifiers

FEATURES

source

1. 537
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1932202"
/clone_lib="Soares_NhMPu_S1"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab_host="DH10B"
/note="Organ: mixed (see below); Vector: pT7T3D-Pac
(Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; Equal amounts of Plasmid DNA from three
normalized libraries (melanocyte 2NBHM, pregnant uterus
NBHPU, and fetal heart NBH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of

5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."
BASE COUNT 89 a 172 c 163 g 108 t 5 others
ORIGIN

Alignment Scores:

Pred. No.:	9.62e-33	Length:	537
Score:	333.00	Matches:	67
Percent Similarity:	85.00%	Conservative:	1
Best Local Similarity:	83.75%	Mismatches:	12
Query Match:	80.63%	Indels:	0
DB:	9	Gaps:	0

US-09-993-234-6_COPY_338_417 (1-80) x AI266746 (1-537)

QY 1 ValMetAspAlaValProAlaArgArgTrrPlysgluPheValArgThrLeuglyLeuArg 20
|||
DB 516 GTGATNGACCGGTNCCAGCGCGCGCTGMAAGAGTTCGTGCGCACGCGGGGCTGCGC 457
QY 21 GluAlaGluilegluAlaValGluValGluileglyArgPheArgAspginglnTyrGlu 40
|||||
DB 456 GAGCAGAGATCGAACCCGTGNAGGTGAGATCGCCGCTTCGAGACCAAGTACGAG 397
QY 41 MetLeuysArgTrrPargGlnGlnInProAlaGlyLeuGlyAlaValTyrAlaAlaLeu 60
|||||
DB 396 ATGCTCAAGCGCTGGCGCCAGCAGACGCCCGGGGCTCGAGCCGTTTACCGGCCCTG 337
QY 61 GluArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80
|||||
DB 336 GAGCGCATGGGGCTGGAGCGCTGCTGGAAGACTTGGCAGACGCCGCTGACGGCGGCCG 277

RESULT 14

BM794760 647 bp mRNA linear EST 05-MAR-2002
LOCUS K-EST0076219 S22SNUI6n1 Homo sapiens cDNA clone S22SNUI6n1-48-G11
DEFINITION 5', mRNA sequence.

AI266746
BM794760.1 GI:19142992
EST.

VERSION
KEYWORDS
SOURCE
ORGANISM

human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL

1 (bases 1 to 647)
Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
Kim, Y.S.

COMMENT
21C Frontler Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS

Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr
Plate: 48 row: G column: 11
High quality sequence stop: 647.

Location/Qualifiers

FEATURES

source

1. 647
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="S22SNUI6n1-48-G11"
/clone_lib="S22SNUI6n1"
/sex="F"
/tissue_type="Ascites"
/cell_type="Lymphoblast-like"
/lab_host="DH10B"
/note="Organ: Stomach; Vector: pT7T3-Pac; Site_1: EcoRI;
Site_2: NotI; The S22SNUI6 library was contributed by the
Soares laboratory and it was constructed as described by

Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. RNA was prepared from harvested cells of SNU-16 culture. SNU-16 cell was obtained from Korean Cell Line Bank (KCLB). SNU-16 was established from ascitic fluids of Korean patients by Park J.G. et al. (1990), Cancer Res 50: 2773-2780."

BASE COUNT 110 a 229 c 203 g 105 t
ORIGIN

Alignment Scores:

Pred. No.: 1.7e-32 Length: 647
Score: 332.00 Matches: 65
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 80.39% Indels: 0
DB: 14 Gaps: 0

US-09-993-234-6_COPY_338_417 (1-80) x BM794760 (1-647)

OY 1 ValMetaspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArg 20

DB 451 GTGATGACGCGGTCCACGCGCGCTGGAAGAGTTCGTGCGCAGCTGGGGCTGCGC 510

OY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGlu 40

DB 511 GAGCGAGAGATCGAAGCCGTGAGGTGAGATCGCCGCTTCGAGACACAGCAGTACGAG 570

OY 41 MetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeu 60

DB 571 ATGCTCAGCGCTGGCGCCAGCAGCAGCCCGGGCGCTCGAGCCGTTTACGGCGCCCTG 630

OY 61 GluArgMetGlyLeu 65

DB 631 GAGCGCATGGGGCTG 645

RESULT 15
BB212432

LOCUS BB212432 633 bp mRNA linear EST 31-AUG-2001
DEFINITION BB212432 RIKEN full-length enriched, 0 day neonate thymus Mus
musculus cDNA clone A430110L22 3', mRNA sequence.

ACCESSION BB212432 GI:15410061

VERSION BB212432
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 633)

Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,
Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda
,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki
,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toyota,T.,
Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
On Jun 30, 2000 this sequence version replaced gi:8877385.
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gscl.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/

TITLE
JOURNAL
COMMENT

Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagl,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,

Watabiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Yamanaka,I., Kiyosawa,H., Kondo,S., Saito,T., Shinagawa,A., Aizawa
,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K., Arakawa,T.,
Ishii,Y. and Hayashizaki,Y.
Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct.
Func. Genomics 2 pre, L72-L86 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp/) for
further details.
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.

FEATURES

source
1. 633
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="A430110L22"
/clone_lib="RIKEN full-length enriched, 0 day neonate
thymus"
/tissue_type="thymus"
/dev_stage="0 day neonate"
/lab_host="DH108"

/note="Site_1: SalI; Site_2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTTCTTTVN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot - 10.0 and subtraction to Rot - 459.0. Second
strand cDNA was prepared with the primer adapter of
sequence [5' GAGAGAGAGATCTCGAGTTAATTAATCCCCCCCCCC
3']. cDNA was cleaved with XhoI and BamHI. Vector: a
modified pBluescript KS(+) after bulk excision from Lambda
FLC I."

BASE COUNT 124 a 169 c 190 g 149 t 1 others
ORIGIN

Alignment Scores:

Pred. No.: 5.38e-32 Length: 633
Score: 328.00 Matches: 73
Percent Similarity: 93.75% Conservative: 2
Best Local Similarity: 91.25% Mismatches: 5
Query Match: 79.42% Indels: 3
DB: 10 Gaps: 0

US-09-993-234-6_COPY_338_417 (1-80) x BB212432 (1-633)

OY 1 ValMetaspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArg 20

DB 132 GTGATGATGCGGTCCACGACGAGAGGTGAGAGTTCGTGCGCAGCTGGGGCTGCGG 191

OY 21 GluAlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGlu 40

DB 192 GAAGCGGAATTGAAGCGGTGAGGTGGAATCTGCGCTTCGAGACGACGATATGAG 251

OY 41 MetLeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeu 60

Db 252 ATGCTCAAGCGCTGGCGTCAGCAGCAGCCTGCAAGCCCTCGGTGCCATCTATCG-GCTCTG 310
Qy 61 GLUArgMetGlyLeuAspGlyCysValGluAspLeuArgSerArgLeuGlnArgGlyPro 80
Db 311 GAGCGCATGGGTCTGGAAGGCTGTGCGCCGAGGACCTGNC-AGCCGCCT-CAGCGTGGCCCG 368

Search completed: April 6, 2003, 23:25:25
Job time : 507.409 secs

GenCore version 5.1.4-p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: Apr11 6, 2003, 15:35:34 ; Search time 2161.6 Seconds
(without alignments)
2504.221 Million cell updates/sec

Title: US-09-993-234-6_COPY_19_204
Perfect score: 1101
Sequence: 1 LIGARAQGGTSPRCDCAGD.....GSCPERCAAVCGWRQMFVQ 186

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US09993234/runat_27032003_115455_15349/app_query.fasta_1.2346
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09993234_@CGN_1_1.8534_@runat_27032003_115455_15349 -NCPU=6 -ICPU=3
-NO_XLPHY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*

29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1101	100.0	1254	6 AR119657	AR119657 Sequence
2	1101	100.0	1254	9 HSU72763	U72763 Human death
3	1101	100.0	1254	9 HSU78029	U78029 Human apopto
4	1101	100.0	1254	9 HSU94501	U94501 Human lymph
5	1101	100.0	1257	9 HSU94502	U94502 Human lymph
6	1101	100.0	1634	9 HSU74611	U74611 Human Apo-3
7	1101	100.0	1662	6 AX055442	AX055442 Sequence
8	1101	100.0	1662	6 AX201344	AX201344 Sequence
9	1101	100.0	1783	6 AR119656	AR119656 Sequence
10	1091	99.1	1528	9 HSU83597	U83597 Human death
11	1091	99.1	1557	9 HSU75380	U75380 Human apopt
12	1077	97.8	1355	9 HSU94503	U94503 Human lymph
13	1077	97.8	1743	6 AX331947	AX331947 Sequence
14	1077	97.8	1743	9 HSWSL1	Y09392 H.sapiens m
15	1070	97.2	1143	9 HSU94510	U94510 Human lymph
16	1041	94.6	1250	6 AX150176	AX150176 Sequence
17	1041	94.6	1763	9 AF026071	AF026071 Homo sapi
18	1037	94.2	1669	9 AF026070	AF026070 Homo sapi
19	979	88.9	808	9 HSU75381	U75381 Human apopt
20	979	88.9	809	9 HSU94512	U94512 Human lymph
21	979	88.9	816	6 AX335086	AX335086 Sequence
22	979	88.9	816	9 HSU83598	U83598 Human death
23	965.5	87.7	1198	9 HSU94504	U94504 Human lymph
24	964	87.6	1087	9 HSU94505	U94505 Human lymph
25	794.5	72.2	1119	9 HSU94509	U94509 Human lymph
26	767	69.7	4825	9 AB051850	AB051850 Homo sapi
27	767	69.7	53982	9 AL158217	AL158217 Human DNA
28	760	69.0	4811	9 AB051851	AB051851 Homo sapi
29	657.5	59.7	952	9 HSU94506	U94506 Human lymph
30	636	57.8	651	9 HSU83599	U83599 Human alter
31	613	55.7	1665	10 AF329969	AF329969 Mus muscu
32	501	45.5	838	9 HSU94507	U94507 Human lymph
33	472	42.9	1619	10 BC017526	BC017526 Mus muscu
34	437	39.7	196368	2 AL772240	AL772240 Mus muscu
35	374.5	34.0	665	9 HSU83600	U83600 Human death
36	330.5	30.0	97483	2 AC118359	AC118359 Rattus no
37	231.5	21.0	2600	4 SSJ001202	AJ001202 Sus scrof
38	216	19.6	705	9 HSU94508	U94508 Human lymph
39	216	19.6	2115	10 AF329976	AF329976 Rattus no
40	216	19.6	2115	10 AF329977	AF329977 Rattus no
41	216	19.6	2115	10 AF329978	AF329978 Rattus no
42	216	19.6	2115	10 AF329979	AF329979 Rattus no
43	216	19.6	2115	10 AF329980	AF329980 Rattus no
44	216	19.6	2115	10 AF329981	AF329981 Rattus no
45	216	19.6	2130	6 AX401925	AX401925 Sequence

RESULT 1

ALIGNMENTS

AR119657
LOCUS AR119657 1254 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 3 from patent US 6153402.
ACCESSION AR119657
VERSION AR119657
KEYWORDS AR119657.1 GI:14102356
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
BASE COUNT 201 a 420 c 407 g 226 t
ORIGIN

Alignment Scores:
Pred. No.: 2.08e-68 Length: 1254
Score: 1101.00 Matches: 186
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-993-234-6_COPY_19_204 (1-186) x AR119657 (1-1254)

OY 1 LeuLeuGlYAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
Db 55 CTGCTGGGGGGCCGGCCAGGGCGGCGACTGTAGCCCAAGTGTGACTGTGCCGGTGAC 114
OY 21 PheHisLysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLys 40
Db 115 TTCACACAGAAGATTGCTGTGTTGTGCAGAGGCTGCCACGGGGGCACTACCTGAAG 174
OY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
Db 175 GCGCCCTGGCAGCGAGCCCTGCGGCAACTCCACTGCTGTGTGCCCAAGACACCTTC 234
OY 61 LeuAlaTrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80
Db 235 TTGGCCTGGGAGAACCAACATTAATTGATGTGCCCGCTGCCAGGCTGTGATGAGCAG 294
OY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
Db 295 GCCTCCAGGTGGCGCTGGAGAACTGTTCAAGCAGTGGCCGACACCCGCTGTGCTTAAG 354
OY 101 ProGlyTrpPheValGluCysGlnValSerClnCysValSerSerProPheTyrCys 120
Db 355 CCAGGCTGGTTGTGAGTGGCAGGTCAAGTCAATGTGTCAAGCAGTTCACCTTCTACTGC 414
OY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeucysSerArgArg 140
Db 415 CAACCATGCTAGACTGCGGGCCCTGGACCGCCACACAGCGCTACTCTGTCCCGCAGA 474
OY 141 AspThrAspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSer 160
Db 475 GATACGTAGCTGGGACCTGCTGCTGCTTATGAACATGGCGATGGCTGCTGCC 534
OY 161 CysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTyrParg 180
Db 535 TGCCCCACAGACACCTGGGAGAGCTGTCCAGAGCGCTGTGCCGCTGTCTGTGGCTGAGG 594
OY 181 GlnMetPheTrpValGln 186
Db 595 CAGATGTCTGGGTCAG 612

RESULT 2
HSU72763 HSU72763 1254 bp mRNA linear PRI 15-NOV-1996
LOCUS
DEFINITION Human death receptor 3 (DR3) mRNA, complete cds.

ACCESSION U72763
VERSION U72763.1 GI:1669511
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
gene
CDS
/organism="Homo sapiens"
/db_xref="taxon:9606"
1. .1254
/gene="DR3"
1. .1254
/codon_start=1
/product="death receptor 3"
/protein_id="AAC50819.1"
/db_xref="GI:1669512"
/translation="MEQRPKCAVAALLVLVGARAQGGTRSPKDCAGDFHKIG
LPCRGCPAGHYLKAPCTEPCGNSRLVCPQDTFLAMENHNHNSCARQACDEQASQV
ALENCSAVADTRCGCKPGWFEQVSCVSSSPFYCQPCIDGALHRTLRILCSRDT
DCGTRCLPGEYEHGDCVSCPTSLGSCPERCAVCGWRQWQVLLAGLVPLLLGA
TLTYTYRHCPHKPLVTADAEAGMALTPPATHLSPIDSAHTLLAPDSSEKICTVOL
VGNSTWPTGYPETQDALCPQVWMSMDQLPSRALGPAAPATSPSPAGSPAMLOPQPO
LYDVMDAVPARWKEFVRITGLBFAEIEAVEVEIGRFDDQYEMLKRWROQPAIGLA
VVAALERMGLDGVEDLRSLRQRP"

BASE COUNT 201 a 420 c 407 g 226 t
ORIGIN

Alignment Scores:
Pred. No.: 2.08e-68 Length: 1254
Score: 1101.00 Matches: 186
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-993-234-6_COPY_19_204 (1-186) x HSU72763 (1-1254)

OY 1 LeuLeuGlYAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
Db 55 CTGCTGGGGGGCCGGCCAGGGCGGCGACTGTAGCCCAAGTGTGACTGTGCCGGTGAC 114
OY 21 PheHisLysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLys 40
Db 115 TTCACACAGAAGATTGCTGTGTTGTGCAGAGGCTGCCACGGGGGCACTACCTGAAG 174
OY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
Db 175 GCGCCCTGGCAGCGAGCCCTGGGCAACTCCACTGCTGTGTGTGCCCAAGACACCTTC 234
OY 61 LeuAlaTrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80
Db 235 TTGGCCTGGGAGAACCAACATTAATTGAAATGTGCCCGCTGCCAGGCTGTGATGAGCAG 294
OY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
Db 295 GCCTCCAGGTGGCGCTGGAGAACTGTTCAGACAGTGGCCGACACACCCGCTGTGCTTAAG 354

OY 101 ProGlyTTrpPheValGluCysGlnValSerGlnCysValSerSerProphetyrCys 120
|||||
Db 355 CCAGGCTGTTGTGGAGTGCACAGGTACCAATGTGTACAGATTCCACCTTCTACTGC 414
OY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArg 140
|||||
Db 415 CAACCATGCCTAGACTGGGGCCCTGCACCCGACACACGGCTACTCTGTCCCGCAGA 474
OY 141 AspThrAspCysGlyThrCysLeuProGlyPheGluHisGlyAspGlyCysValSer 160
|||||
Db 475 GATACTGACTGTGGACCTGCCTGCCTTCTATGAACATGGCGATGGCTGCTCC 534
OY 161 CysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTrpArg 180
|||||
Db 535 TGCCCCACGAGCACCTGGGGAGCTGTCCAGAGCGCTGTCCGCTGTGTGGCTGAGG 594
OY 181 GlnMetPheTrpValGln 186
|||||
Db 595 CAGATGTTCTGGGTCCAG 612

RESULT 3
HSU78029

LOCUS HSU78029 1254 bp mRNA linear PRI 15-JAN-1997
DEFINITION Human apoptosis inducing receptor AIR mRNA, complete cds.
ACCESSION U78029
VERSION U78029.1 GI:1778763

KEYWORDS
SOURCE
ORGANISM

Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Degli-Esposti, M.A., Din, W.S., Cosman, D., Smith, C.A. and Goodwin, R.G.
TITLE AIR, A Novel Member of the TNF Receptor Family, Is a Strong Inducer of Apoptosis
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1254)
AUTHORS Degli-Esposti, M.A. and Goodwin, R.G.
TITLE Direct Submission
JOURNAL Submitted (12-NOV-1996) Biochemistry, Immunex Corporation, 51 University St., Seattle, WA 98101, USA

FEATURES
source

1. 1254
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/map="1pter"
/cell_type="peripheral blood T-cells"
1. 1254
/codon_start=1
/product="apoptosis inducing receptor AIR"
/protein_id="AAB40918.1"
/db_xref="GI:1778764"

CDS

/translation="MEQRPFGCAVVAALLVLGARAQGGTRSPRCDCAGDFHKKIG
LFCCRGCPAGHYLKAPCTEPCGNSITCLVCPQDTFLAWENHNSECARCQACDEQASQV
ALENCSAVADTRCGCKPGWFEVCQVSSSPFYCQCLDCGALHRTLLCSRDY
DCGTCLPGFEYEHGDGCVSPTISGSCPERCAAVCGWRQMFVYVLLAGLVPLLGA
TLFTYRHCWPHKPLVTADGEMALTPPATHLSPIDSAHTLLAPDSEKICTYQL
VGNSTWPGYPTQALCPQVTVMSDQLPSRALGPAAPTLSPSPAGSPAMMLQPGPO
LYVDMDAVPARRWKEFVRTGLREAEIEAVEVEIGFRDQYEMUKRWQQPAGIGA
VYALERMGLDGCVEDLRSRLQRP"

BASE COUNT 201 a 420 c 407 g 226 t
ORIGIN

Alignment Scores:
Pred. No.: 2.08e-68
Score: 1101.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 9

Length: 1254
Matches: 186
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-09-993-234-6_COPY_19_204 (1-186) x HSU78029 (1-1254)

OY 1 LeuLeuGlyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
|||||
Db 55 CTGCTGGGGGGCCCGGGCCAGGGCCACTGCTAGCCCCAGGTGTGACTGTGCCGGTGAC 114
OY 21 PheHisLysLysIleGlyLeuPheCysArgGlyCysProAlaGlnHisIstYrLeuLys 40
|||||
Db 115 TTCCACAAGAAGATTGCTGTGTTGTGTGCAGAGGCTGCCACGGGGGACTACTGTAAG 174
OY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
|||||
Db 175 GCCCTTGACAGGAGCCCTGGCGCACTCCACCTGCTGTGTGTCCCAAGACACCTTC 234
OY 61 LeuAlaTrpGluAsnHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80
|||||
Db 235 TTGGCCCTGGGAGAACCACTAATTTCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAG 294
OY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
|||||
Db 295 GCCTCCAGGTGGCGCTGGAGACTGTTCAGCAGTGGCCGACACCCGCTGTGGCTGTAG 354
OY 101 ProGlyTTrpPheValGluCysGlnValSerGlnCysValSerSerProphetyrCys 120
|||||
Db 355 CCAGGCTGTTGTGGAGTGCACAGGTACCAATGTGTACAGAGTTACACCTTCTACTGC 414
OY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg 140
|||||
Db 415 CAACCATGCCTAGACTGGGGCCCTGCACCGCCACACAGGGCTACTCTGTCCCGCAGA 474
OY 141 AspThrAspCysGlyThrCysLeuProGlyPheGluHisGlyAspGlyCysValSer 160
|||||
Db 475 GATACTGACTGTGGAGCTGCCTGCCTGCTTCTATGAACATGGCGATGGCTGCTGCC 534
OY 161 CysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTrpArg 180
|||||
Db 535 TGCCCCACGAGCACCTGGGGAGCTGTCCAGAGCGCTGTCCGCTGTGTGGCTGAGG 594
OY 181 GlnMetPheTrpValGln 186
|||||
Db 595 CAGATGTTCTGGGTCCAG 612

RESULT 4
HSU94501

LOCUS HSU94501 1254 bp mRNA linear PRI 15-MAY-1997
DEFINITION Human lymphocyte associated receptor of death 1a mRNA, complete cds.
ACCESSION U94501
VERSION U94501.1 GI:2071948

KEYWORDS
SOURCE
ORGANISM

Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Screation, G.R., Xu, X.N., Olsen, A.L., Cowper, A.E., Tan, R., McMichael, A.J. and Bell, J.I.
TITLE LARD: a new lymphoid-specific death domain containing receptor regulated by alternative pre-mRNA splicing
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)
MEDLINE 97272273
PUBMED 9114039

REFERENCE
AUTHORS
TITLE
JOURNAL

FEATURES
source
1. 1254
/organism="Homo sapiens"
/db_xref="taxon:9606"

Location/Qualifiers
Submitted (19-MAR-1997) Molecular Immunology Group, Institute of Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3 9DU, UK

Db 175 GCCCCTGCACGAGACCCCTGGCGCAACTCCACCTGCCCTGTGTGTCTCCCAAGACACCTTC 234

QY 61 LeuAlaTrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80

Db 235 TTGGCCCTGGAGAACCACTAATCTCTGAATGTGCCCTGCCAGGCGCTGTGATGAGCAG 294

QY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100

Db 295 GCCTCCAGAGTGCGCTGGAGAACTGTTCCAGCAGTGGCCGACACCCGCTGTGGCTGTAAAG 354

QY 101 ProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerProphetyrCys 120

Db 355 CCAGGCTGGTTGTGGAGTGCAGGTCAGCCAATGTGTCCAGATTCCACCCCTTCTACTGC 414

QY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg 140

Db 415 CAACCATGCTAGACTGCGGGGCCCTGCACCGCCACACAGGCTACTCTGTCTCCCGCAGA 474

QY 141 AspThrAspCysGlyThrCysLeuProGlyPheTyrgluHisGlyAspGlyCysValSer 160

Db 475 GATACTGACTGTGGACCTGCTGCTGCTTCTATGAACATGGCGATGGCTGCGTGTCC 534

QY 161 CysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTrpArg 180

Db 535 TGCCCCACGAGCACCCTGGGAGCTGTCCAGAGCGCTGTGCCGCTGTGTGGCTGGAG 594

QY 181 GlnMetPheTrpValGln 186

Db 595 CAGATGTCTGTGGTCCAG 612

RESULT 6

HSU74611

LOCUS HSU74611 1634 bp mRNA linear PRI 02-JAN-1997

DEFINITION Human Apo-3 mRNA, complete cds.

ACCESSION U74611

VERSION U74611.1 GI:1763292

KEYWORDS

SOURCE Homo sapiens.

ORGANISM Homo sapiens.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1634)

AUTHORS Marsters,S.A., Sheridan,J.P., Donahue,C.J., Pittl,R.M., Gray,C.L., Goddard,A.D., Bauer,K.D. and Ashkenazi,A.

TITLE Apo-3, a new member of the tumor necrosis factor receptor family, contains a death domain and activates apoptosis and NF-kB

JOURNAL Curr. Biol. (1996) In press

REFERENCE 2 (bases 1 to 1634)

AUTHORS Marsters,S.A., Sheridan,J.P., Donahue,C.J., Pittl,R.M., Gray,C.L., Goddard,A.D., Bauer,K.D. and Ashkenazi,A.

TITLE Direct Submission

JOURNAL Submitted (15-OCT-1996) Molecular Oncology, Genentech, 460 Pt. San Bruno Blvd., South San Francisco, CA 94080, USA

FEATURES

Source location/Qualifiers

1..1634

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="1"

/map="1p36.3"

/tissue_type="heart"

/dev_stage="fetal"

89..1342

/note="contains death domain, activates apoptosis and NF-kB; TNF receptor family member"

/codon_start=1

/product="Apo-3"

/protein_id="AAB39714.1"

/db_xref="GI:1763293"

CDS

/translation="MEGRPRGCAVAANAALLVLLGARAOGGTRSPRCDCAGDFHKKIG LFCCRGPAGHYLKAPCTEPCGNSTCLVCPQDTFLAMENHNSECARQACDEQASQV ALENCASAVADTRCGCKPGWFEVCQVSSSPFYCQPLDCGALHRTLLCSRDY DCGTCLPGFEHGDGCVSPTSTIGSPERCAVCGWROMFWOVYLAGLVPLLIGA TLTYYTRHGMPHKPLVTADAEAGMEALTPPPATHLSPLDASHTLAPDSSEKICTVOL

VGNSWTPGYPETQEAICPVWTSWDQLPSRALGPAAPTLSPESPAGSPAMLOPGPO LYDMDAVPARRWKEFEVRLGLREAIEAVEVEIGRFDOQYEMLRKRRQOOPAGLGA VYALERMGLDGCVEDURSRLORGP"

BASE COUNT 300 a 528 c 519 g 287 t

ORIGIN

Alignment Scores:

Pred. No.: 2.71e-68 Length: 1634

Score: 1101.00 Matches: 186

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 9 Gaps: 0

US-09-993-234-6_COPY_19_204 (1-186) x HSU74611 (1-1634)

QY 1 LeuLeuGlyAlaArgAlaGlnGlyThrArgSerProArgCysAspCysAlaGlyAsp 20

Db 143 CTGCTGGGGGGCCCGGGCCAGGGGGCACTCGTAGCCCCAGGTGTGACTGTGCGGTGAC 202

QY 21 PheHisLysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLys 40

Db 203 TTCCACAGAAGATTGCTGTGTTGTGTGCAGAGGCTGCCAGGGGGCACTACTGAAG 262

QY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60

Db 263 GCCCCTGCACGAGACCCCTGGCGCACTCCACCTGCTGTGTGTCTCCCAAGACACCTTC 322

QY 61 LeuAlaTrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80

Db 323 TTGGCCCTGGAGAACCACTAATCTCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAG 382

QY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100

Db 383 GCCTCCAGAGTGCGCGCTGGAGAACTGTTCAAGAGTGCCGACACCCGCTGTGGCTGTAA 442

QY 101 ProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerProphetyrCys 120

Db 443 CCAGGCTGGTTGTGGAGTGCAGGTCAGCAATGTGTACAGCAAGTTCACCCCTTCTACTGC 502

QY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg 140

Db 503 CAACCATGCTAGACTGCGGGGCCCTGCACCGCCACACAGGCTACTCTGTCCCGCAGA 562

QY 141 AspThrAspCysGlyThrCysLeuProGlyPheTyrgluHisGlyAspGlyCysValSer 160

Db 563 GATACTGACTGTGGACCTGCTGCTGCTTCTATGAACATGGCGATGGCTGCGTGTCC 622

QY 161 CysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTrpArg 180

Db 623 TGCCCCACGAGCACCCTGGGAGCTGTCCAGAGCGCTGTGCCGCTGTGTGGCTGAGAG 682

QY 181 GlnMetPheTrpValGln 186

Db 683 CAGATGTCTGTGGTCCAG 700

RESULT 7

AX055442

LOCUS AX055442 1662 bp DNA linear PAT 13-JAN-2001

DEFINITION Sequence 72 from Patent WO0073452.

ACCESSION AX055442

VERSION AX055442.1 GI:12228713

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1662)

AUTHORS Ashkenazi,A.J., Baker,K.P., Chan,B., Goddard,A., Godowski,P.J., Gurney,A.L., Hebert,C., Henzel,W., Kabakoff,R.C., Shelton,D.L., Tamas,D., Watanabe,C.K. and Wood,W.I.

TITLE Compositions and methods for the treatment of immune related diseases

JOURNAL Patent: WO 0073452-A 72 07-DEC-2000;
Genentech, Inc. (US)
Location/Qualifiers
1.1662
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 302 a 540 c 531 g 289 t
ORIGIN

Alignment Scores:

Score: 2.75e-68 Length: 1662
Pred. No.: 1101.00 Matches: 186
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-993-234-6_COPY_19_204 (1-186) x AX055442 (1-1662)

QY 1 LeuLeuGLyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
Db 157 CTGCTGGGGGGCCGGCCAGGGGGGCGGCGACTCGTAGCCCAAGGTGTGACTGTGCCGGTGAC 216
QY 21 PheHisLysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLys 40
Db 217 TTGCACAGAAGATGTGCTGTTTGTGTGACAGAGGCTGCCAGCGGGGCGACTACTGGAAG 276
QY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
Db 277 GCCCCTTGACAGGAGCCCTGCGGCAACTCCACTGCTGTGTGTCCCAAGACACCTTC 336
QY 61 LeuAlaTrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80
Db 337 TTGGCCTGGAGAACCAACATATTCTGAATGTGCCCGCTGCCAGGCGCTGTGATGAGCAG 396
QY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
Db 397 GCCTCCAGGTGGCGCTGGAGAACTGTTCAGCAGTGGCCGACACCCCGCTGTGCTGAAG 456
QY 101 ProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerSerProPheTyrCys 120
Db 457 CCAGGCTGGTGTGGAGTGGCAGGTCAAGCAATGTGTCAAGCAGTTACCCCTTCTACTGC 516
QY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg 140
Db 517 CAACCATGCTTAGACTGCGGGGCGCTGCACCGCCACACAGGCTACTCTGTCCCGCAGA 576
QY 141 AspThrAspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSer 160
Db 577 GATACTGACTGTGGGACCTGCTGCTCTATGAACATGGCGATGGCTGCGTGC 636
QY 161 CysProThrSerThrLeuGlySerCysProGluArgCysAlaValCysGlyTyrParg 180
Db 637 TGCCCCACAGACACCCCTGGGAGGCTGTCCAGAGCGGTGTGCCGCTGTGGCTGAGG 696
QY 181 GlnMetPheTrpValGln 186
Db 697 CAGATGTCTGGGTCCAG 714

RESULT 8
AX201344

LOCUS AX201344 1662 bp DNA linear PAT 30-AUG-2001
DEFINITION Sequence 23 from Patent WO0153486.
ACCESSION AX201344
VERSION AX201344.1 GI:15391165
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1662)
Ashkenazi,A.J., Goddard,A., Godowski,P.J., Gurney,A.L.,
Hillan,K.J., Marsters,S.A., Pan,J., Pitti,R.M., Roy,M.A., Smith,V.,

TITLE Stone,D.M., Watanabe,C.K. and Wood,W.I.
JOURNAL Compositions and methods for the treatment of tumour
Patent: WO 0153486-A 23 26-JUL-2001;
Genentech, Inc. (US)

BASE COUNT 302 a 540 c 531 g 289 t
ORIGIN

Alignment Scores:
Score: 2.75e-68 Length: 1662
Pred. No.: 1101.00 Matches: 186
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-993-234-6_COPY_19_204 (1-186) x AX201344 (1-1662)

QY 1 LeuLeuGLyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
Db 157 CTGCTGGGGGGCCGGCCAGGGGGGCGGCGACTCGTAGCCCAAGGTGTGACTGTGCCGGTGAC 216
QY 21 PheHisLysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLys 40
Db 217 TTCCACAGAAGATGTGCTGTTTGTGTGACAGAGGCTGCCAGCGGGGCGACTACTGGAAG 276
QY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
Db 277 GCCCCTTGACAGGAGCCCTGCGGCAACTCCACTGCTGTGTGTGTCCCAAGACACCTTC 336
QY 61 LeuAlaTrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80
Db 337 TTGGCCTGGAGAACCAACATATTCTGAATGTGCCCGCTGCCAGGCGCTGTGATGAGCAG 396
QY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
Db 397 GCCTCCAGGTGGCGCTGGAGAACTGTTCAGCAGTGGCCGACACCCCGCTGTGCTGAAG 456
QY 101 ProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerSerProPheTyrCys 120
Db 457 CCAGGCTGGTGTGGAGTGGCAGGTCAAGCAATGTGTCAAGCAGTTACCCCTTCTACTGC 516
QY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg 140
Db 517 CAACCATGCTTAGACTGCGGGGCGCTGCACCGCCACACAGGCTACTCTGTCCCGCAGA 576
QY 141 AspThrAspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSer 160
Db 577 GATACTGACTGTGGGACCTGCTGCTCTATGAACATGGCGATGGCTGCGTGC 636
QY 161 CysProThrSerThrLeuGlySerCysProGluArgCysAlaValCysGlyTyrParg 180
Db 637 TGCCCCACAGACACCCCTGGGAGGCTGTCCAGAGCGGTGTGCCGCTGTGGCTGAGG 696
QY 181 GlnMetPheTrpValGln 186
Db 697 CAGATGTCTGGGTCCAG 714

RESULT 9
AR119656

LOCUS AR119656 1783 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 1 from patent US 6153402.
ACCESSION AR119656
VERSION AR119656.1 GI:14102355
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE
AUTHORS

Unclassified.
1 (bases 1 to 1783)
Yu,G.-L., Ni,J., Gentz,R.L. and Dillon,P.J.

TITLE Death domain containing receptors
JOURNAL Patent: US 6153402-A 1 28-NOV-2000;
FEATURES Location/Qualifiers
source 1.1783
BASE COUNT 330 a 562 c 564 g 327 t
ORIGIN

Alignment Scores:
Pred. No.: 2.95e-68 Length: 1783
Score: 1101.00 Matches: 186
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-993-234-6_COPY_19_204 (1-186) x AR119656 (1-1783)

QY 1 LeuLeuGlyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
Db 285 CTGCTGGGGGGCCCCGAGGCGGCGACTCGTAGCCCCAGGTGTGACTGTGCCGGTGAC 344
QY 21 PheHisLysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLys 40
Db 345 TTCACAGAAGATTGGTCTGTTTGTGTGACAGAGCTGCCAGCGGGGCGACTACTGAAG 404
QY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
Db 405 GCCCCTTGACAGGAGCCCTGCGGCACTCCACCTGCTGTGTGCCCAAGACCTTC 464
QY 61 LeuAlaTrpGluAsnHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80
Db 465 TTGGCCTGGAGAACCACTAATTTGATGTGCCCGCTGCCAGCGCTGTGATGACAG 524
QY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
Db 525 GCCTCCAGGTGGCGCTGGAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGCTTAAG 584
QY 101 ProGlyTyrPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCys 120
Db 585 CCAGGCTGGTTGTGGAGTGCAGGTCAAGCAATGTGTACAGCAAGTTCAACCTTTACTGTC 644
QY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg 140
Db 645 CAACCATGCTAGACTGGGGGGCCCTGCACCGCCACACAGGGCTACTCTGTCCGACAGA 704
QY 141 AspThrAspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSer 160
Db 705 GATACTGACTGTGGAGCTGCTGCTGCTGTATGAACATGGCGATGGCTGCTGCC 764
QY 161 CysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTyrParg 180
Db 765 TGCCCCACGAGCACCTGGGGAAGTGTCCAGAGCGCTGTGCCGCTGTGTGGCTGAGG 824
QY 181 GlnMetPheTyrValGln 186
Db 825 CAGATGTTCTGGGTCCAG 842

RESULT 10
HSU83597 1528 bp mRNA linear PRI 27-JAN-1997
LOCUS HSU83597 Human death domain receptor 3 (DDR3) mRNA, partial cds.
ACCESSION U83597
VERSION U83597.1 GI:1800292
KEYWORDS

SOURCE
ORGANISM

Homo sapiens.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1528)
AUTHORS Chaudhary, P.M. and Hood, L.E.
TITLE Direct Submission
JOURNAL Submitted (03-JAN-1997) Molecular Biotechnology, University of

Washington, 1705 NE Pacific Street, HSB-K360, Seattle, WA 98195,
USA

FEATURES
source Location/Qualifiers
1.1528
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/map="1p36"
1.1528
/gene="DDR3"
<1.1238
/gene="DDR3"
/function="mediates apoptosis when cross-linked"
/note="A TNFR1-related death-domain containing receptor;
DR3, WSL-LR, Apo-3, TRAMP; transmembrane form; similar to
human EST clone 298913, Genbank Accession Number N71143"
/codon_start=3
/product="death domain receptor 3"
/protein_id="AAB41432.1"
/db_xref="GI:1800293"
/translation="GCAAVAAALLVLGARAQGGTRSPRCDCAGDFHKKIGLFCCRG
CPAGHYLKAPCTEPCGNSTCLVCPDFTFLAMENHNHNSCARCQACBOASQVALENC
AVADTRCGCKPGEVFEQVSSQVSSPFYQPCLDGALHRTILCSRDPTDGTCL
LGFYEHDGCVSCPSTLIGSCPERCAVCGWRQMFVQVLLAGLVPLLLGATLTFTY
RHCWPHKPLVTADAGMEALTPPATHTSPDLSAHTLAPDSSSEKICTVQLVNSWT
PGYPTQEALCPQVWTSMDQLPSRALGPAAAPTLSPSPAGSPAMQLPGPOLYDMD
AVPARRWKEVFTLGLREAIEAVEVEIGRFRDQYEMLKRWROQDPAGLAVYAALE
RMGLDGCVEDLRSLRQRP"

gene
CDS
BASE COUNT 280 a 496 c 470 g 282 t
ORIGIN

Alignment Scores:
Pred. No.: 1.26e-67 Length: 1528
Score: 1091.00 Matches: 185
Percent Similarity: 99.46% Conservative: 0
Best Local Similarity: 99.46% Mismatches: 1
Query Match: 99.09% Indels: 0
DB: 9 Gaps: 0

US-09-993-234-6_COPY_19_204 (1-186) x HSU83597 (1-1528)

QY 1 LeuLeuGlyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
Db 39 CTGCTGGGGGGCCCCGAGGCGGCGACTCGTAGCCCCAGGTGTGACTGTGCCGGTGAC 98
QY 21 PheHisLysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLys 40
Db 99 TTCACAGAAGATTGGTCTGTTTGTGTGACAGAGCTGCCAGCGGGGCGACTACTGAAG 158
QY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
Db 159 GCCCCTTGACAGGAGCCCTGCGGCACTCCACCTGCTGTGTGCCCAAGACACTTC 218
QY 61 LeuAlaTrpGluAsnHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80
Db 219 TTGGCCTGGAGAACCACTAATTTGATGTGCCCGCTGCCAGCGCTGTGATGACAG 278
QY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
Db 279 GCCTCCAGGTGGCGCTGGAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGCTTAAG 338
QY 101 ProGlyTyrPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCys 120
Db 339 CCAGGCTGGTTGTGGAGTGCAGGTCAAGCAATGTGTACAGCAAGTTCAACCTTTACTGTC 398
QY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg 140
Db 399 CAACCATGCTAGACTGGGGGGCCCTGCACCGCCACACAGGGCTACTCTGTCCGACAGA 458
QY 141 AspThrAspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSer 160
Db 459 GATACTGACTGTGGAGCTGCTGCTGCTGTATGAACATGGCGATGGCTGCTGCC 518


```

OY 161 CysProthrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTyrParg 180
Db 519 TGCCCCACGAGACCCCTGGGAGCTGTCCAGACGCGCTGTGCGCTGTGCTGAGG 578
OY 181 GlnMetPheTyrValGln 186
Db 579 CAGATGTTCTGGGTCACG 596
RESULT 11
HSU75380
LOCUS HSU75380 1557 bp mRNA linear PRI 05-APR-1997
DEFINITION Human apoptosis-mediating receptor TRAMP mRNA, partial cds.
ACCESSION U75380
VERSION U75380.1 GI:1695924
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE 1 (bases 1 to 1557)
AUTHORS Bodmer, J.L., Burns, K., Schneider, P., Hofmann, K., Steiner, V.,
Thome, M., Bornand, T., Hahne, M., Schroter, M., Becker, K., Wilson, A.,
French, L.E., Browning, J.L., Macdonald, R. and Tschoopp, J.
TITLE TRAMP, a novel apoptosis-mediating receptor with sequence homology
JOURNAL to tumor necrosis factor receptor 1 and Fas(Apo-1/CD95)
MEDLINE Immunity 6 (1), 79-88 (1997)
PUBMED 97205335
REFERENCE 9052839
AUTHORS 2 (bases 1 to 1557)
Bodmer, J.L., Burns, K., Schneider, P., Hofmann, K., Steiner, V.,
Thome, M., Bornand, T., Hahne, M., Schroter, M., Wilson, A.,
French, L.E., Browning, J.L., Macdonald, R. and Tschoopp, J.
TITLE Direct Submission
JOURNAL Submitted (18-OCT-1996) Institute of Biochemistry, University of
Lausanne, 155 Chemin des Boveresses, Epalinges, CH 1066,
Switzerland
FEATURES
source location/Qualifiers
1..1557
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/map="1p36.2"
/tissue-type="fetal lung"
<1..1245
/function="activates NF-kB"
/function="mediates apoptosis"
/note="contains a death domain; similar to TNF receptor"
/codon_start=1
/product="apoptosis-mediating receptor TRAMP"
/protein_id="AAC51192.1"
/db_xref="GI:1695925"
/translation="AAAGCAVAALLLVLGARAGGSTRSPRCDCAGDFHKKIGLFC
CRGCPAGHYLKAPCTEPCGNTSLVCPDFTFLAENHNHNSCARQACDEQASQVALE
NCSAVADTRCGCKPGWFEQVQSQSSSPFCQPCLDGALHRTLLCSRDIDCG
TCLIGFEYEHGDGCVSPTSLGSCPERCAACGWRQMFVQVLLAGLVPLDGLATIT
YTRHCWPHKPLVTADDEAGMALTPPPATHSPLDSAHTLIAPPDSSEKICTVQLVGN
SWTGYPETQALCPQVTSWMDQLPSRAIGPAAPTLSPSPAGSPAMMLQPGPOLYD
VMDAVPARMKFEFVTLGLREAIEAVEVEIGRFDDQYEMLRMRQOPAGLGAVYA
ALERMGLDGCYEDLRSLRQGP"
BASE COUNT 286 a 508 c 477 g 286 t
ORIGIN

Alignment Scores:
Score: 1.29e-67 Length: 1557
Pred. No.: 1091.00 Matches: 185
Percent Similarity: 99.46% Conservative: 0
Best Local Similarity: 99.46% Mismatches: 1
Query Match: 99.09% Indels: 0
DB: 9 Gaps: 0

US-09-993-234-6_COPY_19_204 (1-186) x HSU75380 (1-1557)
OY 1 LeuLeuGlyAlaArgAlaGlnGlyThrArgSerProArgCysAspCysAlaGlyasp 20
CDS
FEATURES
source location/Qualifiers
1..1355
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Hela"
/cell_type="lymphocyte"
1..762
/function="mediates apoptosis"

```


DEFINITION H.sapiens mRNA for WSL-LR, WSL-S1 and WSL-S2 proteins.
ACCESSION Y09392
VERSION Y09392.1 GI:1669690
KEYWORDS wsl-1 gene; WSL-IR protein; WSL-S1 protein; WSL-S2 protein.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 1743)
AUTHORS Kitson, J., Raven, T., Jiang, Y.P., Goeddel, D.V., Giles, K.M., Pun, K.T., Grinham, C.J., Brown, R. and Farrow, S.N.
TITLE A death-domain-containing receptor that mediates apoptosis
JOURNAL Nature 384 (6607), 372-375 (1996)
MEDLINE 97088617
PUBMED 8934525
REFERENCE 2 (bases 1 to 1743)
AUTHORS Kitson, J.
TITLE Direct Submission
JOURNAL Submitted (12-NOV-1996) J. Kitson, GLAXO-Wellcome, Medicines Research Centre, Gunnels Wood Road, Stevenage, SG1 2NY, UK
FEATURES
source 1.1743
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_type="T-lymphocyte"
/tissue_type="lymphoid"
1.1742
/gene="wsl-1"
1.610
/gene="wsl-1"
/number=1
join(69..666,768..1423)
/gene="wsl-1"
/codon_start=1
/product="WSL-IR protein"
/protein_id="CAA70561.1"
/db_xref="GI:1669693"
/db_xref="SWISS-PROT:Q93038"
/translation="MEQPRGCAVAALLLVLLGARAOGGTRSPRCDCAGDFHKKIG
LFCCRGCPAGHYLKAPCTEPCGNSCTLCVPQDTFLAMENHNSECARCOACDEQASQV
ALENCASAVADTRCGCKPGWFEVCQVSCVSSSPFYCQPCIDCGALHRTLLCSRRDT
TLTYTRHCWPHKPLVTADAGMEALTPPATHLSPIDSAHTLAPDSSEKICTVOL
VGNSTWPGYPTETQALCPQVETWSMDQLPSRALGPAPRTLSPEPAGSPAMMLQPGPO
LYDMDAVPARWKEFEVRLTGLREAEIEAVEVEIGLFRDQYEMLKHWROQQPAGLGA
VYALERMGLDGCVEDLRSRLQRP"
join(69..610,768..882)
/gene="wsl-1"
/codon_start=1
/product="WSL-S1 protein"
/protein_id="CAA70560.1"
/db_xref="GI:1669692"
/db_xref="SWISS-PROT:Q93038"
/translation="MEQPRGCAVAALLLVLLGARAOGGTRSPRCDCAGDFHKKIG
LFCCRGCPAGHYLKAPCTEPCGNSCTLCVPQDTFLAMENHNSECARCOACDEQASQV
ALENCASAVADTRCGCKPGWFEVCQVSCVSSSPFYCQPCIDCGALHRTLLCSRRDT
DCGTCLPGFYEHGDGCVSCPTVLGPGAPGWPCGPPAWGHPDLHIPPLASQAPGYCR
"
69..830
/gene="wsl-1"
/codon_start=1
/product="WSL-S2 protein"
/protein_id="CAA70559.1"
/db_xref="GI:1669691"
/db_xref="SWISS-PROT:Q93038"
/translation="MEQPRGCAVAALLLVLLGARAOGGTRSPRCDCAGDFHKKIG
LFCCRGCPAGHYLKAPCTEPCGNSCTLCVPQDTFLAMENHNSECARCOACDEQASQV
ALENCASAVADTRCGCKPGWFEVCQVSCVSSSPFYCQPCIDCGALHRTLLCSRRDT
GEEGHNPTPTSCFCSCSRSRCSWLALWSPCLGPP"
611..666
/gene="wsl-1"
/number=2
exon

exon 667..767
/gene="wsl-1"
/number=3
768..1742
/gene="wsl-1"
/number=4
BASE COUNT 347 a 543 c 549 g 304 t
ORIGIN
Alignment Scores:
Pred. No.: 1.37e-66
Score: 1077.00
Percent Similarity: 98.91%
Best Local Similarity: 98.91%
Query Match: 97.82%
DB: 9
Gaps: 0
US-09-993-234-6_COPY_19_204 (1-186) x HSWSL1 (1-1743)
QY 1 LeuLeuGIyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
Db 123 CTGCTGGGGGGCCCGGGCCAGGGGGCCACTCTGAGCCCGAGGTGTGACTGTGCCGGTGAC 182
QY 21 PheHisLysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLys 40
Db 183 TTCCACAAGAAGATGTGCTGTTTGTGTGACAGAGGCTGCCACGGGGCCTACTGAAG 242
QY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
Db 243 GCCCCTTGACAGGAGCCCTGCGGCACTCCACTGCTGTGTGTCCCAAGACACCTTC 302
QY 61 LeuAlaTrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80
Db 303 TTGGCTGGGAGAACACCATATTTGTAATGTGCCCGCTGCCAGGCTGTGATGAGCAG 362
QY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
Db 363 GCCCTCCAGGTGGCGCTGGAGACTGTTCAAGCAGTGGCCGACACCCGCTGTGCTGTAA 422
QY 101 ProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCys 120
Db 423 CCAGCGCTGTTGTGTGAGTGCAGGTCAGCCCAATGTGTACAGCAGTTACACCTTACTGC 482
QY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg 140
Db 483 CAACCATGCTAGACTGCGGGGCCCTGCACCCGACACACAGGCTACTGTTCCCGCAGA 542
QY 141 AspThrAspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSer 160
Db 543 GATACGTACTGTGGAGACCTGCTGCTGCTTATGAAACATGGCATGGCTGCTGTGCC 602
QY 161 CysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTyrParg 180
Db 603 TGCCCCAGCAGACACCTGGGAGCTGTCCAGAGCGCTGTGCCGCTGTGTGGCTGAGAG 662
QY 181 GlnMetPheTyr 184
Db 663 CAGAGTAGGTGG 674
RESULT 15
HSU94510
LOCUS HSU94510
DEFINITION Human lymphocyte associated receptor of death 9 mRNA, alternatively spliced, complete cds.
ACCESSION U94510.1 GI:2071966
VERSION U94510.1
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 1143)
AUTHORS Screaton, G.R., Xu, X.N., Olsen, A.L., Cowper, A.E., Tan, R.,

TITLE MCMichael,A.J. and Bell,J.I.
LARD: a new lymphoid-specific death domain containing receptor
regulated by alternative pre-mRNA splicing
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)
MEDLINE 97272273
PUBMED 9114039
REFERENCE 2 (bases 1 to 1143)
AUTHORS Screation,G.R.
TITLE Direct Submission
JOURNAL Submitted (19-MAR-1997) Molecular Immunology Group, Institute of
Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3
9DU, UK

FEATURES
source location/Qualifiers
1..1143 /organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Hela"
/cell_type="lymphocyte"
1..1143
/function="mediates apoptosis"
/note="LARD-9; NGFR family member; similar to Fas and
TNF-R1"
/codon_start=1
/product="lymphocyte associated receptor of death 9"
/protein_id="AAC51315.1"
/db_xref="GI:2071967"
/translation="MEQRPKGCAVAALLLVLGARAOGGTRSPRCDCAGDFHKKIG
LFCCRGCPCAGHYLKAPCTEPCGNSTCLVCPQDTFLAMENHNSECARQCDEQASQV
ALENCASAVADTRCGCKPGWFVECOVSQCVSSPFYCPQLDCGALHRTRLCSRDT
DCGTCLPGEYHGDGCVSTSTLGSCEPCAAVCGWRQNEAGMEALTPPATHTLSPL
DSAHTLAPDSSEKICTVOLGNSWTPGYPTQELCPQVTSMDLPSPALGPAA
PTLSPESPAGSPAMMLQPGPOLYDMADAVPARMKFEVRTLGLREAETEAIVEIGRE
RDOQYEMLKRMWQQQPAIGAVYAALERMGLDCVEDLRSRLQRP"
598..599
/note="deletion compared to LARD 1a, deposited in GenBank
Accession Number U94501, probable skipping of putative
exon 7 encoding the transmembrane domain"

CDS
BASE COUNT 188 a 378 c 378 g 199 t
ORIGIN
misc_feature
598..599
/note="deletion compared to LARD 1a, deposited in GenBank
Accession Number U94501, probable skipping of putative
exon 7 encoding the transmembrane domain"

Alignment Scores:
Pred. No.: 2.76e-66 Length: 1143
Score: 1070.00 Matches: 181
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 97.18% Indels: 0
DB: 9 Gaps: 0

us-09-993-234-6_copy_19_204 (1-186) x HSU94510 (1-1143)

QY 1 LeuLeuGlyAlaArgAlaGlnGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
Db 55 CTGCTGGGGGGCCCGGGCCAGGGCGCACTCGTAGCCCAAGGTGTGACTGTGCCGGTGAC 114
QY 21 PheHisLysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlnHisTyrLeuLys 40
Db 115 TTCCACAAGAAGATTGGTCTGTTTGTTCAGAGAGCTGCCAGCGGGCACTACCTGAAG 174
QY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
Db 175 GCCCTTGCAAGGAGCCCTGGCGCACTCACTGCTGTGTGTCCCAAGACACCTTC 234
QY 61 LeuAlaTyrGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80
Db 235 TTGGCTGGGAGAACACCATTAATTCGAATGTGCCCGCTGCCAGCCTGTGATGAGCAG 294
QY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
Db 295 GCCTCCAGAGTGGCGCTGAGAACTGTTCAGACAGTGGCCGACACCGCTGTGCTGAAG 354
QY 101 ProGlyTyrPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCys 120
Db 355 CCAGGCTGTGTGTGAGTGCACAGGACCAATGTGTACAGAGTTCAACCTTCTACTGC 414

QY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg 140
Db 415 CAACCATGCTTAGACTGCGGGGCGCTGCACCGCCACACACAGGCTACTGTGTCCCGCAGA 474
QY 141 AspThrAspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSer 160
Db 475 GATACTGACTGTGGAGACCTGCGCTGCTTCTATGAACATGGCGATGGCTGCTGCC 534
QY 161 CysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTyrParg 180
Db 535 TGCCCCACGACACACCTGGGGAGCTGTCCAGAGCGCTGTGCCGCTGTGTGGCTGAGAG 594
QY 181 Gln 181
Db 595 CAG 597

Search completed: April 6, 2003, 21:08:09
Job time : 2168.6 secs

THIS PAGE BLANK (USPTO)



140

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: Apr11 6, 2003, 15:33:09 ; Search time 173.187 Seconds
(without alignments)
2418.610 Million cell updates/sec

Title: US-09-993-234-6_COPY_19_204
Perfect score: 1101
Sequence: 1 LIGARAGCGTRSPRCDCAGD.....GSCPERCAVCGMRQMFVQ 186

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+p2n.model -DEV=xlh
-O=/cgn2_1/USPTO.spool/US09993234/runat_27032003_115454_15312/app_query.fasta_1.2346
-DB=N_geneseq_101002 -QWTF=fastap -SUFFIX=tnq -MINMATCH=0.1 -LOOPEL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS-human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09993234_@CGN_1_1_660_@runat_27032003_115454_15312 -NCPU=6 -ICPU=3
-NO_XLPUXY -NO_MMAP -LARGQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_101002:*
1: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
8: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
9: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
11: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1101	100.0	1254	18	AAT89427	Death domain conta
2	1101	100.0	1254	20	AAK00925	Death domain conta
3	1101	100.0	1254	21	AAC68777	Human death domain
4	1101	100.0	1634	18	AAT91180	Human apoptosis pr
5	1101	100.0	1634	22	AAH27782	Human genomic DNA
6	1101	100.0	1634	24	AAI47186	Human rheumatoid a
7	1101	100.0	1662	22	AAC91477	Human PRO779 CDNA.
8	1101	100.0	1662	24	ABK40265	CDNA encoding huma
9	1101	100.0	1783	18	AAT89426	Death domain conta
10	1101	100.0	1783	20	AAK00924	Death domain conta
11	1101	100.0	1783	21	AAC68776	Human death domain
12	1101	100.0	1847	19	AAV28700	Human apoptosis in
13	1077	97.8	1743	24	ABL64119	Breast cancer rela
14	1041	94.6	1250	22	AAF83770	Nucleotide sequenc
15	979	88.9	816	24	ABL67258	Thyroid cancer rel
16	979	88.9	1438	18	AAT91179	Human apoptosis pr
17	964	87.6	787	24	AAI47187	Human rheumatoid a
18	767	69.7	4825	24	AAI47185	Human DR3 gene ass
19	767	69.7	10797	23	ABK42690	Genomic sequence #
20	615	55.9	1251	19	AAV28701	Mouse apoptosis in
21	216	19.6	2130	24	ABK63694	Rat sequence diffe
22	212.5	19.3	1049	18	AAT94007	CDNA for TBP(20-16
23	212	19.3	5870	21	AAAI5044	Nucleotide sequenc
24	205.5	18.7	1301	18	AAT94022	CDNA for TBP(20-19
25	203.5	18.5	1202	18	AAT94008	CDNA for TBP(20-16
26	203	18.4	608	13	AAQ24441	Encodes truncated
27	203	18.4	1334	11	AAQ06282	Plasmid Tumour Nec
28	203	18.4	1368	14	AAQ49932	lambda-derived TNF
29	203	18.4	1368	14	AAQ5105	Human TNFR1 coding
30	203	18.4	2062	13	AAQ24440	TNF-alpha binding
31	203	18.4	2062	13	AAQ10883	Encodes TNF-alpha
32	203	18.4	2088	12	AAQ10883	30kd TNF inhibitor
33	203	18.4	2088	22	AAC83946	Human 30 kDa TNF 1
34	203	18.4	2111	12	AAQ10955	Encodes human 55kd
35	203	18.4	2111	20	AAZ09170	Human tumour necro
36	203	18.4	2111	22	AAH48859	Human TNFBP-associ
37	203	18.4	2111	24	ABK84039	Human CDNA differe
38	203	18.4	2111	24	ABN95862	Gene #2360 used to
39	203	18.4	2141	11	AAQ06285	Human Tumour Necro
40	203	18.4	2161	21	AAZ48475	Human tumour necro
41	203	18.4	2161	24	ABK13194	Human tumour necro
42	203	18.4	2175	16	AAQ0513	p55 TNF-R gene. H
43	203	18.4	6889	17	AAT15931	DHFR/Inttron (WTas
44	203	18.4	6926	18	AAV04431	Vector pCDNA3-IgG1
45	202	18.3	2170	14	AAQ50870	p55 Tumour necrosi

ALIGNMENTS

RESULT 1
AAT89427
ID AAT89427 standard; CDNA; 1254 BP.
XX
AC AAT89427;
XX
DT 02-MAR-1998 (first entry)
XX
DE Death domain containing receptor DR3 CDNA.
XX
KW Death domain containing receptor; DR3; human; apoptosis;
KM Inflammation; NF-kappaB; ds.
XX
OS Homo sapiens.
XX
FH Key
FT sig_peptide 1..72
FT /*tag= a

FT mat_peptide 73..1251
FT /*tag= b
XX PN W09733904-A1.
XX 18-SEP-1997.
XX PD
XX PF 17-OCT-1996; 96WO-US16849.
XX PR 12-MAR-1996; 96US-0013285.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PA (UNMI) UNIV MICHIGAN.
XX PI Dillon PJ, Dixit VM, Gentz RL, Ni J, Yu G;
XX WPI; 1997-470812/43.
XX DR P-PSDB; AAW31517.

PT Death domain containing receptor polypeptide(s) DR3 and DR3-V1
PT for activation of apoptosis and NF-kappaB, antagonists can be used
PT to treat inflammatory diseases

PS Claim 6; Page 75-77; 108pp; English.

XX This cDNA clone codes for human death domain containing receptor
CC DR3 (see AAW31517), a novel member of the tumour necrosis factor
CC receptor family. It was isolated from a HUVEC cDNA library.
CC Related death domain containing receptor DR3-V1 cDNA (see AAT89426)
CC was isolated from a human testis tumour cDNA library. The genes
CC have also been identified in cDNA libraries of foetal liver,
CC foetal brain, tonsil and leukocyte. Nucleic acids encoding full-
CC length or mature DR3, or the extracellular, transmembrane,
CC intracellular or especially the death domain of DR3, can be used to
CC produce recombinant polypeptides in transformed host cells. These
CC polypeptides can be used to treat diseases and disorders associated
CC with the inhibition of apoptosis. Antagonists can be used to treat
CC diseases and disorders associated with increased apoptosis and for
CC treating inflammatory diseases and disorders.

XX SQ Sequence 1254 BP; 201 A; 420 C; 407 G; 226 T; 0 other;

Alignment Scores:
Pred. No.: 7.95e-75 Length: 1254
Score: 1101.00 Matches: 186
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-09-993-234-6_copy_19_204 (1-186) x AAT89427 (1-1254)

QY 1 LeuLeuGlyAlaArgAlaGlnGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
Db 55 CTGCTGGGGGCGCGGCCAGGGGGGCGGCACTCGTAGCCCCAGGTGTGACTGTGCCGGTGAC 114
QY 21 PheHisLysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLys 40
Db 115 TTCCACAAGAAGATTGCTGTTTGTTCAGAGCGTGCAGGGGGGCACTACTGTAAG 174
QY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
Db 175 GCCCCTTGACAGGAGCCCTGCCCACTCCACCTGCTGTGTGTCCCAAGACACCTTC 234
QY 61 LeuAlaTrpGluAsnHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80
Db 235 TTGGCCTGGAGAACCACTAATTTGATGTGCCCGCTGCCAGGCTGTGATGACAG 294
QY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
Db 295 GCCTCCAGGTGGCGGTGAGAACTGTTACAGACAGTGGCGACACACCCGCTGTGCTTAAG 354
QY 101 ProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCys 120

Db 355 CCAGGCTGTTGTGGAGTGCAGAGTCAATGTGTACAGAGTTCACCTTCTACTGC 414
QY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArg 140
Db 415 CAACCATGCTAGACTGCGGGGCCCTGCACGCCACACAGCGCTACTGTCTCCGCAGA 474
QY 141 AspThrAspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSer 160
Db 475 GATACCTAGCTGGGAGCTGCCTGCTGTATGACATGCGCATGCGTGCCTGCC 534
QY 161 CysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTyrParg 180
Db 535 TGCCCCACAGCACCCCTGGGAGCTGTCCAGAGCGTGTGCCGCTGTGTGCTGAGG 594
QY 181 GlnMetPheTrpValGln 186
Db 595 CAGATGTTCTGGGTCACAG 612

RESULT 2

AAAX00925
ID AAX00925 standard; cDNA; 1254 BP.

AC AAX00925;

DT 25-MAR-1999 (first entry)

DE Death domain containing receptor polypeptide (DR3) encoding cDNA.

KW Death domain; receptor; DR3-V1; DR3; recombinant; ds.

XX Homo sapiens.

XX FH Key Location/Qualifiers
XX FT CDS 1..1254
XX FT /*tag= a
XX FT /product= "Death domain containing receptor DR3"
XX FT sig_peptide 1..72
XX FT /*tag= b
XX FT mat_peptide 73..1251
XX FT /*tag= c

PN JP11000170-A.

PD 06-JAN-1999.

PF 12-MAR-1997; 97JP-0057503.

PR 06-FEB-1997; 97US-0037341.

PR 12-MAR-1996; 96US-0013285.

XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PA (UNMI) UNIV MICHIGAN.

XX DR WPI; 1999-124390/11.
XX DR P-PSDB; AAW95538.

PT New death domain containing receptor and recombinant vector -
PT optionally comprising leader sequence
PS Claim 6; Fig 3; 50pp; Japanese.

XX The invention provides nucleotide sequences encoding death domain
CC containing receptor polypeptides DR3-V1 and DR3. The DR3-V1 cDNA clone
CC is contained in ATCC deposition No. 97456 and the DR3 cDNA clone is
CC contained in ATCC deposition No. 97757. Recombinant vectors comprising
CC the nucleic acid sequences and optionally the leader sequences are
CC used for the recombinant production of the proteins. The present
CC sequence represents a cDNA encoding the death domain containing
XX receptor polypeptide (DR3).

SQ Sequence 1254 BP; 201 A; 420 C; 407 G; 226 T; 0 other;

Alignment Scores:

Pred. No.: 7.95e-75 Length: 1254
Score: 1101.00 Matches: 186
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 20 Gaps: 0

US-09-993-234-6_COPY_19_204 (1-186) x AAX00925 (1-1254)

OY 1 LeuLeuGLyAlaArgAlaInglnglyGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
Db 55 CTGCTGGGGGGCCCCGGCCAGGGGGGCGACATCGTAGCCCAAGGTGTGACTGTGCCGGTGAC 114
OY 21 PheHisLysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLys 40
Db 115 TTCCACAAGAAGATTGGTCTGTTTGTTCAGAGAGGCTGCCAGCGGGGCACTACTGTGAAG 174
OY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
Db 175 GCCCTTGACAGGAGCCCTGGCGCAACTCCACCTGCTGTGTCCCAAGACACTTC 234
OY 61 LeuAlaTrpGluAsnHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80
Db 235 TTGGCCTGGGAGAACCACTAATTTCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAG 294
OY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
Db 295 GCCTCCAGGTGGCGGTGAGAACTGTTCAGACAGTGGCCGACACCCGCTGTGGCTGAAG 354
OY 101 ProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCys 120
Db 355 CCAGGCTGTTGTGGAGTGCAGGTCAGCCAAATGTGTCAAGCATTCACCCCTTCTACTGC 414
OY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg 140
Db 415 CAACCATGCCCTAGACTGGGGGGCCCTGCACCGCCACACAGGGCTACTCTGTGCCGAGA 474
OY 141 AspThrAspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSer 160
Db 475 GATACTGACTGTGGGACCTGCCTGCCTGCTTATGAACATGGCGATGGCTGCCTGCC 534
OY 161 CysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTrpArg 180
Db 535 TGCCCCACGAGCACCTGGGAGCTGTCCAGAGCGCTGTGCCGTGTGTGGGTGAGG 594
OY 181 GlnMetPheTrpValGln 186
Db 595 CAGATGTTCTGGGTCCAG 612

RESULT 3

AAC68777
ID AAC68777 standard; cDNA; 1254 BP.
XX
AC AAC68777;
XX
DT 20-FEB-2001 (first entry)
XX
DE Human death domain containing receptor DR3 coding sequence.
XX
KW Human; death domain containing receptor; DR3; cancer;
KW autoimmune disorder; inflammation; cardiovascular disorder; infection;
KW neurodegenerative disease; angiogenesis; ss.
XX
OS Homo sapiens.
XX
PN WO200064465-A1.
XX
XX 02-NOV-2000.
PD
XX
PF 21-APR-2000; 2000WO-US10741.
XX

PR 22-APR-1999; 99US-0130488.
PR 28-MAY-1999; 99US-0136741.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (UNMI) UNIV MICHIGAN.
PA (YUGG/) YU G.
PA (NIJ/) NI J.
PA (GENT/) GENTZ R L.
PA (DILL/) DILLON P J.
PA (DIXI/) DIXIT V M.
XX

PI Yu G, Ni J, Gentz RL, Dillon PJ, Dixit VM;
XX
XX WPI; 2000-687263/67.
DR P-PSDB; AAB36265.
DR

PT Treating graft-versus-host disease, cancer, immunodeficiency or an
PT autoimmune disease comprising administering an antibody to Death Domain
PT Containing Receptor proteins and a second therapeutic agent -
XX
PS Example 2B; Fig 2; 273pp; English.
XX

CC The present invention provides the protein and coding sequences for two
CC death domain containing receptors, designated DR3 and DR3-V1. These
CC receptors are involved in apoptosis, and the sequences given can be used
CC in the treatment of cancers, infections, cardiovascular disorders such as
CC arrhythmias, ischaemia, aneurysms, arterial occlusive diseases, embolisms
CC and congenital heart defects, neurodegenerative diseases including
CC Alzheimer's and Parkinson's diseases, autoimmune disease such as multiple
CC sclerosis, arthritis, diabetes, Graves' disease, asthma and psoriasis,
CC and to promote angiogenesis and wound healing.
XX

SQ Sequence 1254 BP; 201 A; 420 C; 407 G; 226 T; 0 other;

Alignment Scores:

Pred. No.: 7.95e-75 Length: 1254
Score: 1101.00 Matches: 186
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-09-993-234-6_COPY_19_204 (1-186) x AAC68777 (1-1254)

OY 1 LeuLeuGLyAlaArgAlaInglnglyGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
Db 55 CTGCTGGGGGGCCCCGGCCAGGGGGGCGACATCGTAGCCCAAGGTGTGACTGTGCCGGTGAC 114
OY 21 PheHisLysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLys 40
Db 115 TTCCACAAGAAGATTGGTCTGTTTGTTCAGAGAGGCTGCCAGCGGGGCACTACTGTGAAG 174
OY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
Db 175 GCCCTTGACAGGAGCCCTGGCGCAACTCCACCTGCTGTGTCCCAAGACACTTC 234
OY 61 LeuAlaTrpGluAsnHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80
Db 235 TTGGCCTGGGAGAACCACTAATTTCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAG 294
OY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
Db 295 GCCTCCAGGTGGCGGTGAGAACTGTTCAGACAGTGGCCGACACCCGCTGTGGCTGAAG 354
OY 101 ProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCys 120
Db 355 CCAGGCTGTTGTGGAGTGCAGGTCAGCCAAATGTGTCAAGCATTCACCCCTTCTACTGC 414
OY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg 140
Db 415 CAACCATGCCCTAGACTGGGGGGCCCTGCACCGCCACACAGGGCTACTCTGTGCCGAGA 474
OY 141 AspThrAspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSer 160

|||||
DB 475 GATACCTGACTGTGGGACCTGCTGCTGCTGCTATGACATGCGGCTGCGTGTCC 534
QY 161 CysProthSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTrpArg 180
DB 535 TGCCCCACGAGACCCCTGGGAGCTGTCCAGACGCGCTGTGCCGCTGTCTGTGGCTGAGG 594
QY 181 GlnMetPheTrpValGln 186
DB 595 CAGATGTCTCTGGGCTCCAG 612
RESULT 4
AAT91180
ID AAT91180 standard; cDNA; 1634 BP.
XX
AC AAT91180;
XX 14-APR-1998 (first entry)
DT
XX Human apoptosis protein Apo-3 cDNA clone FH20.57.
DE
XX Apo-3; apoptosis; human; therapy; drug screening; ss.
XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT CDS 89..1342
FT /*tag= a
FT sig_peptide 89..160
FT /*tag= b
FT /*note= "determined by hydropathy analysis"
FT mat_peptide 161..1339
FT /*tag= c
XX
PN WO9737020-A1.
XX
PD 09-OCT-1997.
XX
PF 31-MAR-1997; 97WO-US05230.
XX
PR 23-SEP-1996; 96US-0710802.
PR 01-APR-1996; 96US-0625328.
XX
PA (GETH) GENENTECH INC.
XX
XX Ashkenazi AJ;
PI
XX
DR WPI; 1997-503105/46.
XX
PT Polypeptide(s) Apo-3 and Apo-2LI - useful for regulating apoptosis
PT in mammalian cells
PS
PS Example 1; Page 45-46; 70pp; English.
XX
CC cDNA clone FH20.57 (ATCC 55820) codes for a novel polypeptide (see
CC W26709), designated Apo-3, that stimulates or induces apoptotic
CC activity in mammalian cells. It was isolated from a human foetal
CC heart cDNA library by screening with probes (see T91183-84) based
CC on an EST sequence (GenBank locus W71984) that showed homology to
CC the intracellular domain of human TNFRI and CD95. Amino acid
CC residues 1-181 of Apo-3 are identical to another novel apoptosis
CC polypeptide, Apo-2LI (see W26708). Nucleic acids encoding Apo-3
CC can be used diagnostically for tissue-specific typing and to
CC produce recombinant Apo-3 polypeptides, especially the
CC extracellular domain (amino acids 1-198) or death domain (amino
CC acids 338-417). Apo-3 can be used to induce apoptosis or
CC NF-kappa-N- or JNK-mediated gene expression for therapeutic
CC purposes. Non-human transgenic animals containing cells that
CC express Apo-3 nucleic acid, and knockout animals containing
CC cells that have an altered Apo-3 gene, can be used in drug
CC screening and development.
XX
SQ Sequence 1634 BP; 300 A; 528 C; 519 G; 287 T; 0 other;

Alignment Scores:
Pred. No.: 1.08e-74 Length: 1634
Score: 1101.00 Matches: 186
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0
US-09-993-234-6_copy_19_204 (1-186) x AAT91180 (1-1634)
QY 1 LeuLeuGlyAlaAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
DB 143 CTGCTGGGGGCCCGGGCCAGGGGCGCACCTCGTAGCCCCAGGCTGTGACCTGCGGTGAC 202
QY 21 PheHisLysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLys 40
DB 203 TTCCACAAGAAGATTGCTCTGTTTGTTCAGAGGCTGCCACGGGGCAGCTACCTGAAG 262
QY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
DB 263 GCCCTTGACAGGAGCCCTGGCGCAACTCCACCTGCTGTGTGCCAAGACACCTTC 322
QY 61 LeuAlaTrpGluAsnHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80
DB 323 TTGGCCTGGGAGAACCACTAATCTGATGTGCCCGCTGCCAGGCTGTGATGACAG 382
QY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
DB 383 GCCTCCAGGTGGCGCTGGAGAACTGTTCAAGCAGTGGCGGACACCCGCTGTGGCTGAAG 442
QY 101 ProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCys 120
DB 443 CCAGGCTGTTGTGTGGAGTCCAGGTCAGCCAAATGTGTACAGAGTTACCTACTGC 502
QY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg 140
DB 503 CAACCATGCTAGACTGGGGGGCCCTGCACCGCCACACACGGCTACTCTGTCCCGCAGA 562
QY 141 AspThrAspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSer 160
DB 563 GATACCTGACTGTGGGACCTGCTGCTGCTGTATGACATGGCGATGGCTGCTGCC 622
QY 161 CysProthSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTrpArg 180
DB 623 TGCCCCACGAGACCCCTGGGAGCTGTCCAGAGCGCTGTGCCGCTGTCTGTGGCTGAGG 682
QY 181 GlnMetPheTrpValGln 186
DB 683 CAGATGTCTCTGGGCTCCAG 700
RESULT 5
AAH27782
ID AAH27782 standard; DNA; 1634 BP.
XX
XX AAH27782;
AC
XX 15-AUG-2001 (first entry)
DT
XX
DE Human genomic DNA encoding a rheumatoid arthritis associated protein.
XX
XX Rheumatoid arthritis; transmembrane protein; human; ds.
OS
XX Homo sapiens.
FH
FH Key Location/Qualifiers
FT CDS 89..1342
FT /*tag= a
FT /*product= "Rheumatoid arthritis associated protein"
XX
PN WO200132921-A2.
XX
PD 10-MAY-2001.

XX 01-NOV-2000; 2000WO-JP07690.
PF
XX
PR 01-NOV-1999; 99JP-0310805.
XX
PA (SHIO/) SHIOZAWA S.
XX
PI Shiozawa S, Konishi Y;
XX
DR WPI: 2001-308750/32.
DR P-PSDB; AAB97370.
XX

PT Diagnosing rheumatoid arthritis by probing digested human genomic DNA
PT or comparing expression of mRNA or polypeptide of a region of
PT transmembrane protein -
XX

PS Claim 1; Page 14-18; 21pp; Japanese.

XX This invention relates to a method of diagnosing chronic rheumatoid
CC arthritis by digesting human genomic DNA with EcoRI and hybridizing it
CC with a probe containing a fragment of the present sequence which
CC represents DNA encoding a transmembrane protein. The method is used for
CC the diagnosis of chronic rheumatoid arthritis, and for developing new
CC treatments.
XX

SQ Sequence 1634 BP; 300 A; 528 C; 519 G; 287 T; 0 other;

Alignment Scores:

Pred. No.:	1.08e-74	Length:	1634
Score:	1101.00	Matches:	186
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	22	Gaps:	0

US-09-993-234-6_COPY_19_204 (1-186) x AAN27782 (1-1634)

QY 1 LeuLeuGlyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
Db 143 CTGCTGGGGGGCCCGGGCCAGGGGGGCACTGCTAGCCCCAGGTGTGACTGTGCCGGTGAC 202
QY 21 PheHisLysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLys 40
Db 203 TTCCACAGAAGAATGTGTGTGTGTCAGAGGCTGCCAGGGGGGCACTACTGAAG 262
QY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
Db 263 GCCCCTTGACAGGAGCCCTGCGCACTCCACCTGCTGTGTCTCCCAAGACACCTTC 322
QY 61 LeuAlaTrpGluAsnHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80
Db 323 TTGGCCTGGGAGAACCACTAATTCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAG 382
QY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
Db 383 GCCTCCAGGTGGCGCTGAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGGCTGAAG 442
QY 101 ProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCys 120
Db 443 CCAGCCTGTGTGTGAGTGCAGTCCAGTCAACATGTGTACAGTGTTCACCCCTTACTGTC 502
QY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg 140
Db 503 CAACCATGCTAGACTGCGGGGCTGCACCCGACACACAGGCTACTCTGTCCCGCAGA 562
QY 141 AspThrAspCysGlyThrCysLeuProGlyPheTyrGlnHisGlyAspGlyCysValSer 160
Db 563 GATACTGACTGTGGGACCTGCCCTGCTGTCTATGACATGGCGATGGCTGCTGCC 622
QY 161 CysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTyrArg 180
Db 623 TGCCCCACGAGCACCTGGGGAGCTGTCCAGAGCGCTGTGCCCTGTCTGTGGCTGAGG 682

QY 181 GlnMetPheTrpValGln 186
Db 683 CAGATGTCTGTGGTCCAG 700

RESULT 6

AAL47186

ID AAL47186 standard; cDNA; 1634 BP.

AC AAL47186;

DT 22-AUG-2002 (first entry)

DE Human rheumatoid arthritis associated DR3 gene related cDNA #1.

KW Human; DR3; rheumatoid arthritis; antirheumatic; antiarthritic;

XX gene therapy; gene; ss.

OS Homo sapiens.

XX Key location/Qualifiers

FT CDS 89..1342

FT /*tag= a

FT /product= "AAO17879"

XX WO200234912-A1.

XX PD 02-MAY-2002.

XX PF 24-OCT-2001; 2001WO-JP09313.

XX PR 24-OCT-2000; 2000JP-0324296.

XX PR 27-MAR-2001; 2001JP-0090546.

XX PR 30-MAR-2001; 2001JP-0099990.

XX PA (NEWI-) NEW IND RES ORG.

XX PA (SHIO/) SHIOZAWA S.

XX PI Shiozawa S, Konishi Y;

XX DR WPI: 2002-417132/44.

XX DR P-PSDB; AAO17879.

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

The present invention relates to the human DR3 gene, which is associated
CC with rheumatoid arthritis. Certain mutations in the gene can be linked to
CC the disease. The sequences can be used to evaluate disease onset and its
CC possibility and to provide therapy and remedies. The present sequence is
CC a coding sequence described in the exemplification of the invention.
XX
SQ Sequence 1634 BP; 300 A; 528 C; 519 G; 287 T; 0 other;

Alignment Scores:

Pred. No.:	1.08e-74	Length:	1634
Score:	1101.00	Matches:	186
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	24	Gaps:	0

US-09-993-234-6_COPY_19_204 (1-186) x AAL47186 (1-1634)

QY 1 LeuLeuGlyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
Db 143 CTGCTGGGGGGCCCGGGCCAGGGGGGCACTGCTAGCCCCAGGTGTGACTGTGCCGGTGAC 202
QY 21 PheHisLysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLys 40
Db 203 TTCCACAGAAGAATGTGTGTGTGTCAGAGGCTGCCAGGGGGGCACTACTGAAG 262

QY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
DB 263 GCCCCTTGACGAGACCCCTGCGGCACTCCACCTGCTGTGTGTCTCCCAAGACACCTTC 322
QY 61 LeuAlaTrpGluAsnHisHisAsnSerGlyCysAlaArgCysGlnAlaCysAspGluGln 80
DB 323 TTGGCCTGGGAGAACACCATTAATTCATGTGATGTGCCCGCTGCCAGGCTGTGATGAGCAG 382
QY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
DB 383 GCCTCCAGGTGGCGCTGAGAGAACTGTTAGCAGTGCGCCGACACCCGCTGTGCTGAAG 442
QY 101 ProGlyTTrpPheValGlyCysGlnValSerGlnCysValSerSerProPheTyrCys 120
DB 443 CCAGGCTGTGTTGTGAGTGCCAGGTCACCAATGTGTGTCAGCAGTTCACTTCTACTGC 502
QY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg 140
DB 503 CAACCATGCTAGACTGCGGGCCCTGCACCGCACACAGGCTACTCTGTCCCGCAGA 562
QY 141 AspThrAspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSer 160
DB 563 GATACTGACTGTGGGACCTGCGCTGCTTCTATGAAACATGGCGATGGCTGCGTGTCC 622
QY 161 CysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTyrArg 180
DB 623 TGCCCCACGAGACACCTGGGGAGCTGTCCAGACGCGTGTGCGCTGTGTGGTGAGG 682
QY 181 GlnMetPheTrpValGln 186
DB 683 CAGATGTTCTGGGTCCAG 700
RESULT 7
AAC91477
ID AAC91477 standard; cDNA; 1662 BP.
XX AAC91477;
AC AAC91477;
XX 21-MAR-2001 (first entry)
DT 21-MAR-2001 (first entry)
XX Human PRO779 cDNA.
DE Human PRO779 cDNA.
XX Human; PRO; antiinflammatory; dermatological; antiarthritic;
KW antirheumatic; cardiant; antianaemic; immunosuppressive; antithyroid;
KW antidiabetic; nootropic; neuroprotective; hepatotropic; virucide;
KW antiallergic; antiasthmatic; immune related disorder;
KW hepatobiliary disease; autoimmune disease; allergy; ss.
XX Homo sapiens.
OS Homo sapiens.
XX WO200073452-A2.
PN WO200073452-A2.
XX 07-DEC-2000.
PD 07-DEC-2000.
XX 02-JUN-2000; 2000WO-US15264.
PF 02-JUN-2000; 2000WO-US15264.
XX 02-JUN-1999; 99WO-US12252.
PR 20-JUL-1999; 99US-0144732.
PR 20-JUL-1999; 99US-0144758.
PR 28-JUL-1999; 99US-0146222.
PR 01-SEP-1999; 99WO-US20111.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 29-OCT-1999; 99US-0162506.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28634.
PR 09-DEC-1999; 99US-0170262.
PR 20-DEC-1999; 99WO-US30911.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.

PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
XX (GETH) GENENTECH INC.
PI Ashkenazi AJ, Baker KP, Chan B, Goddard A, Godowski PJ, Gurney AL;
PI Hebert C, Henzel W, Kabakoff RC, Shelton DL, Tumas D, Watanabe CK;
PI Wood WI;
XX WPI; 2001-025253/03.
DR P-PSDB; AAB50918.
DR
XX
PT Thirty three nucleic acids encoding PRO polypeptides which are useful
PT in the diagnosis and treatment of immune related disorders, e.g.
PT systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
PT thyroiditis and diabetes mellitus -
XX Claim 48; Fig 33; 218pp; English.
XX
XX The present sequence is one of thirty three nucleic acids encoding PRO
XX polypeptides. The PRO polypeptides, anti-PRO antibodies, agonists and
XX antagonists are useful for treating and diagnosing immune related
XX disorders such as systemic lupus erythematosus, rheumatoid arthritis,
XX osteoarthritis, juvenile chronic inflammatory myopathies, Sjogren's
XX systemic sclerosis, idiopathic inflammatory myopathies, Sjoegen's
XX syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
XX anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,
XX immune-mediated renal disease, demyelinating diseases of the central
XX and peripheral nervous systems (such as multiple sclerosis, idiopathic
XX demyelinating polynuropathy or Guillain-Barre syndrome, and chronic
XX inflammatory demyelinating polynuropathy), hepatobiliary diseases
XX (such as infectious, autoimmune chronic active hepatitis, primary
XX biliary cirrhosis, granulomatous hepatitis and sclerosing cholangitis),
XX inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's
XX disease, autoimmune or immune-mediated skin diseases (such as bullous
XX skin diseases, erythema multiforme, contact dermatitis, psoriasis),
XX allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,
XX food hypersensitivity and urticaria), immunological diseases of the
XX lung (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis
XX and hypersensitivity pneumonitis), transplantation associated diseases
XX including graft rejection and graft-versus-host diseases.
XX
SQ Sequence 1662 BP; 302 A; 540 C; 531 G; 289 T; 0 other;
Alignment Scores:
Pred. No.: 1.1e-74 Length: 1662
Score: 1101.00 Matches: 186
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0
US-09-993-234-6_COPY_19_204 (1-186) x AAC91477 (1-1662)
QY 1 LeuLeuGlyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
DB 157 CTGCTGGGGGCGCGCCAGGCGGCACCTGTAGCCCAAGGTGTGACTGTGCCGGTGAC 216
QY 21 PheHisLysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLys 40
DB 217 TTCACACAGAGATTTGCTGTGTTGTTCAGAGAGGCTGCGCCAGCGGCGACTACTGAAG 276
QY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
DB 277 GCCCCTTGACGAGACCCCTGCGGCACTCCACCTGCTGTGTGTCTCCCAAGACACCTTC 336

QY 61 LeuAlaTrpGluAsnHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80
Db 337 TTGGCCTGGAGAACACCAATAATCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAG 396
QY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
Db 397 GCCTCCAGAGTGGCGCTGGAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGGCTGTAG 456
QY 101 ProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCys 120
Db 457 CCAGGCTGGTTGTGGAGTGCAGGTCAGCCAAATGTGTACAGAGTTCAACCTTCTACTGC 516
QY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg 140
Db 517 CAACCATGCCTAGACTGGGGCCCTGCACCGCACACGGCTACTCTGTCCCGCAGA 576
QY 141 AspThrAspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSer 160
Db 577 GATTAAGTACTGTGGAGACCTGCCTGGCTTCTATGAACATGGCGATGGCTGCGTGTCC 636
QY 161 CysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTyrArg 180
Db 637 TGCCCCACGAGACACCTGGGGAGCTGTCCAGAGCGCTGTGCCGTGTGTGGCTGGAGG 696
QY 181 GlnMetPheTrpValGln 186
Db 697 CAGATGTCTGTGGTCCAG 714
RESULT 8
ABK40265
ID ABK40265 standard; cDNA; 1662 BP.
XX
AC ABK40265;
DT 15-JUL-2002 (first entry)
XX
DE cDNA encoding human PRO779 polypeptide.
XX
KW Human; PRO; benign tumour; malignant tumour; lymphoid malignancy;
KW leukaemia; neuronal disorder; stromal disorder; blastocoealic disorder;
KW inflammatory disorder; immune disorder; angiogenic disorder;
KW gene therapy; cytosstatic; neuroprotective; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200153486-A1.
XX
PD 26-JUL-2001.
XX
PF 11-FEB-2000; 2000WO-US03565.
XX
PR 08-MAR-1999; 99WO-US05028.
PR 11-MAR-1999; 99US-123972P.
PR 11-MAY-1999; 99US-133459P.
PR 02-JUN-1999; 99WO-US12252.
PR 22-JUN-1999; 99US-140650P.
PR 22-JUN-1999; 99US-140653P.
PR 20-JUL-1999; 99US-144758P.
PR 26-JUL-1999; 99US-145698P.
PR 28-JUL-1999; 99US-146222P.
PR 17-AUG-1999; 99US-149395P.
PR 31-AUG-1999; 99US-151689P.
PR 01-SEP-1999; 99WO-US20111.
PR 15-SEP-1999; 99WO-US21090.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.
PR 05-JAN-2000; 2000WO-US00219.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL, Hillan KJ;
PI Marsters SA, Pan J, Pitsi RM, Roy MA, Smith V, Stone DM;

PI Watanabe CK, Wood WI;
XX
DR WPI; 2002-205567/26.
DR P-PSDB; AA086139.
XX
PT Thirty five nucleic acids encoding PRO polypeptides, useful for
PT treating benign or malignant tumours, leukaemias and lymphoid
PT malignancies, inflammatory, angiogenic and immunologic disorders -
XX
PS Claim 50; Fig 23; 302pp; English.
XX
CC The present invention relates to the isolation of novel human PRO
CC polypeptides and the polynucleotide sequences encoding them. The
CC PRO polypeptides, agonists, antagonists or anti-PRO antibodies are
CC useful for treating benign or malignant tumours (e.g. renal, kidney,
CC bladder, breast, etc), leukaemias and lymphoid malignancies, other
CC disorders such as neuronal, glial, astrocytal, hypothalamic, glandular,
CC macrophagal, stromal and blastocoealic disorders, inflammatory, immune
CC and angiogenic disorders. The polynucleotide sequences are also
CC useful in gene therapy. ABK40254-ABK40288 encode for the human PRO
CC polypeptides of the invention.
XX
SQ Sequence 1662 BP; 302 A; 540 C; 531 G; 289 T; 0 other;
Alignment Scores:
Pred. No.: 1.1e-74 Length: 1662
Score: 1101.00 Matches: 186
Percent Similarity: 100.00% Conservative: 0
Best local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 24 Gaps: 0
US-09-993-234-6_COPY_19_204 (1-186) x ABK40265 (1-1662)
QY 1 LeuLeuGlyAlaAlaArgAlaGlnGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
Db 157 CTGCTGGGGGGCCCCGGGCCAGGGCGGCACCTCGTAGCCCCAGGTGTGACTGTGCCGTGAC 216
QY 21 PheHisLysLysIleGlyLeuPheCysArgGlyCysProAlaGlyHisTyrLeuLys 40
Db 217 TTCCACAGAAGATTGCTGTGTTGTTGTCAGAGGCTGCCACGGGGGCACTACCTGAAG 276
QY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
Db 277 GCCCCTTGACGAGGCCCTGGGCACTCCACCTGCTGTGTGTCCCAAGACACCTTC 336
QY 61 LeuAlaTrpGluAsnHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80
Db 337 TTGGCCTGGAGAACACCAATAATCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAG 396
QY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
Db 397 GCCTCCAGAGTGGCGCTGGAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGGCTGTAG 456
QY 101 ProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCys 120
Db 457 CCAGGCTGGTTGTGGAGTGCAGGTCAGCCAAATGTGTACAGAGTTCAACCTTCTACTGC 516
QY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg 140
Db 517 CAACCATGCCTAGACTGGGGCCCTGCACCGCACACGGCTACTCTGTCCCGCAGA 576
QY 141 AspThrAspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSer 160
Db 577 GATTAAGTACTGTGGAGACCTGCCTGGCTTCTATGAACATGGCGATGGCTGCGTGTCC 636
QY 161 CysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTyrArg 180
Db 637 TGCCCCACGAGACACCTGGGGAGCTGTCCAGAGCGCTGTGCCGTGTGTGGCTGGAGG 696
QY 181 GlnMetPheTrpValGln 186
Db 697 CAGATGTCTGTGGTCCAG 714

```
RESULT 9
AAT89426
ID AAT89426 standard; cDNA; 1783 BP.
XX
AC AAT89426;
XX
DT 02-MAR-1998 (first entry)
XX
DE Death domain containing receptor DR3-V1 cDNA.
XX
KW Death domain containing receptor; DR3-V1; human; apoptosis;
XX inflammation; NF-kappaB; ds.
OS Homo sapiens.
XX
FH Key
FT CDS Location/Qualifiers
FT sig_peptide /tag= a
FT mat_peptide /tag= b
FT /tag= c
XX
PN WO9733904-A1.
XX
PD 18-SEP-1997.
XX
PF 17-OCT-1996; 96WO-US16849.
XX
PR 12-MAR-1996; 96US-0013285.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX (UNMI ) UNIV MICHIGAN.
XX
PI Dillon PJ, Dixit VM, Gentz RL, Ni J, Yu G;
XX
DR WPI: 1997-470812/43.
XX P-PSDB; AAW31516.
XX
PT Death domain containing receptor polypeptide(s) DR3 and DR3-V1
PT for activation of apoptosis and NF-kappaB, antagonists can be used
PT to treat inflammatory diseases
XX
PS Claim 2; Page 71-73; 108pp; English.
XX
CC This cDNA clone, deposited as ATCC 97456, codes for human death
CC domain containing receptor DR3-V1 (see AAW31516), a novel member of
CC the tumour necrosis factor receptor family. It was isolated from a
CC cDNA library derived from cells of a human testis tumour. Related
CC death domain containing receptor DR3 cDNA (see AAT89427) was isolated
CC from a HUVEC cDNA library. The genes have also been identified in
CC cDNA libraries of foetal liver, foetal brain, tonsil and leukocyte.
CC Nucleic acids encoding full-length or mature DR3-V1 can be used to
CC produce recombinant polypeptides in transformed host cells. These
CC polypeptides can be used to treat diseases and disorders associated
CC with the inhibition of apoptosis. Antagonists, such as antibodies
CC raised against DR3-V1, can be used to treat diseases and disorders
CC associated with increased apoptosis and for treating inflammatory
CC diseases and disorders.
XX
SQ Sequence 1783 BP; 330 A; 562 C; 564 G; 327 T; 0 other;

Alignment Scores:
Pred. No.: 1.19e-74 Length: 1783
Score: 1101.00 Matches: 186
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-09-993-234-6_COPY_19_204 (1-186) x AAT89426 (1-1783)
```

```
QY 1 LeuLeuGlyAlaArgAlaGlnGlyThrArgSerProArgCysAspCysAlaGlyasp 20
DB 285 CTGCTGGGGCCCCGGGGCCAGGGGGCACTGTAACCCAGGTGTGACCTGCGGTGAC 344
QY 21 PheHisLysLysIleGlyLeuPheCysArgGlyCysProAlaGlyHisTyrLeuLys 40
DB 345 TTCACACAGAAGATTGCTGTGTTTGTTCAGAGGCTGCCAGGGGGCACTACCTGAAG 404
QY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
DB 405 GCCCTTGACAGGAGCCCTGGCGCACTCCACCTGCTGTGTGTCCCAAGACACCTTC 464
QY 61 LeuAlaTrpGluAsnHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80
DB 465 TTGGCCTGGAGAACCAACCAATATTCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAG 524
QY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
DB 525 GCCTCCAGGTGGCGCTGAGACTGTTCAGCAGTGGCCACACCCGCTGTGCTGTAAAG 584
QY 101 ProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCys 120
DB 585 CCAGCTGTGTTGTGAGTGTCCAGGTCAACCAATGTTCAGAGTTCAACCTTCTACTGC 644
QY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArg 140
DB 645 CAACCATGCTAGACTGTGGGGGCCCTGCACCGCCACACAGGCTACTCTGTCCGACAGA 704
QY 141 AspThrAspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSer 160
DB 705 GATACCTGACTGTGGAGCTGCTGCTGCTGCTGTATGAACATGGCGATGGCTGTCTCC 764
QY 161 CysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTyrParg 180
DB 765 TGCCCCACGAGACACCTGGGGAGAGTGTCCAGAGAGCGCTGTGCCGCTGTGTGCTGAGG 824
QY 181 GlnMetPheTyrPargGln 186
DB 825 CAGATGTTCTGGGTCCAG 842

RESULT 10
AAX00924
ID AAX00924 standard; cDNA; 1783 BP.
XX
AC AAX00924;
XX
DT 25-MAR-1999 (first entry)
XX
DE Death domain containing receptor polypeptide (DR3-V1) encoding cDNA.
XX
KW Death domain; receptor; DR3-V1; DR3; recombinant; ds.
XX
OS Homo sapiens.
XX
FH Key
FT CDS Location/Qualifiers
FT sig_peptide /tag= a
FT /product= "Death domain containing receptor DR3-V1"
FT /tag= b
FT 301..1481
FT mat_peptide /tag= c
XX
PN JP11000170-A.
XX
PD 06-JAN-1999.
XX
PF 12-MAR-1997; 97JP-0057503.
XX
PR 06-FEB-1997; 97US-0037341.
PR 12-MAR-1996; 96US-0013285.
PR 17-OCT-1996; 96US-0028711.
XX
```


PA (HUMA-) HUMAN GENOME SCI INC.
PA (UNMI) UNIV MICHIGAN.
XX
DR WPI: 1999-124390/11.
DR P-PSDB; AAW95537.
XX
PT New death domain containing receptor and recombinant vector -
PT optionally comprising leader sequence
XX
PS Claim 2; Fig 1, 2; 50pp; Japanese.
XX
CC The invention provides nucleotide sequences encoding death domain
CC containing receptor polypeptides DR3-V1 and DR3. The DR3-V1 cDNA clone
CC is contained in ATCC deposition No. 97456 and the DR3 cDNA clone is
CC contained in ATCC deposition No. 97757. Recombinant vectors comprising
CC the nucleic acid sequences and optionally the leader sequences are
CC used for the recombinant production of the proteins. The present
CC sequence represents a cDNA encoding the death domain containing
CC receptor polypeptide (DR3-V1).
XX
SQ Sequence 1783 BP; 330 A; 562 C; 564 G; 327 T; 0 other;

Alignment Scores:
Pred. No.: 1.19e-74 Length: 1783
Score: 1101.00 Matches: 186
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 20 Gaps: 0

US-09-993-234-6_COPY_19_204 (1-186) x AAX00924 (1-1783)

QY 1 LeuLeuGLyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
DB 285 CTGCTGGGGGGCCCGCCAGGGCGGCACTCTGAGCCCAAGGTGTGACTGTGCCGGTGAC 344
QY 21 PheHisLysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLys 40
DB 345 TTCACAGAAGATTGCTGTTTGTGTGAGAGGCTGCCAGCGGGGCACTACTGAG 404
QY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
DB 405 GCCCCTTGACAGGAGCCCTCGGCAACTCCACCTGCTGTGTCCCAAGACACCTTC 464
QY 61 LeuAlaTrpGluAsnHisAsnSerGluCysAlaArgCysGlnAlaCysAspGln 80
DB 465 TTGGCTGGGAGAACCACTAATCTGAATGTGCCCGGCCAGGCTGTGATGAGCAG 524
QY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
DB 525 GCCTCCCAAGTGGCGGTGAGAACTGTTCAGACAGTGGCCGACACCCGCTGTGCTGTAAG 584
QY 101 ProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCys 120
DB 585 CCAGGCTGCTTGTGGAGTGCAGGTCAGCCATGTGTACAGTTCACCTTCTACTGC 644
QY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg 140
DB 645 CAACCATGCTAGACTGCGGGGCCCTGCACCGCCACACAGGCTACTGTGCCCGCAGA 704
QY 141 AspThrAspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSer 160
DB 705 GATACTGACTGTGGACCTGCTGCTGCTTATGAACATGGCGATGGCTGCGTGC 764
QY 161 CysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTyrParg 180
DB 765 TGCCCCACGAGCACCTGGGGAGCTGTCCAGAGCGCTGTGCCGCTGTCTGTGCTGAGG 824
QY 181 GlnMetPheTyrValGln 186
DB 825 CAGATGTCTTGGGTCCAG 842
RESULT 11

AAC68776
ID AAC68776 standard; cDNA; 1783 BP.
XX
AC AAC68776;
XX
DT 20-FEB-2001 (first entry)
XX
DE Human death domain containing receptor DR3-V1 coding sequence.
XX
KW Human; death domain containing receptor; DR3-V1; cancer;
KW autoimmune disorder; inflammation; cardiovascular disorder; infection;
KW neurodegenerative disease; angiogenesis; ss.
XX
OS Homo sapiens.
XX
PN WO200064465-A1.
XX
PD 02-NOV-2000.
XX
PF 21-APR-2000; 2000WO-US10741.
XX
PR 22-APR-1999; 99US-0130488.
PR 28-MAY-1999; 99US-0136741.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (UNMI) UNIV MICHIGAN.
PA (YUGG/) YU G.
PA (NIJ/) NI J.
PA (GENT/) GENTZ R L.
PA (DILL/) DILLON P J.
PA (DIXI/) DIXIT V M.
XX

PI YU G, NI J, Gentz RL, Dillon PJ, Dixit VM;

DR WPI: 2000-687263/67.
DR P-PSDB; AAB36264.

PT Treating graft-versus-host disease, cancer, immunodeficiency or an
PT autoimmune disease comprising administering an antibody to Death Domain
PT Containing Receptor proteins and a second therapeutic agent -

PS Example 1; Fig 1; 273pp; English.

CC The present invention provides the protein and coding sequences for two
CC death domain containing receptors, designated DR3 and DR3-V1. These
CC receptors are involved in apoptosis, and the sequences given can be used
CC in the treatment of cancers, infections, cardiovascular disorders such as
CC arrhythmias, ischaemia, aneurysms, arterial occlusive diseases, embolisms
CC and congenital heart defects, neurodegenerative diseases including
CC Alzheimer's and Parkinson's diseases, autoimmune disease such as multiple
CC sclerosis, arthritis, diabetes, Graves' disease, asthma and psoriasis,
CC and to promote angiogenesis and wound healing.

SQ Sequence 1783 BP; 330 A; 562 C; 564 G; 327 T; 0 other;

Alignment Scores:
Pred. No.: 1.19e-74 Length: 1783
Score: 1101.00 Matches: 186
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-09-993-234-6_COPY_19_204 (1-186) x AAC68776 (1-1783)

QY 1 LeuLeuGLyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
DB 285 CTGCTGGGGGGCCCGCCAGGGCGGCACTCTGAGCCCAAGGTGTGACTGTGCCGGTGAC 344
QY 21 PheHisLysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLys 40
DB 345 TTCACAGAAGATTGCTGTTTGTGTGAGAGGCTGCCAGCGGGGCACTACTGAG 404

QY	41	AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe	60
Db	405	GGCCCTTGACGAGGAGCCCTGGCGCAACTCCACTGCCTGTGTGTCCCAAGACACCTTC	464
QY	61	LeuAlaTrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln	80
Db	465	TTGGCTGGGAGAAACCACCATTAATCTGAAATGTGCCCGCTGCCAGGCTGTGATGAGCAG	524
QY	81	AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys	100
Db	525	GGCTTCCAGGTGGCGCTGGAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGGCTGTAA	584
QY	101	ProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCys	120
Db	585	CCAGGCTGGTTTGTGGAGTGCACAGTTCAGCCCAATGTGTACAGCAGATTACCCCTTACTGC	644
QY	121	GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg	140
Db	645	CAACCATGCGCTAGACTGCGGGGCGCTGCACCGCCACACACAGGCTACTCTGTTC	704
QY	141	AspThrAspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSer	160
Db	705	GATACTGACTGTGGGACCTGCCCTGCCTTCTATGAACATGGCGATGGCTGCGTGC	764
QY	161	CysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTrpArg	180
Db	765	TGCCCCACGAGCACCCCTGGGGAGCTGTCCAGAGCGCTGTGCCCTGTCTGTGGCTGAGG	824
QY	181	GlnMetPheTrpValGln	186
Db	825	CAGATGTTCTGGGTCCAG	842

RESULT 12	
AAV28700	
ID	AAV28700 standard; cDNA; 1847 BP.
XX	
AC	AAV28700;
XX	
DT	20-AUG-1998 (first entry)
XX	
DE	Human apoptosis inducing receptor coding sequence.
XX	
KW	Apoptosis inducing receptor; AIR protein; human; cell death regulator;
KW	Type I transmembrane protein; tumour cell death; autoimmune disease;
KW	therapy; ss.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	CDS
FT	236..1489
FT	/*tag= a
FT	/product= AIR
XX	
PN	W09814565-A1.
XX	
PD	09-APR-1998.
XX	
PF	03-OCT-1997; 97WO-US17876.
XX	
PR	04-OCT-1996; 96US-0044456.
XX	
PA	(IMMV) IMMUNEX CORP.
XX	
PI	Perkins PA;
XX	
DR	WPI; 1998-240077/21.
DR	P-PSDB; AAW57045.
XX	
PT	DNA encoding apoptosis inducing receptor - which is type I
PT	transmembrane protein, useful for regulating cell death
XX	
PS	Claim 2; Page 28-30; 45pp; English.
XX	

CC This sequence encodes the human apoptosis inducing receptor (AIR) of the
CC invention. AIR is a Type I transmembrane protein, soluble forms of which
CC can be used to regulate cell death in a therapeutic setting. Soluble AIR
CC can also be used in vitro to block apoptosis or AIR-expressing cells, or
CC to screen agonists or antagonists of AIR activity. The cytoplasmic domain
CC of AIR can be used to develop assays for inhibitors of AIR-induced cell
CC death, which is useful to regulate cell death in a therapeutic setting as
CC well as in vitro. Agonists of AIR activity can be used to kill tumour
CC cells that express AIR, or T cells expressing AIR in autoimmune diseases.
XX
SQ Sequence 1847 BP; 316 A; 605 C; 579 G; 347 T; 0 other;

Alignment Scores:	
Pred. No.:	1.24e-74
Score:	1101.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	19
Length:	1847
Matches:	186
Conservative:	0
Mismatches:	0
Gaps:	0

US-09-993-234-6_COPY_19_204 (1-186) x AAV28700 (1-1847)

QY	1	leuLeuGlYlaaRgaIaGInGInGlyGlyThrAnGserProArGcYsaSpCYsaIaGlyAsp	20
Db	290	CTGCTGGGGGGCCCGCCAGGGCGGCACGTCTAGCCCCAGGTGTGACTGTGCCGGGTGAC	34
QY	21	PheHisLysIleGlyLeuPheCysCysArGlyCysProIaGlyHisTyrLeuLys	40
Db	350	TTCACACAGACATTTGCTGTTTGTTCAGAGGGCTGCCACGGGGGTACTTACTTGAC	400

QY 41 AlaProCysThnGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
 |||||
 Db 410 GCCCCTTGACGGAGGCCCTGCGGCAACTCCACCTGTGTTGTGTCCCAAGACACCTTC 465

QY 61 LeuAlaTrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysaspGluGln 80
 |||
 Db 470 TTGGCGTGGAGAACCAACCATTAATTCTGAATGTGCCCGCTGCCAGGCGCTGTGATGAGCAG 529

QY 81 ALASerGlnValAlaLeuGlnAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
|||||
Db 530 GCCTCCAGGTGGCGCTGGAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGGCTGTAC 589

QY 101 ProGlyTrrPheValGIuCySGlnValSerGlnCysValSerSerProphetyrCys 120
 |||||
 590 CCAGGCTGGTTGTGAGAGTGCCAGGTCAGCCAAATGTGTACACAGTTCACCCCTTCTACTGC 649
 Dp

QY	121	GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgarg	140
Db	650	CACCATGCCTAGACTGGCGGCCCTGCACCGCCACACACGGCTACTGTGTCCCGCAGA	709

141 ASPINRSPCYSGLYTHRCYSEUPROGLYPHETRYGLUHSGLYASPGLYCYVALSER 160
 710 GATACTGACTGTGGGACCTGCCTGCCTTCTATGACATGGCGATGGCTGCCTGTCC 769

QY	161	CysProThrSerThrLeuClYserCysProGluArgCysAlaAlaValCysGlyTrpArg	180
Db	770	TGCCCCACGAGCACCCCTGGGGAGCTGTCCAGAGCGCTGTCCGCTGTCTGTGGCTGGAGG	829

QY	181	GlnMetPheTrrPvalGln	186
Db	830	CAgATGTTCTGGGTCCAG	847

RESULT 13

ABL64119 standard; DNA; 1743 BP.

XX
AC ABL64119;

15-MAY-2002 (first entry)

Breast cancer related gene sequence SEQ ID NO:2456

Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;

KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
XX gene; ds.
OS Homo sapiens.
XX
PN WO200194629-A2.
XX
PD 13-DEC-2001.
XX
PF 30-MAY-2001; 2001WO-US10838.
XX
PR 05-JUN-2000; 2000US-209473P.
PR 05-JUN-2000; 2000US-209531P.
PR 18-SEP-2000; 2000US-233133P.
PR 18-SEP-2000; 2000US-233617P.
PR 20-SEP-2000; 2000US-234009P.
PR 20-SEP-2000; 2000US-234034P.
PR 20-SEP-2000; 2000US-234052P.
PR 22-SEP-2000; 2000US-234509P.
PR 22-SEP-2000; 2000US-234567P.
PR 25-SEP-2000; 2000US-234923P.
PR 25-SEP-2000; 2000US-234924P.
PR 25-SEP-2000; 2000US-235077P.
PR 25-SEP-2000; 2000US-235082P.
PR 25-SEP-2000; 2000US-235134P.
PR 25-SEP-2000; 2000US-235280P.
PR 26-SEP-2000; 2000US-235637P.
PR 26-SEP-2000; 2000US-235638P.
PR 27-SEP-2000; 2000US-235711P.
PR 27-SEP-2000; 2000US-235720P.
PR 27-SEP-2000; 2000US-235840P.
PR 27-SEP-2000; 2000US-235863P.
PR 28-SEP-2000; 2000US-236028P.
PR 28-SEP-2000; 2000US-236032P.
PR 28-SEP-2000; 2000US-236033P.
PR 28-SEP-2000; 2000US-236034P.
PR 28-SEP-2000; 2000US-236109P.
PR 28-SEP-2000; 2000US-236111P.
PR 29-SEP-2000; 2000US-236842P.
PR 29-SEP-2000; 2000US-236891P.
PR 02-OCT-2000; 2000US-237172P.
PR 02-OCT-2000; 2000US-237173P.
PR 02-OCT-2000; 2000US-237278P.
PR 02-OCT-2000; 2000US-237294P.
PR 02-OCT-2000; 2000US-237295P.
PR 02-OCT-2000; 2000US-237316P.
PR 03-OCT-2000; 2000US-237425P.
PR 03-OCT-2000; 2000US-237598P.
PR 03-OCT-2000; 2000US-237604P.
PR 03-OCT-2000; 2000US-237606P.
PR 03-OCT-2000; 2000US-237608P.
PR 01-NOV-2000; 2000US-244867P.
PR 01-NOV-2000; 2000US-245084P.
XX
PA (AVAL-) AVALON PHARM.
XX
PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppet DR, Weaver Z;
XX
XX WPI; 2002-188264/24.
XX
PT Screening for anti-neoplastic agent involves exposing cells to a
PT chemical agent to be tested for anti-neoplastic activity, and
PT determining a change in expression of a gene of a signature gene set -
XX
PS Claim 1; SEQ ID 2456; 44pp; English.
XX
CC The present invention describes a method (M1) for screening for an
CC anti-neoplastic agent. The method involves exposing cells to a chemical
CC agent to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664

CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening
CC an anti-neoplastic agent, and can be used for producing a product which
CC is the data collected with respect to the anti-neoplastic agent as a
CC result of M1, and the data is sufficient to convey the chemical
CC structure and/or properties of the agent. M1 can be used in the
CC treatment of cancer such as colon, breast, stomach, lung, thyroid,
CC oesophageal, ovarian, kidney, prostate or pancreatic cancer,
CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
CC carcinoma, papillary carcinoma and Wilm's tumour.
XX
SQ Sequence 1743 BP; 347 A; 543 C; 549 G; 304 T; 0 other;
XX
Alignment Scores:
Pred. No.: 7.74e-73 Length: 1743
Score: 1077.00 Matches: 182
Percent Similarity: 98.91% Conservative: 0
Best Local Similarity: 98.91% Mismatches: 2
Query Match: 97.82% Indels: 0
DB: 24 Gaps: 0
US-09-993-234-6_COPY_19_204 (1-186) x ABL64119 (1-1743)
QY 1 LeuLeuGlyAlaIarGAlaInglyGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
DB 123 CTGCTGGGGGGCCCGGGCCAGGGGGCACTCGTAGCCCCAGGTGTGACTGTGCCGGTAC 182
QY 21 PheHisLysLysIleGlyLeuPheCysArgGlyCysProAlaGlyHisTyrLeuLys 40
DB 183 TTCCACAAGAAAGATTGCTGTGTTGTTCAGAGGCTGCCACGGGGCACTACCTGAAG 242
QY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
DB 243 GCCCTTGACACGAGCCCTGGCGCACTCCACCTGCTGTGTGCCCAAGACACCTTC 302
QY 61 LeuAlaTrrGluAsnHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluIn 80
DB 303 TTGGCCTGGGAGAACCACCATTAATTCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAG 362
QY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
DB 363 GCCTCCAGGTGGCGCTGGAGACTGTTCAGCAGTGGCCGACACCCGCTGTGGCTGTAA 422
QY 101 ProGlyTrrPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCys 120
DB 423 CCAGGCTGGTTTGTGGAGTGCAGGTCACCAATGTGTACAGACTTCACCTTCTACTGC 482
QY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArg 140
DB 483 CAACCATGCTTAGACTGCGGGCCCTGCACCGCACACACAGGCTACTGTGTCCCGCAGA 542
QY 141 AspThrAspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSer 160
DB 543 GATACGTGACTGTGGACCTGCTGCTGCTGCTTCTATGAACATGGCGATGGCTGCTCC 602
QY 161 CysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTrrArg 180
DB 603 TGCCCCACGACGACACCTGGGGAGCTGTCCAGAGCGCTGTGCCGTGTGTGGCTGAGG 662
QY 181 GlnMetPheTrr 184
DB 663 CAGAGTAGGTGG 674
RESULT 14
AAF83770
ID AAF83770 standard; DNA; 1250 BP.
XX
AC AAF83770;
XX
DT 06-AUG-2001 (first entry)
XX

DE Nucleotide sequence of human TR3 gene.
XX
KW TR3; cell proliferation; leukemia; immunosuppressive; cytostatic;
KW dermatological; antiarthritic; antidiabetic; neuroprotective; cardiant;
KW antithyroid; antiinflammatory; antiallergic; T-cell-inhibitor; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1250
FT /tag= a
FT /transl_except= "(pos:481..482, aa:asp)"
FT /note= "this codon has an apparent 1 nucleotide
FT deletion which alters the reading frame"
FT /transl_except= "(pos:558..559, aa:Cys)"
FT /note= "this codon has an apparent 1 nucleotide
FT deletion which alters the reading frame"
FT /transl_except= "(pos:638..639, aa:Leu)"
FT /note= "this codon has an apparent 1 nucleotide
FT deletion which alters the reading frame"
FT /transl_except= "(pos:718..719, aa:Met)"
FT /note= "this codon has an apparent 1 nucleotide
FT deletion which alters the reading frame"
FT sig_peptide 1..72
FT /tag= b
FT mat_peptide 73..1247
FT /tag= c
XX
PN WO200135995-A2.
XX PD 25-MAY-2001.
XX PF 17-NOV-2000; 2000WO-US31692.
XX PR 19-NOV-1999; 99US-0166583.
XX PA (TITT/) TITTLE T V.
XX PA (WEGM/) WEGMANN K W.
XX PI Tittle TV, Wegmann KW;
XX DR WPI; 2001-343711/36.
XX DR P-PSDB; AAB84941.
XX
PT Composition for treatment of T-cell mediated disease e.g. arthritis,
PT cancer comprises a biologically active TR3-specific binding agent
PT especially a monoclonal antibody -
XX
PS Disclosure; Page 72; 77pp; English.
XX
CC The invention relates to a composition comprising a biologically active
CC TR3-specific binding agent (I) that binds to TR3 and inhibits the
CC proliferation of cells expressing TR3. (I) identified by the methods are
CC useful for treating a subject suspected of having a disease associated
CC with a proliferation of cells expressing TR3 especially leukemias or
CC lymphomas or a T-cell mediated disease especially autoimmune diseases
CC such as myasthenia gravis, systemic lupus erythamatosus, rheumatoid
CC arthritis, diabetes, multiple sclerosis, sarcoidosis, myocarditis,
CC thyroiditis and tumours. (I) is also useful for treating a subject
CC suspected of having graft-versus-host disease, rejection of a
CC transplanted organ such as heart, liver, lung, kidney, pancreas, bowel,
CC skin or an appendage, or inflammatory diseases, allergies and contact
CC dermatitis. The present sequence represents the nucleotide sequence of
CC human TR3 gene.
XX
SQ Sequence 1250 BP; 201 A; 419 C; 406 G; 224 T; 0 other;

Alignment Scores:
Pred. No.: 2.88e-70 Length: 1250
Score: 1041.00 Matches: 184
Percent Similarity: 98.92% Conservative: 0
Best Local Similarity: 98.92% Mismatches: 2
Query Match: 94.55% Indels: 2

DB: 22 Gaps: 0
US-09-993-234-6_COPY_19_204 (1-186) x AAF83770 (1-1250)
QY 1 LeuLeuGlYAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
DB 55 CTGCTGGGGCCCGGGCCAGGGCGGCACTGAGCCCAAGTGTGACTGTGCCGGTGAC 114
QY 21 PheHisLysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLys 40
DB 115 TTCACAGAGAAGATTGGTCTGTTGTTCAGAGAGCTGCCAGCGGGCAGCTACTGAAG 174
QY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
DB 175 GCCCCTGCACGGAGAGCCCTGCCGCACTCCACCTGCTGTGTGCCCAAGACACCTTC 234
QY 61 LeuAlaTrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80
DB 235 TTGGCCTGGGAGAACCAACCATTAATTCGAAATGTGCCCGCTGCCAGGCTGTGATGAGCAG 294
QY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
DB 295 GCCTCCAGGTGGCGCTGGAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGGCTGAAG 354
QY 101 ProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCys 120
DB 355 CCAGGCTGGTGTGTGGAGTGCAGGTCACCAATGTGTACAGAGTTCAACCTTCTACTGC 414
QY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg 140
DB 415 CAACCATGCTAGACTGCGGGCCCTGCACCGCACACAGCGGCTACTCTGTCCCGCAGA 474
QY 141 AspThrAspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSer 160
DB 475 GATAC-GACTGTGGGAGACCTGCTGCTGCTGTATGAACATGGCAGTGCGTGC 533
QY 161 CysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTyrArg 180
DB 534 TGCCCCACGAGACCCCTGGGAGCGT-CCAGAGCGCTGTGCCGCTGTGTGGCTGAGG 592
QY 181 GlnMetPheTrpValGln 186
DB 593 CAGATGTTCTGGGCTCCAG 610
RESULT 15
ABL67258
ID ABL67258 standard; DNA; 816 BP.
XX
AC ABL67258;
XX
DT 15-MAY-2002 (first entry)
XX
DE Thyroid cancer related gene sequence SEQ ID NO:5595.
XX
KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW gene; ds.
XX
OS Homo sapiens.
XX
PN WO200194629-A2.
XX PD 13-DEC-2001.
XX
PF 30-MAY-2001; 2001WO-US10838.
XX
PR 05-JUN-2000; 2000US-209473P.
PR 05-JUN-2000; 2000US-209531P.
PR 18-SEP-2000; 2000US-233133P.
PR 18-SEP-2000; 2000US-233617P.
PR 20-SEP-2000; 2000US-234009P.
PR 20-SEP-2000; 2000US-234034P.

PR 20-SEP-2000; 2000US-234052P.
PR 22-SEP-2000; 2000US-234509P.
PR 22-SEP-2000; 2000US-234567P.
PR 25-SEP-2000; 2000US-234923P.
PR 25-SEP-2000; 2000US-234924P.
PR 25-SEP-2000; 2000US-235077P.
PR 25-SEP-2000; 2000US-235082P.
PR 25-SEP-2000; 2000US-235134P.
PR 25-SEP-2000; 2000US-235280P.
PR 26-SEP-2000; 2000US-235637P.
PR 26-SEP-2000; 2000US-235638P.
PR 27-SEP-2000; 2000US-235711P.
PR 27-SEP-2000; 2000US-235720P.
PR 27-SEP-2000; 2000US-235840P.
PR 27-SEP-2000; 2000US-235863P.
PR 28-SEP-2000; 2000US-236028P.
PR 28-SEP-2000; 2000US-236032P.
PR 28-SEP-2000; 2000US-236033P.
PR 28-SEP-2000; 2000US-236034P.
PR 28-SEP-2000; 2000US-236109P.
PR 28-SEP-2000; 2000US-236111P.
PR 29-SEP-2000; 2000US-236842P.
PR 29-SEP-2000; 2000US-236891P.
PR 02-OCT-2000; 2000US-237172P.
PR 02-OCT-2000; 2000US-237173P.
PR 02-OCT-2000; 2000US-237278P.
PR 02-OCT-2000; 2000US-237294P.
PR 02-OCT-2000; 2000US-237295P.
PR 02-OCT-2000; 2000US-237316P.
PR 03-OCT-2000; 2000US-237425P.
PR 03-OCT-2000; 2000US-237598P.
PR 03-OCT-2000; 2000US-237604P.
PR 03-OCT-2000; 2000US-237606P.
PR 03-OCT-2000; 2000US-237608P.
PR 01-NOV-2000; 2000US-244867P.
PR 01-NOV-2000; 2000US-245084P.

(AVAL-) AVALON PHARM.
XX PA
XX Young PE, Augustus M, Carter KC, Edner R, Endress G, Horrigan S;
PI Sopet DR, Weaver Z;
XX DR
XX WPI; 2002-188264/24.

Screening for anti-neoplastic agent involves exposing cells to a
chemical agent to be tested for anti-neoplastic activity, and
determining a change in expression of a gene of a signature gene set -

Claim 1; SEQ ID 5595; 44pp; English.
XX PS
XX
CC The present invention describes a method (M1) for screening for an
CC anti-neoplastic agent. The method involves exposing cells to a chemical
CC agent to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening
CC an anti-neoplastic agent, and can be used for producing a product which
CC is the data collected with respect to the anti-neoplastic agent as a
CC result of M1, and the data is sufficient to convey the chemical
CC structure and/or properties of the agent. M1 can be used in the
CC treatment of cancer such as colon, breast, stomach, lung, thyroid,
CC oesophageal, ovarian, kidney, prostate or pancreatic cancer,
CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
CC carcinoma, papillary carcinoma and Wilm's tumour.
XX
XX Sequence 816 BP; 149 A; 235 C; 264 G; 168 T; 0 other;

Alignment Scores:	
Pred. No.:	9.1e-66
Score:	979.00
	Length: 816
	Matches: 169

Percent Similarity:	93.92%	Conservative:	1
Best Local Similarity:	93.37%	Mismatches:	3
Query Match:	88.92%	Indels:	8
DB:	24	Gaps:	1

US-09-993-234-6_COPY_19_204 (1-186) x ABL67258 (1-816)

QY	1	LeuLeuGluAlaAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAsp	20
Db	39	CTGCTGGGGGGCCCCGAGGGGGGGGGCACTGCTAGCCCCAGGTGTGACTGTGCCGGTGAC	98
QY	21	PheHisLysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLys	40
Db	99	TTCCACAAGAAGATTGGTCTGTTTGTGTGCAGAGGCTGCCAGCGGGGCACTACCTGAAG	158
QY	41	AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe	60
Db	159	GCCCCCTGGACAGGAGGCCCTCGGGCACTCCACCTGCCCTGTGTGTCTCCCAAGACACCTTC	218
QY	61	LeuAlaTyrGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln	80
Db	219	TTGGCCCTGGGAGAACCACCATTAATCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAG	278
QY	81	AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys	100
Db	279	GCCTCCAGGTGGCGCTGGAGAACTGTTCAGCAGTGGCCGACACCCGGCTGTGCTGAAG	338
QY	101	ProGlyTyrPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCys	120
Db	339	CCAGGCTGGTTTGTGGAGTGCCAGGTACGCCAATGTGTACAGCAGTTACCCCTTCTACTGC	398
QY	121	GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg	140
Db	399	CAACCATGCCCTAGACTGGCGGGCCCTGCACCGCCACACACAGCGCTACTCTGTGCCCGCAGA	458
QY	141	AspThrAspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSer	160
Db	459	GATACTGACTGTGGAGACCTGCCTGCCTTCTATGAACATGGCGATGGCTGCGTGCC	518
QY	161	CysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTyrParg	180
Db	519	TGCCCCACGTAATTCCTA-----GCTGTCTGTGGATGGAGG	554
QY	181	Gln 181	
	...		
Db	555	GAA 557	

Search completed: April 6, 2003, 16:53:27
Job time : 216.187 secs

W7

THIS PAGE BLANK (USPTO)

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 6, 2003, 16:28:24 ; Search time 31.3989 Seconds
(without alignments)
1816.682 Million cell updates/sec

Title: US-09-993-234-6_COPY_19_204
Perfect score: 1101
Sequence: 1 LIGARAQGGTRSPRCDCAGD.....GSCPERCAAVCGWRQMFVQ 186

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 441362 segs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US0993234/runat_27032003_115457_15378/app_query.fasta_1.2346
-DB=Issued_Patents_NA -QFMT=fastlap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=biosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US0993234_@CGN_1_1_116_@runat_27032003_115457_15378 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1101	100.0	1254	3	US-08-815-469-3	Sequence 3, Appli
2	1101	100.0	1634	4	US-08-928-069-11	Sequence 11, Appl
3	1101	100.0	1634	4	US-08-828-683A-9	Sequence 9, Appli
4	1101	100.0	1783	3	US-08-815-469-1	Sequence 1, Appli
5	979	88.9	1438	4	US-08-928-069-5	Sequence 5, Appli
6	979	88.9	1438	4	US-08-828-683A-5	Sequence 5, Appli
7	692	62.9	433	4	US-08-928-069-2	Sequence 2, Appli
8	692	62.9	433	4	US-08-828-683A-2	Sequence 2, Appli
9	213	19.3	1956	2	US-08-762-308-10	Sequence 10, Appl
10	212.5	19.3	1049	4	US-08-804-166-1	Sequence 1, Appli
11	212.5	19.3	1049	4	US-08-910-991-1	Sequence 1, Appli
12	205.5	18.7	1301	4	US-08-804-166-7	Sequence 7, Appli

13	205.5	18.7	1301	4	US-08-910-991-7	Sequence 7, Appli
14	205	18.6	600	1	US-08-050-319B-47	Sequence 47, Appl
15	205	18.6	600	2	US-08-465-982-47	Sequence 47, Appl
16	203.5	18.5	1202	4	US-08-804-166-3	Sequence 3, Appli
17	203.5	18.5	1202	4	US-08-910-991-3	Sequence 3, Appli
18	203	18.4	2062	1	US-08-050-319B-24	Sequence 24, Appl
19	203	18.4	2062	1	US-08-465-982-24	Sequence 24, Appl
20	203	18.4	2161	3	US-09-106-038A-1	Sequence 1, Appli
21	203	18.4	2161	4	US-09-505-250-3	Sequence 3, Appli
22	203	18.4	2175	1	US-08-321-668-1	Sequence 1, Appli
23	203	18.4	2175	1	US-08-837-941-1	Sequence 1, Appli
24	203	18.4	2175	1	US-08-126-016-1	Sequence 1, Appli
25	203	18.4	2175	4	US-08-054-970-1	Sequence 1, Appli
26	203	18.4	6889	1	US-08-286-740-2	Sequence 2, Appli
27	203	18.4	6889	5	PCT-US95-09576-2	Sequence 2, Appli
28	203	18.4	6896	2	US-08-627-151A-6	Sequence 6, Appli
29	201	18.3	1147	4	US-08-804-166-5	Sequence 5, Appli
30	201	18.3	1147	4	US-08-910-991-5	Sequence 5, Appli
31	200.5	18.2	483	4	US-09-326-394-1	Sequence 1, Appli
32	200.5	18.2	1478	4	US-09-149-922-6	Sequence 6, Appli
33	191	17.3	543	4	US-09-513-007-3	Sequence 3, Appli
34	191	17.3	2440	4	US-09-513-007-1	Sequence 1, Appli
35	190	17.3	1724	5	PCT-US96-12374-1	Sequence 1, Appli
36	189	17.2	1724	4	US-08-509-024-1	Sequence 1, Appli
37	189	17.2	1724	4	US-09-333-279-1	Sequence 1, Appli
38	182	16.5	579	4	US-09-146-950-3	Sequence 3, Appli
39	182	16.5	591	4	US-09-146-950-19	Sequence 19, Appl
40	182	16.5	1596	4	US-09-146-950-17	Sequence 17, Appl
41	182	16.5	1929	4	US-09-146-950-1	Sequence 1, Appli
42	182	16.5	4622	4	US-08-509-024-6	Sequence 6, Appli
43	182	16.5	4622	4	US-09-333-279-6	Sequence 6, Appli
44	170.5	15.5	477	1	US-08-050-319B-53	Sequence 53, Appl
45	170.5	15.5	477	2	US-08-465-982-53	Sequence 53, Appl

ALIGNMENTS

RESULT 1
US-08-815-469-3
; Sequence 3, Application US/08815469
; Patent No. 6153402
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Dixit, Vishva
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dillon, Patrick J.
; TITLE OF INVENTION: Death Domain Containing Receptors
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/815,469
; FILING DATE: HERewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: NO. 6153402 Yet Assigned
; FILING DATE: 06-FEB-1997
; APPLICATION NUMBER: US 60/028,711
; FILING DATE: 17-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,285

FILING DATE: 12-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1254 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1251
US-08-815-469-3

Alignment Scores:
Pred. No.: 1.47e-90 Length: 1254
Score: 1101.00 Matches: 186
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-993-234-6_COPY_19_204 (1-186) x US-08-815-469-3 (1-1254)

QY 1 LeuLeuGIyAlaArgAlaGlnGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
Db 55 CTGCTGGGGCCCGGGCCAGGGGGGCACTGAGCCCAAGGTGTGACTGTGCCGGTGAC 114
QY 21 PheHisLysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLys 40
Db 115 TTCACACAGAAGATGTGTCTGTTGTCAGAGGCTGCCAGCGGGCACTACTACCTGAAG 174
QY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
Db 175 GCCCTTGACACGAGAGCCCTGCCGCACTCCACCTGCTGTGTGCCCAAGACACCTTC 234
QY 61 LeuAlaTrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80
Db 235 TTGGCTGGGAGAACCACCATTAATCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAG 294
QY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
Db 295 GCCTCCAGGTGGCGCTGAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGCTGAAG 354
QY 101 ProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCys 120
Db 355 CCAGGCTGTTGTGTGAGTCCAGGTCAACCAATGTGTACAGCAGTTCACCCCTTCTACTGC 414
QY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg 140
Db 415 CAACCATGCTAGACTGCGGGGCCCTGCACCGCACACACGGCTACTCTGTCCCGCAGA 474
QY 141 AspThrAspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSer 160
Db 475 GATACTGACTGTGGACCTGCTGCTGCTTCTATGAACATGGCGATGGCTGCGTTC 534
QY 161 CysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTrpArg 180
Db 535 TGCCCAAGAGACACCTGGGGAGCTGTCCAGAGCGCTGTGCCGCTGTGTGCTGAGAG 594
QY 181 GlnMetPheTrpValGln 186
Db 595 CAGATGTCTGTGGTCCAG 612

RESULT 2
US-08-928-069-11
; Sequence 11, Application US/08928069

Patent No. 6462176
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-3 POLYPEPTIDE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,069
FILING DATE: 11-Sep-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/026943
FILING DATE: 09/23/1996
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1052R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1634 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-928-069-11

Alignment Scores:
Pred. No.: 2.08e-90 Length: 1634
Score: 1101.00 Matches: 186
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-993-234-6_COPY_19_204 (1-186) x US-08-928-069-11 (1-1634)

QY 1 LeuLeuGIyAlaArgAlaGlnGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
Db 143 CTGCTGGGGCCCGGGCCAGGGGGGCACTGAGCCCAAGGTGTGACTGTGCCGGTGAC 202
QY 21 PheHisLysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLys 40
Db 203 TTCACAGAAGATGTGTCTGTTGTCAGAGGCTGCCAGCGGGCACTACTACTGAG 262
QY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
Db 263 GCCCTTGACACGAGAGCCCTGCCGCACTCCACCTGCTGTGTGCCCAAGACACCTTC 322
QY 61 LeuAlaTrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80
Db 323 TTGGCTGGGAGAACCACCATTAATCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAG 382
QY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
Db 383 GCCTCCAGGTGGCGCTGAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGCTGTAAG 442
QY 101 ProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCys 120
Db 443 CCAGGCTGTTGTGTGAGTCCAGGTCAACCAATGTGTACAGCAGTTCACCCCTTCTACTGC 502

QY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg 140
|||||
Db 503 CAACCATGCTAGACTGGGGGGCCCTGCACCGCACACAGGCTACTGTGCCCGCAGA 562
QY 141 AspThrAspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSer 160
|||||
Db 563 GATACTGACTGTGGACCTGCTGCTGCTGCTATGACATGGCGATGGCTGCTGCC 622
QY 161 CysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTrpArg 180
|||||
Db 623 TGCCCCACGACGACCTGGGAGCTGTCCAGAGCGCTGTGCCGCTGTCTGTGGCTGAGG 682
QY 181 GlnMetPheTrpValGln 186
|||||
Db 683 CAGATGTCTGTGGTCCAG 700

RESULT 3
US-08-828-683A-9

; Sequence 9, Application US/08828683A
; Patent No. 6469144

GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/828,683A
; FILING DATE: 31-Mar-1997
; CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/625328
; FILING DATE: 1-Apr-1996
; APPLICATION NUMBER: 08/710802
; FILING DATE: 23-Sep-1996

ATTORNEY/AGENT INFORMATION:

; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1007P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 1634 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-08-828-683A-9

Alignment Scores:

Pred. No.: 2.08e-90 Length: 1634
Score: 1101.00 Matches: 186
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-993-234-6_COPY_19_204 (1-186) x US-08-828-683A-9 (1-1634)

QY 1 LeuLeuGlyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
|||||

Db 143 CTGCTGGGGGGCCCCGGGGCCAGGGGGGCACCTGCTAGCCCCCAGGTGTGACTGTGCCGGTGAC 202
QY 21 PheHisLysLysIleGlyLeuPheCysArgGlyCysProAlaGlyHisTyrLeuLys 40
|||||
Db 203 TTCCACAGAAGATTGTTCTGTGTTTGTGACAGAGGCTGCCACGGGGGCACTACTGTAAG 262
QY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGluAspThrPhe 60
|||||
Db 263 GCCCCTTGACACGAGCCCTGGCGCACTCCACCTGCTGTGTGTCCCAAGACACCTTC 322
QY 61 LeuAlaTrpGluAsnHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80
|||||
Db 323 TTGGCCCTGGAGAACCACTAATTCTGAATGTGCCCGCTGCCAGGCCCTGTGATGAGCAG 382
QY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
|||||
Db 383 GCCCTCCAGGTGGCGCTGGAGAACTGTCAGCAGTGGCCGACACCCGCTGTGCTGTAA 442
QY 101 ProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCys 120
|||||
Db 443 CCAGGCTGTTTGTGAGTGTCCAGGTCAAGCAATGTGTACAGAGTTACCCCTTACTGC 502
QY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg 140
|||||
Db 503 CAACCATGCTAGACTGGGGGGCCCTGCACCGCACACAGGCTACTGTGCCCGCAGA 562
QY 141 AspThrAspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSer 160
|||||
Db 563 GATACTGACTGTGGACCTGCTGCTGCTGCTATGACATGGCGATGGCTGCTGCC 622
QY 161 CysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTrpArg 180
|||||
Db 623 TGCCCCACGACGACCTGGGAGCTGTCCAGAGCGCTGTGCCGCTGTCTGTGGCTGAGG 682
QY 181 GlnMetPheTrpValGln 186
|||||
Db 683 CAGATGTCTGTGGTCCAG 700

RESULT 4

US-08-815-469-1

; Sequence 1, Application US/08815469
; Patent No. 6153402

GENERAL INFORMATION:

; APPLICANT: YU, Guo-Liang
; APPLICANT: NI, Jian
; APPLICANT: Dixit, Vishva
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dillon, Patrick J.
; TITLE OF INVENTION: Death Domain Containing Receptors
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., NW, Suite 600
; CITY: Washington
; STATE: DC

COUNTRY: USA
ZIP: 20005-3934

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/815,469
; FILING DATE: HEREWITH

; CLASSIFICATION: 435

PRIOR APPLICATION DATA:

; APPLICATION NUMBER: NO. 6153402 Yet Assigned
; FILING DATE: 06-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,711
; FILING DATE: 17-OCT-1996
; PRIOR APPLICATION DATA:

```

: APPLICATION NUMBER: US 60/013,285
: FILING DATE: 12-MAR-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Steffe, Eric K.
: REGISTRATION NUMBER: 36,688
: REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-371-2600
: TELEFAX: 202-371-2540
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1783 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: both
: MOLECULE TYPE: CDNA
: FEATURE:
:
: NAME/KEY: CDS
: LOCATION: 198..1481
US-08-815-469-1

```

Alignment Scores:		
Pred. No.:	2.34e-90	1783
Score:	1101.00	186
Percent Similarity:	100.00%	0
Best Local Similarity:	100.00%	0
Query Match:	100.00%	0
DB:	3	0

US-09-993-234-6_COPY_19_204 (1-186) x US-08-815-469-1 (1-1783)

[illegible]

QY 21 PheHisLysLysIleGlyLeuPheCysCysArgGlyCysProIaGlyHisTyrLeuLys 40
 |||||
 Db 345 TTCACAGAGAATTGGTCTGTTTGTTCACAGAGCGTCCACGCGGCACTACCTGAAG 40

QY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
|||||
Db 405 GCGCCCTTGCACGGAGCCCTGCGGCACTCCACCTGCTTGTGTGTCCCAAGACACCTTC 464

QY 61 LeuAla1rPGluAsnHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80
|||||
Db 465 TTGGCCCTGGAGAACACCACCATAATTTCTGAATGTGCCCGCTGCCAGCCTGTGATGAGCAG 524

QY	81	AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys	100
Db	525	GCCTCCAGGTGGCGCTGGAGACTGTTACAGCAGTGGCCGACACCCGCTGTGGCTTAAG	584

QY	101	ProGlyTTPPhveValGluCysGlnValSerGlnCysValSerSerProPhetyrCys	120
Db	585	CCAGGCTGGTTTGTGGAGTGCACGAGTTCACCCCTTCTACTGC	644

QY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg 140
|||||
Db 645 CAACCATGCCCTAGACTCGCGGGCCCTGCACCGCCACACAGGCTACTCTGTTCGCGAGA 704

QY	141	Asp	Thr	Asp	Cys	Gly	Leu	Pro	Gly	Phe	Tyr	Glu	His	Gly	Asp	Arg	Cys	Val	Ser	160
Db	705	GAT	ACT	GACT	GTTGG	ACCTG	CCCTG	CGCTT	CTAT	ATGA	ACATG	GGC	ATG	CGCTG	CGCTG	TCC				764

QY	161	CysProThrSerThrLeuGlySerCysProGluuArgCysalaalaValaCysGlyTyrparg	180
Db	765	TGCCCCACGAGCACCCCTGGGAGCTGTCCAGAGCGCTGTGCCGCTGTCTGTGGCTGAGG	824

QY	181	GlnMetPheTrpValGln	186
Db	825	CAGATGTTCTGGGTCCAG	842

RESULT 5
US-08-928-069-5

; Sequence 5, Application US/08928069
; Patent NO. 6462176

```

; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-3 POLYPEPTIDE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:

```

ADDRESSEE: Genentech, Inc
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA

```

; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

```

```

; SOFTWARE: WinPatlin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,069
; FILING DATE: 11-Sep-1997
; CLASSIFICATION: 435
;
```

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/026943
FILING DATE: 09/23/1996
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.

REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1052R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881

```

; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1438 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: single

```

US-08-928-069-5
 TOPOLOGY: Linear
 Alignment Scores:
 Pred NO.

freq. no.:	1.73e-15	length:	1438
Score:	979.00	Matches:	169
Percent Similarity:	93.92%	Conservative:	1
Best Local Similarity:	93.37%	Mismatches:	3
Query Match:	88.92%	Indels:	8
DB:	4	Gaps:	1

US-09-993-234-6_COPY_19_204 (1-186) x US-08-928-069-5 (1-1438)

QY 1 leuleuGLyAlaarglaInglYlYThrargSerProargcysaspCysAlaGlYasp 20
 Db 431 CTGCTGGGGGCCCGGCCAGGGCGGCACCTCTAGCCCCAGGTGTGACTGTGCCGTGAC 490

QY 21 PheHisLysLysIleGlyLeuPheCysCysArgIcysProAlaGlyHisTyrLeuLys 40
 |||||
 Db 491 TTCACAGAGAGATGGTCTGTTTGTTCACAGAGCTGCCACGGGGCACTACTGAAG 550

41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
 551 GCCCCTTGACAGGAGCCCTGCGCAACTCCACCTGCTGTGTGTCCCAAGACACCTTC 610

61 LeuAlaItrpGluasnHisHisasnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80
 |||||
 611 TTGGCCTGGGAACACCACCATATTTCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAG 670

Qy	81	A l a s e r g I n V a l a l a l e u G l u a s n c y s s e t a l a V a l A l a s p t h r a r g c y s g l y c y s l y s	100
Db	671	G C C T C C A G G T G G G C C T G G A G A A C T G T T C A G C A G T G G C C G A C A C C G C G T G G C T G T A A G	730

QY 101 ProGlyTyrPheValGlnCysGlnValSerGlnCysValSerSerProphethyrCys 120
 |||||
 Db 731 CcAGGCTGTTTGGAGTGCcAGGTcAGcCAATGTGTcAGcAGTTCACcCTTCTACTGC 790

QY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArg 140
|||||
Db 791 CAACCATGCTAGACTGCGGGCCCTGCACCGCACACAGGCTACTGTTCCCGCAGA 850
QY 141 AspThrAspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSer 160
|||||
Db 851 GATACCTGACTGTGGACCTGCTGCTGCTTCTATGAACATGCGCATGGCTGCGTGTCC 910
QY 161 CysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTyrArg 180
|||||
Db 911 TGCCCCACGTAATTCCTA-----GCTGTCGTGGGATGAGG 946
QY 181 Gln 181
:::
Db 947 GAA 949
RESULT 6
US-08-828-683A-5
Sequence 5, Application US/08828683A
Patent No. 6469144
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828, 683A
FILING DATE: 31-Mar-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/625328
FILING DATE: 1-Apr-1996
APPLICATION NUMBER: 08/710802
FILING DATE: 23-Sep-1996
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1438 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-08-828-683A-5
Alignment Scores:
Pred. No.: 1.75e-79 Length: 1438
Score: 979.00 Matches: 169
Percent Similarity: 93.92% Conservative: 1
Best Local Similarity: 93.37% Mismatches: 3
Query Match: 88.92% Indels: 8
DB: 4 Gaps: 1
US-09-993-234-6_COPY_19_204 (1-186) x US-08-828-683A-5 (1-1438)
QY 1 LeuLeuGlyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAsp 20

Db 431 CTGCTGGGGCCCCGGGGCCAGGGCGGCGACTGTAGCCCCAGGTGTGACTGTGCCGCTGAC 490
QY 21 PheHisIysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlnHisTyrLeuLys 40
|||||
Db 491 TTCCACAGAGAATTTGGTCTGTTGTTGTCAGAGGCTGCCACGGGGGCACTACTGTAAG 550
QY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
|||||
Db 551 GCCCTTCACGAGAGCCCTGCGGCACTCCACCTGCTGTGTGTCCTCCAAAGACACCTTC 610
QY 61 LeuAlaTyrGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80
|||||
Db 611 TTGGCTGGGAGAACCACCATTAATTCGAATGTGCCCGCTGCGCAGGCTGTGATGAGCAG 670
QY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
|||||
Db 671 GCCTCCAGGTGGCGCTGAGAGACTGTCAGCAGTGGCCGACACCCGCTGTGCTGTAAG 730
QY 101 ProGlyTyrPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCys 120
|||||
Db 731 CCAGCTGTGTTGTGAGTGGCCAGGTACGCCAATGTGTACAGCATCACCTTCTACTGC 790
QY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArg 140
|||||
Db 791 CAACCATGCTAGACTGCGGGCCCTGCACCGCACACAGGCTACTGTTCCCGCAGA 850
QY 141 AspThrAspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSer 160
|||||
Db 851 GATACCTGACTGTGGACCTGCTGCTGCTTCTATGAACATGCGCATGGCTGCGTGTCC 910
QY 161 CysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTyrArg 180
|||||
Db 911 TGCCCCACGTAATTCCTA-----GCTGTCGTGGGATGAGG 946
QY 181 Gln 181
:::
Db 947 GAA 949
RESULT 7
US-08-928-069-2
Sequence 2, Application US/08928069
Patent No. 6462176
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-3 POLYPEPTIDE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928, 069
FILING DATE: 11-Sep-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/026943
FILING DATE: 09/23/1996
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1052R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 433 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; US-08-928-069-2

Alignment Scores:
Pred. No.: 2.66e-54 Length: 433
Score: 692.00 Matches: 133
Percent Similarity: 93.10% Conservative: 2
Best Local Similarity: 91.72% Mismatches: 6
Query Match: 62.85% Indels: 5
DB: 4 Gaps: 0

US-09-993-234-6_COPY_19_204 (1-186) x US-08-928-069-2 (1-433)

QY 1 LeuLeuGlyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
DB 1 CTGCTGGGGGGCCCGCCAGNGGCGGCACCTGTAAGCCCAAGGTGTGACTGTGCGGTGAC 60
QY 21 PheHisLysLysIleGlyLeuPheCysCysArgGlyCysProAla-GlyHisTyrLeuLy 40
DB 61 TTCACACAGAAGATTGGTCTGTTTGTTCAGAGGCTGCCACGCGGGGCACTACCTGAA 120
QY 40 sAlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPh 60
DB 121 GGCCCTTGACGAGCCCTGCGC-AACTCCACCTGCTTGTGTGTCCTCCCAAGACACCTT 179
QY 60 eLeuAlaTrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluG 80
DB 180 CTTGGCTGGGAGAACCAACCATTAATTCGATGTGCCGCTGCCAGGCTGTGATGAGCA 239
QY 80 nAlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLy 100
DB 240 GGCTCCCGAGGCGCGCTGAGAACTGTTCAGACAGTGGCCGACACCCGCTGTGCTAA 299
QY 100 sProGlyTrpPheValGluCysGln-ValSerGlnCysValSerSer-SerProPheTyr 119
DB 300 GCAGGCTGGTGTGAGAGTGCCAGGCTGACCAATGTGTACAGCAGTTTCACCTTCTAA 359
QY 120 CysGlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCys-SerAr 139
DB 360 TGCCAACCATGCTAGACTGCGGGGCTGCAACGCAACACACGCGCTAATNTGTTCCCG 419
QY 139 gArgAsp 141
DB 420 CAGAGAT 426

RESULT 8
US-08-828-683A-2

; Sequence 2, Application US/08828683A
; Patent No. 6469144

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES

; NUMBER OF SEQUENCES: 28

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 1 DNA Way

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Winpatin (Genentech)

; CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,683A
FILING DATE: 31-Mar-1997

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/625328

; FILING DATE: 1-Apr-1996

; APPLICATION NUMBER: 08/710802

; FILING DATE: 23-Sep-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Marschang, Diane L.

; REGISTRATION NUMBER: 35,600

; REFERENCE/DOCKET NUMBER: P1007P1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650/225-5416

; TELEFAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 433 base pairs

; TYPE: Nucleic Acid

; STRANDEDNESS: Single

; TOPOLOGY: Linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Alignment Scores:
Pred. No.: 2.66e-54 Length: 433
Score: 692.00 Matches: 133
Percent Similarity: 93.10% Conservative: 2
Best Local Similarity: 91.72% Mismatches: 6
Query Match: 62.85% Indels: 5
DB: 4 Gaps: 0

US-09-993-234-6_COPY_19_204 (1-186) x US-08-828-683A-2 (1-433)

QY 1 LeuLeuGlyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
DB 1 CTGCTGGGGGGCCCGCCAGNGGCGGCACCTGTAAGCCCAAGGTGTGACTGTGCGGTGAC 60
QY 21 PheHisLysLysIleGlyLeuPheCysCysArgGlyCysProAla-GlyHisTyrLeuLy 40
DB 61 TTCACACAGAAGATTGGTCTGTTTGTTCAGAGGCTGCCACGCGGGGCACTACCTGAA 120
QY 40 sAlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPh 60
DB 121 GGCCCTTGACGAGCCCTGCGC-AACTCCACCTGCTTGTGTGTCCTCCCAAGACACCTT 179
QY 60 eLeuAlaTrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluG 80
DB 180 CTTGGCTGGGAGAACCAACCATTAATTCGATGTGCCGCTGCCAGGCTGTGATGAGCA 239
QY 80 nAlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLy 100
DB 240 GGCTCCCGAGGCGCGCTGAGAACTGTTCAGACAGTGGCCGACACCCGCTGTGCTAA 299
QY 100 sProGlyTrpPheValGluCysGln-ValSerGlnCysValSerSer-SerProPheTyr 119
DB 300 GCAGGCTGGTGTGAGAGTGCCAGGCTGACCAATGTGTACAGCAGTTTCACCTTCTAA 359
QY 120 CysGlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCys-SerAr 139
DB 360 TGCCAACCATGCTAGACTGCGGGGCTGCAACGCAACACACGCGCTAATNTGTTCCCG 419
QY 139 gArgAsp 141
DB 420 CAGAGAT 426

RESULT 9

US-08-762-308-10

; Sequence 10, Application US/08762308

; Patent No. 5925548

; GENERAL INFORMATION:

; APPLICANT: Beutler, Bruce A.

; TITLE OF INVENTION: MODIFIED RECEPTORS THAT CONTINUOUSLY

; SIGNAL

Db 329 CAAGAGGCGAGTGGCGATAGTGTGTCTCCCAAGAAATATATATCCACCCTCAAAATAAT 388
QY 27 LeupheCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 46
Db 389 TCCATTGTGCTGTACCAAGTGCACAAAGAACTACTTGTACAAATGACTGTCCAGGCCCG 448
QY 47 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 66
Db 449 GGGCAGGATACGAGCTGCAGGAGTGTAGAGCGGCTCTTCCACCGCTTCAGAAACAC 508
QY 67 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluAlaSerGlnValAlaLeu 86
Db 509 CTCAGA--CACTGCTTCAGCTGCCAAATGCCGAAAGAAATGGTCAAGTGCAGATC 565
QY 87 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 106
Db 566 TCTTCTTGACAGTGCACCGGACACCGTGTGTGGCTGCAGAGAAGAACAGTACCGGCAT 625
QY 107 Cys-----GlnValSerGlnCysValSerSerProPheTyrCysGlnProCys 123
Db 626 TATTGAGTGAAGAACCTTTTCCAGTGC-----TTCAATTGCAGCCCTCTGC 670
QY 124 LeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAsp 143
Db 671 CTCAT--GGGACCGTGCAC-----CTCTCTGCAGAGAAACAGAACACC 715
QY 144 CysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThr 163
Db 716 GTGTGCACCTGCCATGCAGGTTTCTTTTAAGAGAAACAGAGTGTGTCTCTGCGCGGT 775
QY 164 SerThrLeuGlySerCysProGlu 171
Db 776 GCTGCCCCAGGT--TGCCACAGAA 796
RESULT 11
US-08-910-991-1
; Sequence 1, Application US/08910991
; Patent No. 6194177
; GENERAL INFORMATION:
; APPLICANT: Campbell, Robert K.
; APPLICANT: Jameson, Bradford A.
; APPLICANT: Chappel, Scott C.
; TITLE OF INVENTION: HYBRID PROTEINS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 22207
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,991
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/804,166
; FILING DATE: 20 February 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/011,936
; FILING DATE: 20 February 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: CAMPBELL-2B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528

; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1049 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 278..1047
; US-08-910-991-1
Alignment Scores:
Pred. No.: 1.44e-10 Length: 1049
Score: 212.50 Matches: 52
Percent Similarity: 42.26% Conservative: 19
Best Local Similarity: 30.95% Mismatches: 82
Query Match: 19.30% Indels: 15
DB: 4 Gaps: 6
US-09-993-234-6_COPY_19_204 (1-186) x US-08-910-991-1 (1-1049)
QY 7 GlnGlyLThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGly 26
Db 329 CAAGAGGCGAGTGGCGATAGTGTGTCTCCCAAGAAATATATATCCACCCTCAAAATAAT 388
QY 27 LeupheCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 46
Db 389 TCCATTGTGCTGTACCAAGTGCACAAAGAACTACTTGTACAAATGACTGTCCAGGCCCG 448
QY 47 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 66
Db 449 GGGCAGGATACGAGCTGCAGGAGTGTAGAGCGGCTCTTCCACCGCTTCAGAAACAC 508
QY 67 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluAlaSerGlnValAlaLeu 86
Db 509 CTCAGA--CACTGCTTCAGCTGCCAAATGCCGAAAGAAATGGTCAAGTGCAGATC 565
QY 87 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 106
Db 566 TCTTCTTGACAGTGCACCGGACACCGTGTGTGGCTGCAGAGAAGAACAGTACCGGCAT 625
QY 107 Cys-----GlnValSerGlnCysValSerSerProPheTyrCysGlnProCys 123
Db 626 TATTGAGTGAAGAACCTTTTCCAGTGC-----TTCAATTGCAGCCCTCTGC 670
QY 124 LeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAsp 143
Db 671 CTCAT--GGGACCGTGCAC-----CTCTCTGCAGAGAAACAGAACACC 715
QY 144 CysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSerCysProThr 163
Db 716 GTGTGCACCTGCCATGCAGGTTTCTTTTAAGAGAAACAGAGTGTGTCTCTGCGCGGT 775
QY 164 SerThrLeuGlySerCysProGlu 171
Db 776 GCTGCCCCAGGT--TGCCACAGAA 796
RESULT 12
US-08-804-166-7
; Sequence 7, Application US/08804166
; Patent No. 6193972
; GENERAL INFORMATION:
; APPLICANT: Campbell, Robert K.
; APPLICANT: Jameson, Bradford A.
; APPLICANT: Chappel, Scott C.
; TITLE OF INVENTION: HYBRID PROTEINS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.

```
COUNTRY: USA
ZIP: 22207
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,166
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/011,936
FILING DATE: 20 February 1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: CAMPBELL-2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1301 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 279..1287
US-08-804-166-7
```

```
Alignment Scores:
Pred. No.: 8.18e-10 Length: 1301
Score: 205.50 Matches: 51
Percent Similarity: 40.91% Conservative: 21
Best Local Similarity: 28.98% Mismatches: 83
Query Match: 18.66% Indels: 21
DB: 4 Gaps: 7
```

US-09-993-234-6_COPY_19_204 (1-186) x US-08-804-166-7 (1-1301)

```
QY 7 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGly 26
DB 330 CAAGAGGGCAGTGGCGATAGTGTGTCTCCCAAGAAATATATCCACCCTCAAAATAAT 389
QY 27 LeupheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 46
DB 390 TCGATTGTGTGTACCAAGTGCACAAAGGAACCTACTGTACATGACTGTCCAGGCCG 449
QY 47 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHis 66
DB 450 GGGCAGGATACGAGCTGCAGGAGTGTGAGAGCGGCTCTTACCGCTTCAGAAACCAC 509
QY 67 HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnValAlaLeu 86
DB 510 CTCAGA---CACTGCCTCAGCTGCTCCAAATGCCGAAAGAAATGGGTGAGTGGAGATC 566
QY 87 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 106
DB 567 TCTTCTTGACAGTGGACCGGACACCGTGTGTGCTGCAGGAAGAACAGTACCGCAT 626
QY 107 Cys-----GlnValSerGlnCysValSerSerSerProPheTyrCysGlnProCys 123
DB 627 TATTGAGTGAACCTTTTCCAGTGC-----TTCAATTCGACCTCTGC 671
QY 124 LeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAsp 143
DB 672 CTCAT---GGGACCGTGCAC-----CTCTCCTGCCAGAGAAACAGAACACC 716
QY 144 CysGlyThrCysLeuProGlyPheTyrGlnHisGlyAspGlyCysValSerCysProThr 163
```

```
DB 717 GTGTGCACCTGCATGACAGTTTCTTCTAAGAGAAACGAGTGTCTCTCTGT----- 770
QY 164 SerThrLeuGlySerCysProGlu-----ArgCysAlaAlaValCys 177
DB 771 -----AGTAAGTGTAGAAAGCCCTGAGTGCACAGAGTTGTGC 809
```

RESULT 13
US-08-910-991-7
Sequence 7, Application US/08910991
Patent No. 6194177

GENERAL INFORMATION:
APPLICANT: Campbell, Robert K.
APPLICANT: Jameson, Bradford A.
APPLICANT: Chapel, Scott C.
TITLE OF INVENTION: HYBRID PROTEINS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 22207
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,991
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/804,166
FILING DATE: 20 February 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/011,936
FILING DATE: 20 February 1996
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: CAMPBELL-2B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1301 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 279..1287
US-08-910-991-7

```
Alignment Scores:
Pred. No.: 8.18e-10 Length: 1301
Score: 205.50 Matches: 51
Percent Similarity: 40.91% Conservative: 21
Best Local Similarity: 28.98% Mismatches: 83
Query Match: 18.66% Indels: 21
DB: 4 Gaps: 7
```

US-09-993-234-6_COPY_19_204 (1-186) x US-08-910-991-7 (1-1301)

```
QY 7 GlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPheHisLysIleGly 26
DB 330 CAAGAGGGCAGTGGCGATAGTGTGTCTCCCAAGAAATATATCCACCCTCAAAATAAT 389
QY 27 LeupheCysCysArgGlyCysProAlaGlyHisTyrLeuLysAlaProCysThrGluPro 46
```

Db 390 TCGATTGCTGTACCAAGTGCACCAAGAACTACTGTACAAATGACTGTCCAGGCCG 449
QY 47 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGlnAsnHis 66
Db 450 GGGCAGGATACGAGCTGACGAGGAGTGTGAGAGCGGCTCTCCACCGCTTCAGAAAACAC 509
QY 67 HisAsnSerGlyCysAlaArgCysGlnAlaCysAspGlnAlaSerGlnValAlaLeu 86
Db 510 CTCAGA---CACTGCCTCAGCTGCTCCAATGCGGAAGAAATGGGTCAAGTGGAGATC 566
QY 87 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 106
Db 567 TCTTCTGTGACAGTGGACCGGACACCGTGTGTGGCTGCAGGAAGAACAGTACCGGCAT 626
QY 107 Cys-----GlnValSerGlnCysValSerSerProPheTrpCysGlnProCys 123
Db 627 TATTGGAGTGAACCTTTTCCAGTGC-----TTCAATTGACAGCTCTGTC 671
QY 124 LeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArgAspThrAsp 143
Db 672 CTCAT---GGGACCGTGCAC-----CTCTCCTGCCAGAGAAACAGAACACAC 716
QY 144 CysGlyThrCysLeuProGlyPheTrpGluHisGlyAspGlyCysValSerCysProThr 163
Db 717 GTGTGACCTGCATGACAGTTTCTTCTAAGAGAAACAGAGTGTCTCTCTG----- 770
QY 164 SerThrLeuGlySerCysProGlu-----ArgCysAlaAlaValCys 177
Db 771 -----AGTAACTGTAGAAAGCCTGGAGTGCACGAGTGTGTC 809

RESULT 14
US-08-050-319B-47
; Sequence 47, Application US/08050319B
; Patent No. 5633145

GENERAL INFORMATION:
APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M. Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Receptor
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Reed & Robbins
STREET: 635 Bryant Street
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94301

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/050,319B
FILING DATE: 10-May-1993
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Robbins, Roberta L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150-0030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 600 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
FEATURE:
NAME/KEY: CDS

LOCATION: 1..597
US-08-050-319B-47

Alignment Scores:
Pred. No.: 3.26e-10 Length: 600
Score: 205.00 Matches: 53
Percent Similarity: 40.88% Conservative: 21
Best Local Similarity: 29.28% Mismatches: 83
Query Match: 18.62% Indels: 24
DB: 1 Gaps: 8

US-09-993-234-6_COPY_19_204 (1-186) x US-08-050-319B-47 (1-600)

QY 2 LeuGlyAlaArgAlaGlnGlyThrArgSerProArgCysAspCysAlaGlyAspPhe 21
Db 100 CTAGGGACAGGAGAGAG-----AGAGATAGTGTGTGTCCACAGAAATATATATC 150
QY 22 HisLysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTrpLeuLysAla 41
Db 151 CACCCGCAAAATAATTGATTTGCTGTACCAAGTGCACAAAGAACCTACTGTACAAAT 210
QY 42 ProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeu 61
Db 211 GACTGTCCAGGCGCGGGGAGGATACGACTGCAGGAGTGTGAGAGCGGCTCTTCACC 270
QY 62 AlaTrpGlnAsnHisHisAsnSerGlyCysAlaArgCysGlnAlaCysAspGlnAla 81
Db 271 GCTTCAGAAACCACTCAGAC---CACTGCCTCAGCTGCTCCAATGCCGAAAGAAATG 327
QY 82 SerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysPro 101
Db 328 GGTCAAGTGGAGATCTCTTCTTGCACGTGACCGGACCGGACACCGTGTGTGCTGCAGAG 387
QY 102 GlyTrpPheValGluCys-----GlnValSerGlnCysValSerSerProPhe 118
Db 388 AACCACTACCGGCAATTATTGAGTGAACCTTTTCCAGTGC-----TTC 432
QY 119 TyrCysGlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSer 138
Db 433 AATTGCAGCTCTGCTCAAT---GGGACCGTGCAC-----CTCTCCTGCCAG 477
QY 139 ArgArgAspThrAspCysGlyThrCysLeuProGlyPheTrpGluHisGlyAspGlyCys 158
Db 478 GAGAAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTCTAAGAGAAACAGAGTGT 537
QY 159 ValSerCysProThrSerThrLeuGlySerCysProGlu-----ArgCysAlaAlaVal 176
Db 538 GTCTCTGT-----AGTAACTGTAGAAAGCCTGGAGTGCACGAGTGTG 582
QY 177 Cys 177
Db 583 TGC 585

RESULT 15
US-08-465-982-47
; Sequence 47, Application US/08465982
; Patent No. 5863786

GENERAL INFORMATION:
APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M. Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Receptor
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Reed & Robbins
STREET: 635 Bryant Street
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94301

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible


```
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,982
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/050,319
FILING DATE: 10-May-1993
ATTORNEY/AGENT INFORMATION:
NAME: Robbins, Roberta L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150-0030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 600 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..597
US-08-465-982-47
```

```
Alignment Scores:
Pred. No.: 3,26e-10 Length: 600
Score: 205.00 Matches: 53
Percent Similarity: 40.88% Conservative: 21
Best Local Similarity: 29.28% Mismatches: 83
Query Match: 18.62% Indels: 24
DB: 2 Gaps: 8
```

US-09-993-234-6_COPY_19_204 (1-186) x US-08-465-982-47 (1-600)

```
OY 2 LeuGlyAlaArgAlaGlnGlyThrArgSerProArgCysAspCysAlaGlyAspPhe 21
Db 100 CTAGGGGACAGGAGAGAG-----AGAGATAGTGTGTGTCCACAGGAAATATATC 150
OY 22 HisLysLysIleGlyLeuPheCysArgGlyCysProIleGlyHisTyrLeuLysAla 41
Db 151 CACCCTCAAAATATTCGATTGCTGTACCAAGTGCACAAAGAACCTACTGTACCAAT 210
OY 42 ProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeu 61
Db 211 GACTGTCCAGGCCCGGGGAGATACGACTGCAGGAGGTGAGAGCGGCTCCTTACC 270
OY 62 AlaTrpGluAsnHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAla 81
Db 271 GCTTCAGAAACACACCTCAGA---CACTGCCTCAGCTGCTCCAATGCGGAAAGAAATG 327
OY 82 SerGlnValAlaLeuGluAsnGlySerAlaValAlaAspThrArgCysGlyCysLysPro 101
Db 328 GGTCCAGGTGAGATCTCTCTTGCACAGTGACCGGACACCGTGTGTGCTGCAGGAAG 387
OY 102 GlyTrpPheValGluCys-----GlnValSerGlnCysValSerSerSerProPhe 118
Db 388 AACCAAGTACCGGCATTATGAGTGAACCAACCTTTCCAGTGC-----TTC 432
OY 119 TyrCysGlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSer 138
Db 433 AATTGACGCTCTGCTCAAT---GGGACCGTGCAC-----CTCTCCTGCCAG 477
OY 139 ArgArgAspThrAspCysGlyThrCysLeuProGlyPheTyrGlnHisGlyAspGlyCys 158
Db 478 GAGAAACAGAACACCGTGTGCACCTGCATGACAGTTTCTTCTAAAGAGAAACGAGTGT 537
OY 159 ValSerCysProThrSerThrLeuGlySerCysProGlu-----ArgCysAlaAlaVal 176
Db 538 GTCTCCTGT-----AGTAACTGTAAAGAAAGCCTGAGTGCACGAAAGTGTG 582
```

OY 177 Cys 177
Db 583 TGC 585

Search completed: April 6, 2003, 23:29:58
Job time : 37.3989 secs

150

THIS PAGE BLANK (USPTO)

THIS PAGE BLANK (USPTO)

GenCore version 5.1.4-p5-4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 6, 2003, 21:08:18 ; Search time 70.8236 Seconds
(without alignments)
2303.655 Million cell updates/sec

Title: US-09-993-234-6_COPY_19_204
Perfect score: 1101
Sequence: 1 LLGARAQGGTRSPRCACG.....GSCPERCAVCGWRQMFVQ 186

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 593429 seqs, 438583890 residues

Total number of hits satisfying chosen parameters: 1186858

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=x1h
-Q=/cgn2_1/USPTO_spool/US09993234/runat_27032003_115459_15466/app_query.fasta_1.2346
-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blsum62
-TRANS=human40.cdi -LIST=45 -DOCLIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09993234.@CGN_1_1_249 @runat_27032003_115459_15466
-NCPU=6 -ICPU=3 -NO_XLPHY -NO_MMMP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1101	100.0	1254	10 US-09-333-966-3	Sequence 3, Appl1
2	1101	100.0	1634	9 US-10-081-280-9	Sequence 9, Appl1
3	1101	100.0	1634	9 US-10-112-793-9	Sequence 9, Appl1
4	1101	100.0	1634	9 US-10-112-193-11	Sequence 11, Appl1

5	1101	100.0	1634	10 US-09-993-234-9	Sequence 9, Appl1
6	1101	100.0	1783	10 US-09-333-966-1	Sequence 1, Appl1
7	1077	97.8	1743	9 US-09-954-531-1389	Sequence 1389, Ap
8	979	88.9	816	10 US-09-964-824A-292	Sequence 292, Ap
9	979	88.9	1438	9 US-10-081-280-5	Sequence 5, Appl1
10	979	88.9	1438	9 US-10-112-793-5	Sequence 5, Appl1
11	979	88.9	1438	9 US-10-112-193-5	Sequence 5, Appl1
12	979	88.9	1438	10 US-09-884-733-5	Sequence 5, Appl1
13	979	88.9	1438	10 US-09-993-234-5	Sequence 5, Appl1
14	767	69.7	10797	9 US-10-092-154-1577	Sequence 1577, Ap
15	767	69.7	10797	10 US-09-764-847-1577	Sequence 1577, Ap
16	692	62.9	433	9 US-10-081-280-2	Sequence 2, Appl1
17	692	62.9	433	9 US-10-112-793-2	Sequence 2, Appl1
18	692	62.9	433	9 US-10-112-193-2	Sequence 2, Appl1
19	692	62.9	433	10 US-09-884-733-2	Sequence 2, Appl1
20	692	62.9	433	10 US-09-993-234-2	Sequence 2, Appl1
21	216	19.6	2130	10 US-09-917-800A-1601	Sequence 1601, Ap
22	212.5	19.3	1049	10 US-09-756-186-1	Sequence 1, Appl1
23	212	19.3	5870	10 US-09-838-718A-8	Sequence 8, Appl1
24	208	18.9	1674	9 US-09-359-595-12	Sequence 12, Appl1
25	205.5	18.7	1301	10 US-09-756-186-7	Sequence 7, Appl1
26	203.5	18.5	570	9 US-09-899-429A-17	Sequence 17, Appl1
27	203.5	18.5	600	9 US-09-899-429A-11	Sequence 11, Appl1
28	203.5	18.5	1202	10 US-09-756-186-3	Sequence 3, Appl1
29	203	18.4	519	9 US-09-899-429A-15	Sequence 15, Appl1
30	203	18.4	549	9 US-09-899-429A-9	Sequence 9, Appl1
31	203	18.4	603	9 US-09-899-429A-13	Sequence 13, Appl1
32	203	18.4	633	9 US-09-899-429A-7	Sequence 7, Appl1
33	203	18.4	1334	9 US-09-898-234-11	Sequence 11, Appl1
34	203	18.4	1334	9 US-09-792-356-11	Sequence 11, Appl1
35	203	18.4	1334	10 US-09-899-422-11	Sequence 11, Appl1
36	203	18.4	1368	9 US-09-898-234-1	Sequence 1, Appl1
37	203	18.4	1368	9 US-09-899-429A-1	Sequence 1, Appl1
38	203	18.4	1368	9 US-09-792-356-1	Sequence 1, Appl1
39	203	18.4	1368	10 US-09-899-422-1	Sequence 1, Appl1
40	203	18.4	2111	10 US-09-880-107-2360	Sequence 1, Appl1
41	203	18.4	2141	9 US-09-898-234-16	Sequence 16, Appl1
42	203	18.4	2141	9 US-09-899-429A-26	Sequence 26, Appl1
43	203	18.4	2141	9 US-09-792-356-16	Sequence 16, Appl1
44	203	18.4	2141	10 US-09-899-422-16	Sequence 16, Appl1
45	203	18.4	2175	12 US-10-120-397-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-09-333-966-3
Sequence 3, Application US/09333966
Patent No. US20020009773A1
GENERAL INFORMATION:
APPLICANT: YU, Guo-Liang
APPLICANT: NI, Jian
APPLICANT: Dixit, Vishva
APPLICANT: Gentz, Reiner L.
APPLICANT: Dillon, Patrick J.
TITLE OF INVENTION: Death Domain Containing Receptors
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/333,966
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/815,469
FILING DATE:
APPLICATION NUMBER: No. US20020009773A1 yet Assigned
FILING DATE: 06-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,711
FILING DATE: 17-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,285
FILING DATE: 12-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1254 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1251
US-09-333-966-3

Alignment Scores:
Pred. No.: 1.5e-103 Length: 1254
Score: 1101.00 Matches: 186
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-993-234-6_COPY_19_204 (1-186) x US-09-333-966-3 (1-1254)

QY 1 LeuLeuGIyAlaAArgAlaGInGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
DB 55 CTGCTGGGGGGCCGGCCAGGGCGCACATCTAGCCCGAGGTGTGACTGTGCCGGTGAC 114
QY 21 PheHisLysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLys 40
DB 115 TTCCACAAGAAGATTGGTCTGTTTGTTCAGAGGCTGCCAGCGGGGCACTACCTGAAG 174
QY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
DB 175 GCGCCCTGCACGAGCCCTGCGGCACTCACCCTGCTGTGTCCTCCCAAGACACCTTC 234
QY 61 LeuAlaTPrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80
DB 235 TTGGCCCTGGGAGAACCACTAATTCTGATGTGCCCGCTGCCAGGCTGTGATGAGCAG 294
QY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
DB 295 GCCTCCAGGTGGCGCTGGAGAACTGTTCAAGCAGTGGCCGACACCCGCTGTGCTGAAG 354
QY 101 ProGlyTPrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCys 120
DB 355 CCAGGCTGGTTGTGAGTGCAGGTCAAGCAATGTGTACAGCACTACCTTCTACTGC 414
QY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg 140
DB 415 CAACCAATGCTAGACTGCGGGGCCCTGCACCGCCACACACGCGTACTCTGTTCCGACAG 474
QY 141 AspThrAspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSer 160
DB 475 GATACTGACTGTGGGACCTGCTGCTGCTTCTATGAACATGGGATGGCTGCGTGTCC 534
QY 161 CysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTyrParg 180

DB 535 TGCCCCACGAGACACCTGGGAGCTGTCCAGAGCGCTGTGCTGTGCTGAGG 594
QY 181 GlnMetPheTPrpValGln 186
DB 595 CAGATGTTCTGGGTCCAG 612

RESULT 2
US-10-081-280-9

Sequence 9, Application US/10081280
Patent No. US20020165157A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/081,280

FILING DATE: 21-Feb-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/829,270

FILING DATE: 31-Mar-1997

ATTORNEY/AGENT INFORMATION:

NAME: Marschang, Diane L.

REGISTRATION NUMBER: 35,600

REFERENCE/DOCKET NUMBER: P1007R1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-5416

TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 1634 base pairs

TYPE: Nucleic Acid

STRANDEDNESS: Single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-10-081-280-9

Alignment Scores:
Pred. No.: 2.06e-103 Length: 1634
Score: 1101.00 Matches: 186
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-993-234-6_COPY_19_204 (1-186) x US-10-081-280-9 (1-1634)

QY 1 LeuLeuGIyAlaAArgAlaGInGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
DB 143 CTGCTGGGGGCCCGGGCCAGGGCGCACATCTAGCCCGAGGTGTGACTGTGCCGTGAC 202
QY 21 PheHisLysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLys 40
DB 203 TTCCACAAGAAGATTGGTCTGTTTGTTCAGAGGCTGCCAGCGGGGCACTACCTGAAG 262
QY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
DB 263 GCGCCCTGCACGAGCCCTGCGGCACTCACCCTGCTGTGTCCTCCCAAGACACCTTC 322

QY 61 LeuAlaTrpGluAsnHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80
|||||
Db 323 TTGGCCTGGAGAACCACTAATTTCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAG 382
QY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
|||||
Db 383 GCCTCCAGGTGGCGCTGGAGAACTGTTCAGACAGTGGCCGACACCCGCTGTGGCTGTAG 442
QY 101 ProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerProPheTrpCys 120
|||||
Db 443 CCAGGCTGTTGTGGAGTGCAGGTCCAGCCAAATGTGTACAGTTCCACCCCTTCTACTGC 502
QY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg 140
|||||
Db 503 CAACCATGCTAGACTGGGGGCCCTGCACCGCCACACAGGCTACTCTGTCCCGCAGA 562
QY 141 AspThrAspCysGlyThrCysLeuProGlyPheTrpGluHisGlyAspGlyCysValSer 160
|||||
Db 563 GATACTGACTGTGGAGCTGCCCTGCCCTTCTATGACATGGCGATGGCTGCCGTGCC 622
QY 161 CysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTrpArg 180
|||||
Db 623 TGCCCCACGAGCACCCCTGGGGAGCTGTCCAGAGCGCTGTGCCGCTGTGGAGG 682
QY 181 GlnMetPheTrpValGln 186
|||||
Db 683 CAGATGTTCTGGGTCCAG 700

RESULT 3
US-10-112-793-9

; Sequence 9, Application US/10112793
; Publication No. US20020192729A1

GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
; NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/112,793
; FILING DATE: 28-Mar-2002
; CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/828,683A
; FILING DATE: 31-Mar-1997
; APPLICATION NUMBER: 08/625328
; FILING DATE: 1-Apr-1996
; APPLICATION NUMBER: 08/710802
; FILING DATE: 23-Sep-1996

ATTORNEY/AGENT INFORMATION:

; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1007P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 1634 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-10-112-793-9

Alignment Scores:

Pred. No.:	2,06e-103	Length:	1634
Score:	1101.00	Matches:	186
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-993-234-6_COPY_19_204 (1-186) x US-10-112-793-9 (1-1634)

QY 1 LeuLeuGlyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
|||||
Db 143 CTGCTGGGGGGCCCCGGCCAGGGCGGCACCTCGTAGCCCCAGCTGTGACTGTGCCGTGAC 202
QY 21 PheHisLysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTrpLeuLys 40
|||||
Db 203 TTCCACAGAAGATTGCTGTTTGTGTTCAGAGGCTGCCAGCGGGCAGCTTACTGAG 262
QY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
|||||
Db 263 GCCCTTGACAGGAGCCCTGGCGCAACTCCACCTGCTGTGTGTGCCCAAGACACCTTCC 322
QY 61 LeuAlaTrpGluAsnHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80
|||||
Db 323 TTGGCCTGGAGAACCACTAATTTCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAG 382
QY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
|||||
Db 383 GCCTCCAGGTGGCGCTGGAGAACTGTTCAGACAGTGGCCGACACCCGCTGTGGCTGTAG 442
QY 101 ProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerProPheTrpCys 120
|||||
Db 443 CCAGGCTGTTGTGGAGTGCAGGTCCAGCAATGTGTACAGATTCCACCCCTTCTACTGC 502
QY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg 140
|||||
Db 503 CAACCATGCTAGACTGGGGGCCCTGCACCGCCACACAGGCTACTCTGTGCCCGCAGA 562
QY 141 AspThrAspCysGlyThrCysLeuProGlyPheTrpGluHisGlyAspGlyCysValSer 160
|||||
Db 563 GATACTGACTGTGGAGCTGCCCTGCCCTTCTATGACATGGCGATGGCTGCCGTGCC 622
QY 161 CysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTrpArg 180
|||||
Db 623 TGCCCCACGAGCACCCCTGGGGAGCTGTCCAGAGCGCTGTGCCGCTGTGGAGG 682
QY 181 GlnMetPheTrpValGln 186
|||||
Db 683 CAGATGTTCTGGGTCCAG 700

RESULT 4
US-10-112-193-11

; Sequence 11, Application US/10112193
; Publication No. US20030004313A1

GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-3 POLYPEPTIDE
; NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/112,193
FILING DATE: 28-Mar-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/928,069
FILING DATE: 11-Sep-1997
APPLICATION NUMBER: 60/026943
FILING DATE: 23-Sep-1996
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1052R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1634 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-112-193-11

Alignment Scores:
Pred. No.: 2.06e-103 Length: 1634
Score: 1101.00 Matches: 186
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-993-234-6_COPY_19_204 (1-186) x US-10-112-193-11 (1-1634)

QY 1 LeuLeuGlyAlaArgAlaGlnGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
Db 143 CTGCTGGGGCCCCGGCCAGGGGGCGGACTGTCAGCCCGAGGTGACTGTGCCGGTGAC 202
QY 21 PheHisLysLysIleGlyLeuPheCysArgGlyCysProAlaGlyHisTyrLeuLys 40
Db 203 TTCCACAAGAAGATTGCTGTTTGTTCAGAGGCTGCCCCAGCGGGGCACCTACCTGAAG 262
QY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
Db 263 GCCCCTGCACGAGAGCCCTGGCGCACTCCACCTGCTGTGTCTCCCAAGACACCTTC 322
QY 61 LeuAlaTrrpGluAsnHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80
Db 323 TTGGCCTGGGAGAACCACTAATCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAG 382
QY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
Db 383 GCCTCCAGGTGGCGCTGGAGAACTGTTCAGCAGTGGCCGACACCGCTGTGGCTGAAG 442
QY 101 ProGlyTrrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCys 120
Db 443 CCAGGCTGGTTTGGAGTGGCCAGGTCAACCAATGTGTACAGCACTTCAACCTTACTGC 502
QY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg 140
Db 503 CAACCATGCTAGACTGGGGGCGCTGCACCGCCACACAGGCTACTGTCTCCCGCAGA 562
QY 141 AspThrAspCysGlyThrCysLeuProGlyPheTyrGlnHisGlyAspGlyCysValSer 160
Db 563 GATACTGACTGTGGACCTGCCCTGGCTTCTATGACATGGCGATGGCTGCTGCC 622
QY 161 CysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTrrpArg 180
Db 623 TGGCCCAAGACACCTGGGGAGCTGTCCAGAGCGCTGTGCCGCTGTCTGTGGCTGAGG 682
QY 181 GlnMetPheTrrpValGln 186
Db 683 CAGATGTTCTGGGTCAG 700

RESULT 5

US-09-993-234-9
Sequence 9, Application US/09993234
Patent No. US20020146768A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/993,234
FILING DATE: 19-No. US20020146768A1-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/828,683
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:

NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007P1
TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-5416
TELEFAX: 415/952-9881
TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 1634 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-09-993-234-9

Alignment Scores:
Pred. No.: 2.06e-103 Length: 1634
Score: 1101.00 Matches: 186
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-993-234-6_COPY_19_204 (1-186) x US-09-993-234-9 (1-1634)

QY 1 LeuLeuGlyAlaArgAlaGlnGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
Db 143 CTGCTGGGGCCCCGGCCAGGGGGCGGACTGTCAGCCCGAGGTGACTGTGCCGGTGAC 202
QY 21 PheHisLysLysIleGlyLeuPheCysArgGlyCysProAlaGlyHisTyrLeuLys 40
Db 203 TTCCACAAGAAGATTGCTGTTTGTTCAGAGGCTGCCAGCGGGGCACCTACCTGAAG 262
QY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
Db 263 GCCCCTGCACGAGAGCCCTGGCGCACTCCACCTGCTGTGTCTCCCAAGACACCTTC 322
QY 61 LeuAlaTrrpGluAsnHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80
Db 323 TTGGCCTGGGAGAACCACTAATCTGAATGTGCCCGCTGTGATGAGCAG 382
QY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
Db 811 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100

Db 383 GCCTCCAGAGTGGCGCTGGAGAACTGTTACAGCAGTGGCCGACACCCGCTGTGGCTGTAG 442
QY 101 ProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCys 120
Db 443 CCAGGCTGGTTGTGGAGTGGCCAGGTCAGCCAAATGTGTACAGCAGTTCACCCCTTCTACTGC 502
QY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg 140
Db 503 CAACCATGCCCTAGACTGGGGGGCCCTGCACCCGCCACACAGGCTACTGTGTCGCCGAGA 562
QY 141 AspThrAspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSer 160
Db 563 GATACCTGACTGTGGAGCTGGCTGCTGCTTCTATGAAATGGCGATGGCTGCTGCTGCC 622
QY 161 CysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTrpArg 180
Db 623 TGCCCCACGACACCTGGGGAGCTGTCCAGAGCGCTGTGCCGCTGTGTGGCTGGAGG 682
QY 181 GlnMetPheTrpValGln 186
Db 683 CAGATGTCTGTGGTCCAG 700

RESULT 6

US-09-333-966-1

; Sequence 1, Application US/09333966

; Patent No. US2002000973A1

; GENERAL INFORMATION:

; APPLICANT: Yu, Guo-Liang

; APPLICANT: Ni, Jian

; APPLICANT: Dixit, Vishva

; APPLICANT: Gentz, Reiner L.

; APPLICANT: Dillon, Patrick J.

; TITLE OF INVENTION: Death Domain Containing Receptors

; NUMBER OF SEQUENCES: 17

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.

; STREET: 1100 New York Ave., NW, Suite 600

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20005-3934

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/333,966

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/815,469

; FILING DATE:

; APPLICATION NUMBER: No. US2002000973A1 yet Assigned

; FILING DATE: 06-FEB-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/028,711

; FILING DATE: 17-OCT-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/013,285

; FILING DATE: 12-MAR-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Steffe, Eric R.

; REGISTRATION NUMBER: 36,688

; REFERENCE/DOCKET NUMBER: 1488.0310003/EXS/KRM

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-371-2600

; TELEFAX: 202-371-2540

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1783 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 198..1481
US-09-333-966-1

Alignment Scores:

Pred. No.:	2,28e-103	length:	1783
Score:	1101.00	Matches:	186
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-09-993-234-6_COPY_19_204 (1-186) x US-09-333-966-1 (1-1783)

QY 1 LeuLeuGlyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAsp 20

Db 285 CTGCTGGGGGGCCCCGGCCAGGGGGCAGCTCGTAGCCCCAGGTGTGACTGTGCCGCTGAC 344

QY 21 PheHisLysLysIleGlyLeuPheCysArgGlyCysProAlaGlyHisTyrLeuLys 40

Db 345 TTCCACAAGAAGATTGGTCTGTTTGTTCAGAGAGCTGCCACGGGGGCACTACTCTGAAG 404

QY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60

Db 405 GCCCTTGCACGGAGCCCTGCCGCACTCCACCTGCTGTGTGTCCCAAGACACCTTC 464

QY 61 LeuAlaTrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80

Db 465 TTGGCTGGGAGAACCACTAATTTCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAG 524

QY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100

Db 525 GCCTGCCAGGTGGCGCTGGAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGCTGTAG 584

QY 101 ProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCys 120

Db 585 CCAGGCTGGTTGTGGAGTGGCCAGGTCCAGCAATGTGTACAGCAGTTCACCCCTTCTACTGC 644

QY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg 140

Db 645 CAACCATGCCCTAGACTGGGGGGCCCTGCACCCGACACACGGCTACTCTGTCCCGCAGA 704

QY 141 AspThrAspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSer 160

Db 705 GATACCTGACTGTGGAGCTGCTGCTGCTGCTTCTATGAACATGGCGATGGCTGCTGCC 764

QY 161 CysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTrpArg 180

Db 765 TGCCCCACGACACCCCTGGGAGGTGTCCAGAGCGCTGTGCCGCTGTGTGGCTGAGAG 824

QY 181 GlnMetPheTrpValGln 186

Db 825 CAGATGTCTGTGGTCCAG 842

Db 825 CAGATGTCTGTGGTCCAG 842

RESULT 7

US-09-954-531-1389

; Sequence 1389, Application US/09954531

; Patent No. US20020165180A1

; GENERAL INFORMATION:

; APPLICANT: Weaver, Zoe

; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C

; TITLE OF INVENTION: Gene Sets

; FILE REFERENCE: 689290-77

; CURRENT APPLICATION NUMBER: US/09/954,531

; CURRENT FILING DATE: 2002-05-02

; PRIOR APPLICATION NUMBER: US/60/233,133

; PRIOR FILING DATE: 2000-09-18

; PRIOR APPLICATION NUMBER: US/60/234,009

; PRIOR FILING DATE: 2000-09-20

; PRIOR APPLICATION NUMBER: US/60/234,034

```
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,509
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US/60/234,567
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 1392
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1389
; LENGTH: 1743
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-531-1389

Alignment Scores:
Pred. No.: 6,25e-101      Length: 1743
Score: 1077.00           Matches: 182
Percent Similarity: 98.91% Conservative: 0
Best Local Similarity: 98.91% Mismatches: 2
Query Match: 97.82%      Indels: 0
DB: 9                    Gaps: 0

US-09-993-234-6_COPY_19_204 (1-186) x US-09-954-531-1389 (1-1743)

QY 1 LeuLeuGLyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
Db 123 CTGCTGGGGGGCCCGCCAGGGCGGACACGTAGCCCCAGGTGTGACTGTGCCGGTGAC 182
QY 21 PheHisLysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLys 40
Db 183 TTCCACAAGAAGATTGCTGTGTTGTGTCAGAGGCTGCCACAGCGGGGCACCTAGAG 242
QY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
Db 243 GCCCTTGACAGGAGCCCTGCGGCACTCCACCTGCTGTGTGTCGCCAAGACACCTTC 302
QY 61 LeuAlaTrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80
Db 303 TTGGCCTGGGAGAACCAACATAATTCTGATGTGCCCGCTGCCAGGCTGTGATGAGCAG 362
QY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
Db 363 GCCTCCAGGTGGCGCTGGAGAACCTGTTCAGCAGTGGCCGACACCCCGCTGTGCTAAG 422
QY 101 ProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCys 120
Db 423 CCAGGCTGTGTTGGAGTGGCCAGGTGACCAATGTGTACAGCAGTTCACCTTCTACTGC 482
QY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg 140
Db 483 CAACCATGCTAGACTGCGGGGCCCTGCACCGCCACACACGCGTACTGTGTCCGCAGA 542
QY 141 AspThrAspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSer 160
Db 543 GATACCTGACTGTGGACCTGCTGCTGCTTCTATGAACATGGCGATGGCTGCTGCC 602
QY 161 CysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTyrParg 180
Db 603 TGCCCCAGAGACACCTGGGAGAGCTGCCAGAGAGCGGTGCGCGCTGTGTGGCTGAGG 662
QY 181 GlnMetPheTrp 184
Db 663 CAGAGTAGGTGG 674

RESULT 8
US-09-964-824A-292
; Sequence 292, Application US/09964824A
; Patent No. US20020102531A1
; GENERAL INFORMATION:
; APPLICANT: Horrigan, Stephen
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; FILE REFERENCE: 689290-73
; CURRENT APPLICATION NUMBER: US/09/964,824A
```

```
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/60/236,033
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,032
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,028
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 583
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 292
; LENGTH: 816
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-824A-292

Alignment Scores:
Pred. No.: 2,53e-91      Length: 816
Score: 979.00           Matches: 169
Percent Similarity: 93.92% Conservative: 1
Best Local Similarity: 93.37% Mismatches: 3
Query Match: 88.92%      Indels: 8
DB: 10                  Gaps: 1

US-09-993-234-6_COPY_19_204 (1-186) x US-09-964-824A-292 (1-816)

QY 1 LeuLeuGLyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
Db 39 CTGCTGGGGGGCCCGCCAGGGCGGACACGTAGCCCCAGGTGTGACTGTGCCGGTGAC 98
QY 21 PheHisLysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLys 40
Db 99 TTCCACAAGAAGATTGCTGTGTTGTGTCAGAGGCTGCCACAGCGGGGCACCTAGAG 158
QY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
Db 159 GCCCTTGACAGGAGCCCTGCGGCACTCCACCTGCTGTGTGTCGCCAAGACACCTTC 218
QY 61 LeuAlaTrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80
Db 219 TTGGCCTGGGAGAACCAACATAATTCTGATGTGCCCGCTGCCAGGCTGTGATGAGCAG 278
QY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
Db 279 GCCTCCAGGTGGCGCTGGAGAACCTGTTCAGCAGTGGCCGACACCCCGCTGTGCTAAG 338
QY 101 ProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCys 120
Db 339 CCAGGCTGTGTTGGAGTGGCCAGGTGACCAATGTGTTCAGCAGTTCACCTTCTACTGC 398
QY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg 140
Db 399 CAACCATGCTAGACTGCGGGGCCCTGCACCGCCACACACGCGTACTGTGTCCGCAGA 458
QY 141 AspThrAspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSer 160
Db 459 GATACCTGACTGTGGACCTGCTGCTGCTTCTATGAACATGGCGATGGCTGCTGCC 518
QY 161 CysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTyrParg 180
Db 519 TGCCCCAGGTAAATTCCTA-----GCTGTGCTGGATGAGG 554
QY 181 Gln 181
Db 555 GAA 557

RESULT 9
US-10-081-280-5
; Sequence 5, Application US/10081280
; Patent No. US20020165157A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-2 L1 AND Apo-3 POLYPEPTIDES
; NUMBER OF SEQUENCES: 11
```


CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/081,280
FILING DATE: 21-Feb-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/829,270
FILING DATE: 31-Mar-1997
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5416
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1438 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-081-280-5
Alignment Scores:
Pred. No.: 4.97e-91 Length: 1438
Score: 979.00 Matches: 169
Percent Similarity: 93.92% Conservative: 1
Best Local Similarity: 93.37% Mismatches: 3
Query Match: 88.92% Indels: 8
DB: 9 Gaps: 1
US-09-993-234-6_COPY_19_204 (1-186) x US-10-081-280-5 (1-1438)
OY 1 LeuLeuGlyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
Db 431 CTGCTGGGGGGCCGGCCGAGGGGCGGCACTGCTAGCCCGGAGTGTGACTGTGCCGGTGAC 490
OY 21 PheHisLysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlnHisTyrLeuLys 40
Db 491 TTCCACACAGAAGATTGGTCTGTTTGTTCAGAGAGCGTGCACCGGGGCGACTACCTGAAG 550
OY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
Db 551 GCCCCTTGACAGGAGCCCTGCGGCACTCCACCTGCTGTGTCTCCCAAGACACCTTC 610
OY 61 LeuAlaTyrGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80
Db 611 TTGGCCTGGAGAACCACTAATTCTGAATGTGCCCGCTGCCAGGCGCTGTGATGAGCAG 670
OY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
Db 671 GCCTCCAGGTGGCGGTGGAGACTGTTTCAGCAGTGGCCGACACCCGCTGTGGCTGAAG 730
OY 101 ProGlyTyrPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCys 120
Db 731 CCAGGCTGGTGTGTGAGTGCAGGTCCAGCCAAATGTGTACAGATTACACCTTCTACTGC 790
OY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg 140
Db 791 CAACCATGCTAGACTGGGGGGCCGTGCACCGGCACACACGCGCTACTCTGTTCGCCGAGA 850

OY 141 AspThrAspCysGlyThrCysLeuProGlyPheTyrGlnHisGlyAspGlyCysValSer 160
Db 851 GATACGTGACTGTGGACCTGCGCTGCGCTTCTATGAACATGCGCATGCGTGTCC 910
OY 161 CysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTyrArg 180
Db 911 TGCCCGCAGTAATTCCTA-----GCTGTCTGGGATGAGAG 946
OY 181 Gln 181
Db 947 GAA 949
RESULT 10
US-10-112-793-5
Sequence 5, Application US/10112793
Publication No. US20020192729A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/112,793
FILING DATE: 28-Mar-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/828,683A
FILING DATE: 31-Mar-1997
APPLICATION NUMBER: 08/625328
FILING DATE: 1-Apr-1996
APPLICATION NUMBER: 08/710802
FILING DATE: 23-Sep-1996
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1438 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-112-793-5
Alignment Scores:
Pred. No.: 4.97e-91 Length: 1438
Score: 979.00 Matches: 169
Percent Similarity: 93.92% Conservative: 1
Best Local Similarity: 93.37% Mismatches: 3
Query Match: 88.92% Indels: 8
DB: 9 Gaps: 1
US-09-993-234-6_COPY_19_204 (1-186) x US-10-112-793-5 (1-1438)
OY 1 LeuLeuGlyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
Db 431 CTGCTGGGGGGCCGGCCGAGGGGCGGCACTGCTAGCCCGGAGTGTGACTGTGCCGGTGAC 490

```
QY 21 pheHisLysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLys 40
Db 491 TTCCACAGAGAGATTGCTCTGTTTGTTCAGAGAGGCTGCCAGGGGGCAGCTACTGAAG 550
QY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
Db 551 GCCCTTGCACAGGAGCCCTGGCGCACTCCACCTGCTTGTGTCCCAAGACACCTTC 610
QY 61 LeuAlaTrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80
Db 611 TTGGCTGGGAGAACCACTAATTCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAG 670
QY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
Db 671 GCCTCCACAGGTGGCGCTGAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGGCTGTAAAG 730
QY 101 ProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCys 120
Db 731 CCAGGCTGGTTGTGAGTGGCAGGTCAGCCAAATGTTCAGCAGTTCAACCTTCTACTGC 790
QY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg 140
Db 791 CAACCATGCTAGACTGCGGGGCGCTGCACCGCCACACAGGCTACTGTGTCCCGCAGA 850
QY 141 AspThrAspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSer 160
Db 851 GATACTGACTGTGGAGCTGCTGCTGCTGCTATGAAACATGGCGATGGCTGCTGTCC 910
QY 161 CysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTyrParg 180
Db 911 TGCCCCACGTAATTCTTA-----GCTGTGCTGGGATGAGAG 946
QY 181 Gln 181
Db 947 GAA 949

RESULT 11
US-10-112-193-5
; Sequence 5, Application US/10112193
; Publication No. US20030004313A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-3 POLYPEPTIDE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/112,193
; FILING DATE: 28-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/928,069
; FILING DATE: 11-Sep-1997
; APPLICATION NUMBER: 60/026943
; FILING DATE: 23-Sep-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1052R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
```

```
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1438 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-112-193-5

Alignment Scores:
Pred. No.: 4.97e-91 Length: 1438
Score: 979.00 Matches: 169
Percent Similarity: 93.92% Conservative: 1
Best Local Similarity: 93.37% Mismatches: 3
Query Match: 88.92% Indels: 8
DB: 9 Gaps: 1

US-09-993-234-6_COPY_19_204 (1-186) x US-10-112-193-5 (1-1438)
QY 1 LeuLeuGlyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
Db 431 CTGCTGGGGGGCGGGGCCAGGGCGGCACACTCGTAGCCCCAGGTGTACTGTGCCGGTGAC 490
QY 21 pheHisLysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLys 40
Db 491 TTCCACAGAGAGATTGCTCTGTTTGTTCAGAGAGGCTGCCAGCGGGCAGCTACTGAAG 550
QY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
Db 551 GCCCTTGCACAGGAGCCCTGGCGCACTCCACCTGCTTGTGTGCCCAAGACACCTTC 610
QY 61 LeuAlaTrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80
Db 611 TTGGCTGGGAGAACCACTAATTCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAG 670
QY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
Db 671 GCCTCCAGGTGGCGCTGGAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGCTGAAG 730
QY 101 ProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCys 120
Db 731 CCAGGCTGGTTGTGAGTGGCAGGTCAGCCAAATGTTCAGCAGTTCAACCTTCTACTGC 790
QY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg 140
Db 791 CAACCATGCTAGACTGCGGGGCGCTGCACCGCCACACAGGCTACTGTTCGCCGAGA 850
QY 141 AspThrAspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSer 160
Db 851 GATACTGACTGTGGAGCTGCTGCTGCTTATGAAACATGGCGATGGCTGCTGTCC 910
QY 161 CysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTyrParg 180
Db 911 TGCCCCACGTAATTCTTA-----GCTGTGCTGGGATGAGAG 946
QY 181 Gln 181
Db 947 GAA 949

RESULT 12
US-09-884-733-5
; Sequence 5, Application US/09884733
; Patent No. US20020123116A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-2 Ligand Inhibitor
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
```

ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/884,733
FILING DATE: 19-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/304,003
FILING DATE: 14-JUNE-2000
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5416
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1438 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-884-733-5

Alignment Scores:
Pred. No.: 4.97e-91 Length: 1438
Score: 979.00 Matches: 169
Percent Similarity: 93.92% Conservative: 1
Best Local Similarity: 93.37% Mismatches: 3
Query Match: 88.92% Indels: 8
DB: 10 Gaps: 1

US-09-993-234-6_COPY_19_204 (1-186) x US-09-884-733-5 (1-1438)

OY 1 LeuLeuGlyAlaArgAlaGlnGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
DB 431 CTGCTGGGGCGCCGGCGCCAGGGCGGCACTGCTAGCCGCCAGGTGTGACTGTGCCGGTGAC 490
OY 21 PheHisLysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLys 40
DB 491 TTCACAGAAGATGTGTGTTGTTGTCAGAGAGCTGCCCCAGCGGGGCACCTGACCTGAAG 550
OY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
DB 551 GCCCCTGCACGAGACCCCTGGGCAACTCCACCTGCTGTGTGCCCAAGACACCTTC 610
OY 61 LeuAlaTrpGluAsnHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80
DB 611 TTGGCCTGGGAGAACCACTAATTCGATGTGCCCGCTGCCAGGCTGTGATGAGCAG 670
OY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
DB 671 GCCTCCAGGTGGCGCTGGAGAACTGTTCAAGCAGTGGCCGACACCCGCTGTGGTGAAG 730
OY 101 ProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCys 120
DB 731 CCAGGCTGGTTGTGAGTGCAGGTCAAGCAATGTGTCAAGAGTTCAACCTTCTACTGC 790
OY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg 140
DB 791 CAACCATGCTAGACTGGGGGCTGCACCGCCACACAGGCTACTCTGTCCCGCAGA 850
OY 141 AspThrAspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSer 160
DB 851 GATTAAGTACTGTGGACCTGCGCTGCTCTATGACATGGCGATGGCTGCGTGTCC 910
OY 161 CysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTyrParg 180

DB 911 TGCCCACTAATTCCTA-----GCTGTCTGGGATGAGC 946
OY 181 Gln 181
DB 947 GAA 949

RESULT 13
US-09-993-234-5
Sequence 5, Application US/09993234
Patent No. US20020146768A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/993,234
FILING DATE: 19-NO. US20020146768A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,683
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5416
TELEFAX: 415/952-9881
TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
LENGTH: 1438 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-993-234-5

Alignment Scores:
Pred. No.: 4.97e-91 Length: 1438
Score: 979.00 Matches: 169
Percent Similarity: 93.92% Conservative: 1
Best Local Similarity: 93.37% Mismatches: 3
Query Match: 88.92% Indels: 8
DB: 10 Gaps: 1

US-09-993-234-6_COPY_19_204 (1-186) x US-09-993-234-5 (1-1438)

OY 1 LeuLeuGlyAlaArgAlaGlnGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
DB 431 CTGCTGGGGCGCCGGCGCCAGGGCGGCACTGCTAGCCGCCAGGTGTGACTGTGCCGGTGAC 490
OY 21 PheHisLysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLys 40
DB 491 TTCACAGAAGATGTGTGTTGTTGTCAGAGAGCTGCCCCAGCGGGGCACCTGAAG 550
OY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
DB 551 GCCCCTGCACGAGACCCCTGGGCAACTCCACCTGCTGTGTGTGCCCAAGACACCTTC 610

QY	61	LeuAlaTrpGluAsnHisHisasnsSergLucysAlaArgCysGlnAlaCysAspGluGln	80
Db	611	TTGGCTGGGAGAACACCACCATTAATTCGAAATGTGCCCGCTGCAGGCGCTGTGATGAGCAG	670
QY	81	AlaSerGlnValAlaLeuGluAsnCysSeraIaValAlaAspThrArgCysGlyCysLys	100
Db	671	GGCTTCCAGGTGGCGCTGGAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGGCTGTAAAG	730
QY	101	ProGlyTrpPheValGluCysGlnValSeraIcncysValSerSerSerProphetyrcys	120
Db	731	CCAGGCTGGTTTGTGGAGTGCACGTCAGCCAAATGTGTACAGCAGTTACCCCTTACTGC	790
QY	121	GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSeraArgArg	140
Db	791	CAACCATGCTTAGACTGCGGGGCCCTGCACCCACACACAGCGCTACTCTGTTCGCCGACA	850
QY	141	AspThrAspCysGlyThrCysLeuProGlyPheTyrgluHisGlyAspGlyCysValSer	160
Db	851	GATACTGACTGTGGACCTGCCTGCCTTCTATGAACATGGCGATGGCTGCCTGTCC	910
QY	161	CysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTrpArg	180
Db	911	TGCCCCACCGTAATTCCTA-----GCTGTCTGGGATGGAGG	946
QY	181	Gln 181	
Db	947	GAA 949	

RESULT 14
US-10-092-154-1577
; Sequence 1577, Application US/10092154
; Publication No. US20030054375A1

```

: GENERAL INFORMATION:
: APPLICANT: Rosen et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
: FILE REFERENCE: PC009C1
: CURRENT APPLICATION NUMBER: US/10/092,154
: CURRENT FILING DATE: 2002-03-07
: NUMBER OF SEQ ID NOS: 2003
: Prior Application removed - See File Wrapper or Palm
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1577
: LENGTH: 10797
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-10-092-154-1577

```

Alignment Scores:

Pred. No.:	2.36e-68	Length:	10797
Score:	767.00	Matches:	167
Percent Similarity:	40.98%	Conservative:	1
Best Local Similarity:	40.73%	Mismatches:	5
Query Match:	69.66%	Indels:	239
DB:	9	Gaps:	4

US-09-993-234-6_COPY_19_204 (1-186) x US-10-092-154-1577 (1-10797)

QY	1	LeuLeuGlyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAsp	20
Db	5250	CTGCTGGGGGGCCCCAGGGCGGCACCTCGTAGCCCCAGGTGTGACTGTGCCGTTGAC	5309
QY	21	PheHisLysLysIleGlyLeuPheCysCysArgGlyCysProAla	35
Db	5310	TTCCACAAGAGATTGTTCTGTTTGTTCACAGAGCTGCCACGGGTAAGTGCCACAG	5369
QY	35	-----	35
Db	5370	GGGTGGAGAGGCATGGGGCAGGCAGGCTGAGAGTTGCCGGGCAGGCCGGGAGTTAA	5429
QY	35	-----	35
Db	5430	GAGGAGGCTGGCAGGGGAGGTAGGGGTAGGCTGACAGAGAAAGTAGGGAGCTGAGAGAAA	5489

QY	35	-----	-----	-----	-----	35
Db	5490	GAGGGAAGGAGGCGCAGGGTGGAAAGCAGGTCGGGGTGGCTGGGCAGCCCCCTGGCCTGC				5549
QY	36	-----	-----	-----	-----	
Db	5550	CTGACCCCTGCCTGGTTCACACAGGGCACTACCTGAAGGCCCTTGACAGGAGCCCTGGGG				5609
QY	48	YASNserThrCysLeuValCysProGlnaspThrPheLeuAlaTrpGluAsnHisHisAs				68
Db	5610	CAACTCCACCTGGCTTGTGTGTCCCAAGACACACCTCTTGGCCTGGAGAACACCATTA				5669
QY	68	nserGluCysAlaArgCysGlnAlaCysAspGlu				79
Db	5670	TTCTGAATGTGCCCGCTGCCAGGCCTGTGATGAGCAGGGGTGAGGGCTTCTCAGTGCCTG				5729
QY	79	-----	-----	-----	-----	79
Db	5730	GCAGGGAGTTCCTAAGACAGGCCCTTCTGAAGAAAGTGGCTGGCTCGGGCCCAACTTG				5789
QY	79	-----	-----	-----	-----	79
Db	5790	GGGTGTGAGGGTCTGCACACCAACCCCTTGCCAGAACCCCTCCACCCCTGATCCTTCAGGG				5849
QY	79	-----	-----	-----	-----	79
Db	5850	TGCCCTTGCCCTTCTCTCTCCCTGGTGACCTTCCCATCTCTCCATGTGCTTGGCCTCT				5909

QY 79 ----- 79

Db 5910 GGTGGCCTTAATCTCTGAGCTTCTCTTTT TAGGGTAGCCCTGTACCTGTCTGCTT 5969

QY 79 ----- 79

Db 5970 TCGCCTATTCTGTCTCCATTATCTTGGGATAATGCCCTCTGCCCTCTCCATGGGAGCCTTT 6029

QY 80 -----G1n1a5eRg1nva1A1 85

Db 6030 GGCCTGACTACTCTCCACTCCCATCTCCCTGCACCCCAACAGCC-TCCAGGTGC 6088

QY 85 aLeuGIuASncYssERAlaValAlaAspThrArgCYsGLyCYsLysProGLyTirpPheV 105

Db 6089 GCTGGAGAACTGTTACAGCAGTGGCCGACACCCGCTGTGGCTGTAAGCCAGCGCTGTTGT 6148

QY 105 1GIuGcYglNvaISerGlnCysvaISerSerSerProphetyrCysGlnProCysLeuAs 125

Db 6149 GGAGTGCAGGTCAGCCAATGTGTCAGCAGTTCACCCCTCTACTGCCAACCATGCCCTAGA 6208

QY 125 PCYSGLYALALEUHIARGHISTHrARGLEULEUCYSSEr----- 138

Db: 6209 CTGCGGGCCCTGCACCGCCACACGCGTACTCTGTGA-GTACCCCCACCCAGGCTCT 6267

QY 138 ----- 138

Db 6268 CTACTCCAGACCCCTTCTCCCTGCGCTGACCCACTCCTGTCCCATGGTGACGCATGCCCT 6327

QY 139 -----ArgargaspThrspcysglyThrcysleuproglyphety 152

Db 6328 CTCCTGGATTGCAGGTTCCCGCAGAGATACTGACTGTGGGACCTGCCCTGCCCTTCTA 6387

QY 152 RGIUHLsGLyAspGLyCysValSerCysProThrSerThrLeuGLySerCysProGLuAr 172

Db 6388 TGAACATGGCGATGGCTGCGTGTCCCTGCCCCACGTAATTCCTA----- 6430

QY 172 gCysAlaIaValCysGlyTrrPargGln 181

Db 6431 -----GCTGTCGTGGGATGGAAGGAA 6451

RESULT 15
HS-09-764-847-1577

; Sequence 1577, Application US/09764847
 ; Patent No US20020132767A1

; GENERAL INFORMATION:


```
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009
; CURRENT APPLICATION NUMBER: US/09/764,847
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2003
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1577
; LENGTH: 10797
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-847-1577

Alignment Scores:
Pred. No.: 2,366-68      Length: 10797
Score: 767.00           Matches: 167
Percent Similarity: 40.98%      Conservative: 1
Best Local Similarity: 40.73%    Mismatches: 5
Query Match: 69.66%           Indels: 239
DB: 10                     Gaps: 4

US-09-993-234-6_COPY_19_204 (1-186) x US-09-764-847-1577 (1-10797)

QY 1 LeuLeuGlyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
    |||||||
Db 5250 CTGCTGGGGGGCCCGGGCCAGGGCGGCACTCGTAGCCGCCAGGTGTGACTGTGCGGTGAC 5309

QY 21 PheHisLysLysIleGlyLeuPheCysCysArgGlyCysProAla----- 35
    |||||||
Db 5310 TTCCACAGAAGAATGTGTGTTTGTGTGACAGAGCTGCCACGCGGTAAGTGCCACAG 5369

QY 35 ----- 35
Db 5370 GGCTGGAGAGCATGGGGCCAGGCAGGCGTGGAGAGTGGCGGGCAGGCCCGGAGGTAA 5429

QY 35 ----- 35
Db 5430 GAGGAGCTGGCAGGGAGGAGTAGGGGTAGGCTGACAGAGAAGTAGGAGCTGGAGAGAA 5489

QY 35 ----- 35
Db 5490 GAGGGAGGAGGGCCAGGGTGAAGACAGAGTCCGGGGTTGCTGGGCAGCCCCCTGCGCTGC 5549

QY 36 -----GlyHisTyrLeuLysAlaProCysThrGluProCysG1 48
    |||||||
Db 5550 CTGACCCCTGCGTGGTTCCACAGGGCAGCTACCTGAAGGCCCTTGACAGGAGCCCTGCGG 5609

QY 48 yAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluAsnHisAs 68
    |||||||
Db 5610 CAACTCCACCTGCTGTGTGTGCCCAAGACACCTTCTGGCCTGGAGAACACCATAA 5669

QY 68 nSerGluCysAlaArgCysGlnAlaCysAspGlu----- 79
    |||||||
Db 5670 TTCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGGGTGAGGGCTTCTCAGTCTTG 5729

QY 79 ----- 79
Db 5730 GCAGGGAGTTCCTAAGACAGGCCCTTCTGAAGAAAGTGGCTGGGCGCCAAACTTG 5789

QY 79 ----- 79
Db 5790 GGGGTGAGGGTCTGTGACCCACCCCTTGCCAGAACCCCTGATCCTCTTCAGGG 5849

QY 79 ----- 79
Db 5850 TGCCCTTGCCCTTCTCTTCTCTGCTGAGACCTTCCATCTCTCCATGTGCCCTTGCCCTCT 5909

QY 79 ----- 79
Db 5910 GGTGCGCCTTAATCTGTGAGCTTCTCTTTTAAAGGTAGCCCTGTACCTGTCTGTCTT 5969

QY 79 ----- 79
```

```
Db 5970 TCGCCATTATTCTGTCTCCATTAATCTTGGGATAATGCCCTGCTCTCCATGGAGCCCTTT 6029

QY 80 -----GlnAlaSerGlnVal1 85
    |||
Db 6030 GGCCCTGACTACTCTCCACTTCCCATCTCCCTGACACCCCAACAGCC-TCCCAGGTGGC 6088

QY 85 aleuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTyrPheVa 105
    |||||||
Db 6089 GCTGGAGAAGACTGTTCAGCAGAGTGGCCGACACCCCGCTGTGGCTGTAAAGCAGGCTGTTGT 6148

QY 105 lGluCysGlnValSerGlnCysValSerSerProPheTyrCysGlnProCysLeuAs 125
    |||||||
Db 6149 GGAGTGCACAGGTACGCCAATGTCTCAGCAGTTCACCCCTTCTACTGCCAACCATGCTTGA 6208

QY 125 pCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSer----- 138
    |||||||
Db 6209 CTGGGGGGCCCTGCACCGCCACACACGCGTACTCTGTGA-GTACCCCAACCAAGGCTGCT 6267

QY 138 ----- 138
Db 6268 CTACTCCACAGACCCCTTCTCCCTGCTGACCCACACTCTCTGCCATGTGTGACGATGCT 6327

QY 139 -----ArgArgAspThrAspCysGlyThrCysLeuProGlyPheTy 152
    |||||||
Db 6328 CTCCCTGATTGACAGTTCCCGCAGAGATACTGACTGTGGACCTGCTGCTGCTTCTTA 6387

QY 152 rGluHisGlyAspGlyCysValSerCysProThrSerThrLeuGlySerCysProGluAr 172
    |||||||
Db 6388 TGAACATGGCGATGGCTGCTGCTCTGCCCCACAGTAATTCCTA----- 6430

QY 172 gCysAlaAlaValCysGlyTyrPArgGln 181
    |||||||
Db 6431 -----GCTGTGCTGGGATGAGGGAA 6451
```

Search completed: April 7, 2003, 03:59:13
Job time : 86.8236 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.4-p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 6, 2003, 16:19:54 ; Search time 1163.45 Seconds

(without alignments)
2589.161 Million cell updates/sec

Title: US-09-993-234-6_COPY_19_204
Perfect score: 1101
Sequence: 1 LIGARAQGTSPRCACAGD.....GSCPERCAAVCGWROMFWVQ 186

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+
-O=/cgn2_1/USPTO_spool/US0993234/runat_27032003_115456_15362/app_query.fasta_1.2346
-DB=EST -QFMT=fastap -SUFFIX=first -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US0993234@cgn_1_1_4749@runat_27032003_115456_15362 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:
1: em_estha:*
2: em_esthum:*
3: em_estim:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1075	97.6	767	13	BI909448 603065172
2	1072	97.4	698	9	AI807913
3	1069	97.1	632	10	AM268610
4	1049	95.3	688	9	AI424936
5	1006	91.4	562	9	AI140043
6	979	88.9	552	14	BM783972
7	979	88.9	585	10	AW517358
8	970	88.1	565	14	BM744307
9	964	87.6	514	14	BM756372
10	964	87.6	514	14	BM783979
11	943	85.6	508	9	AI203624
12	935	84.9	492	14	BM741016
13	920	83.6	488	14	BM770798
14	867	78.7	1010	14	BQ068309
15	825.5	75.0	478	10	AW002222
16	795	72.2	427	12	BE696572
17	707	64.2	422	9	AI700459
18	692	62.9	433	14	H41522
19	654	59.4	572	10	BE668836
20	595	54.0	432	14	N71143
21	580.5	52.7	434	14	BM826048
22	521	47.3	345	9	AA934992
23	518.5	47.1	443	14	H46211
24	479	43.5	673	13	BM251737
25	474.5	43.1	755	13	BI655045
26	463	42.1	468	14	H46374
27	451.5	41.0	775	12	BG867742
28	424.5	38.6	322	9	AA971249
29	420	38.1	330	14	N71141
30	410.5	37.3	639	10	BB636341
31	407	37.0	316	14	H49675
32	391.5	35.6	393	14	H41851
33	360.5	32.7	418	14	H46662
34	325	29.5	397	14	H46378
35	296	26.9	246	14	H46424
36	294	26.7	246	14	H19739
37	283.5	25.7	368	10	BB872434
38	277.5	25.2	517	14	BM692368
39	221	20.1	556	10	AV664984
40	214	19.4	252	14	BM695862
41	213	19.3	779	9	AI119338
42	212	19.3	725	12	BG863025
43	212	19.3	984	12	BF164835
44	209.5	19.0	775	13	BI555040
45	209	19.0	651	13	BM009354

ALIGNMENTS

RESULT 1
BI909448
LOCUS BI909448 767 bp mRNA EST 16-OCr-2001
DEFINITION 603065172F1 NIH_MGC_118 Homo sapiens CDNA clone IMAGE:5214568 5',
ACCESSION BI909448
VERSION BI909448.1 GI:16172666
KEYWORDS
SOURCE EST.
ORGANISM human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 767)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL COMMENT

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLM11538 row: 0 column: 17
High quality sequence stop: 754.
Location/Qualifiers

FEATURES
Source

1. 767
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5214568"
/clone_lib="NIH_MGC_118"
/tissue_type="leukocyte"
/lab_host="DH10B"
/note="Vector: PCMV-SF0RT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH_MGC library."
BASE COUNT 122 a 243 c 241 g 161 t
ORIGIN

Alignment Scores:

Pred. No.: 1.46e-92 Length: 767
Score: 1075.00 Matches: 186
Percent Similarity: 98.94% Conservative: 0
Best Local Similarity: 98.94% Mismatches: 0
Query Match: 97.64% Indels: 2
DB: 13 Gaps: 0

US-09-993-234-6_COPY_19_204 (1-186) x B1909448 (1-767)

QY 1 LeuLeuGLyAlaArg-AlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAs 20
|||||
DB 90 CTGCTGGGGCCCGTGGCCAGGGCGGACATCGTACCCAGGTGTGACTGTGCCGGTGA 149
QY 20 PheHisLysLysIleGlyLeuPheCysCysArgGlyCysProAla-GlyHisTyrLeuL 40
|||||
DB 150 CTTCCACAAGAAGATTGGTCTGTTTGTGTGACAGAGCTGCCAGCTGGGGCATTACCTGA 209
QY 40 ySaIaProCysThrClnuProCysGlyAsnSerThrCysLeuValCysProGlnAspThrp 60
|||||
DB 210 AGGCCCTTGCAAGAGCCCTGCGCAACTGCCTGTGTGTCCTCCCAAGACACCT 269
QY 60 heLeuAlaTrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluG 80
|||||
DB 270 TCTTGGCCTGGGAGAACCATATTTGATGTGCCCGCTGCCAGGCTGTGATGAGC 329
QY 80 lnaIaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysL 100
|||||
DB 330 AGGCTTCCAGGTGGCGCTGGAGAACTGTTCAAGAGTGGCCGACACCCCGTGTGGCTGTA 389
QY 100 ySProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerSerProPheTyrC 120
|||||
DB 390 AGCCAGGCTGTTGTGAGTGCAGGTCAGGTCAGTGTGTCAGCAGTTCACCTTCTACT 449
QY 120 ySglnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgA 140
|||||
DB 450 GCCAACCATGCTAGACTGCGGGCCCTGCACGCCACACACAGGCTACTGTCCCGCA 509
QY 140 rgAspThrAspCysGlyThrCysLeuProGlyPheTyrGlnHisGlyAspGlyCysValS 160
|||||
DB 510 GAGATACTGACTGTGGGACCTGCTGCTGCTTCTATGAACATGGCGATGGCTGCTGT 569

QY 160 erCysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTrpA 180
|||||
DB 570 CCTGCCCCACAGACACCCCTGGGAGCTGTTCACAGCGCTGTGCCGCTGTCTGTGCTGGA 629
QY 180 rgGlnMetPheTrpValGln 186
|||||
DB 630 GGCAGATGTCTGGGTCCAG 649

RESULT 2

AI807913

LOCUS

AI807913 698 bp mRNA linear EST 19-DEC-1999
DEFINITION w552c03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:2359204 3' similar to SW:WSL1_HUMAN Q93038 WSL-1 PROTEIN
PRECURSOR ; mRNA sequence.

ACCESSION

AI807913

VERSION

AI807913.1

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 698)

AUTHORS

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL

Unpublished (1997)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov

This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 1568 Std Error: 0.00
Seq primer: -40UP from Gibco

High quality sequence stop: 459.

FEATURES

source

Location/Qualifiers

1. 698

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2359204"

/clone_lib="Soares_NFL_T_GBC_S1"

/lab_host="DH10B"

/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NBHL19W, testis NH7, and B-cell
NCL-CGAP-GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo."

BASE COUNT 111 a 218 c 214 g 155 t
ORIGIN
Alignment Scores:
Pred. No.: 2.47e-92 Length: 698
Score: 1072.00 Matches: 182
Percent Similarity: 97.85% Conservative: 0
Best Local Similarity: 97.85% Mismatches: 4
Query Match: 97.37% Indels: 0
DB: 9 Gaps: 0
US-09-993-234-6_COPY_19_204 (1-186) x AI807913 (1-698)
QY 1 LeuLeuGLyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
|||||
DB 18 CTGCTGGGGCCCGGCGCCAGGGGGGCTGTATCCCAAGGTGTGACTGTGCCGGTGAC 77
QY 21 PheHisLysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLys 40
|||||
DB 78 TTCACACAAGAAGATTGGTCTGTTTGTGTGACAGAGCTGCCAGCGGGCACTACCTGAAG 137

was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT	102 a	194 c	192 g	143 t	1 others
ORIGIN					

ORIGIN

Alignment Scores:

Pred. No.:	4,12e-92	Length:	6322
Score:	1069.00	Matches:	1833
Percent Similarity:	98.39%	Conservative:	0
Best Local Similarity:	98.39%	Mismatches:	3
Query Match:	97.09%	Indels:	0
DB:	10	Gaps:	0

US-09-993-234-6_COPY_19_204 (1-186) x AW268610 (1-632)

Db	378	CAACCATGCCCTAGACTGCGGGGCCCTGCACCGCACACAGCGCTACTCTGTCCCGCAGA	437	QY	1	LeuLeuGlyAlaArgAlaGlnGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAsp	20
QY	141	AspThrAspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSer	160	Db	9	CTGCTGGGGGCCCGGGCCAGGGGGGCACACTGTAGCCCCAGGTGTGACTGTGCGGTGAC	68
Db	438	GATACTGACTGTGGACCTGCCTGCCTGCTATGAACATGGCGATGGCTGCCTGCC	497	QY	21	PheHisLysLysIleGlyLeuPheCysArgGlyCysProAlaGlnIstTyrLeuLys	40
QY	161	CysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTyrParg	180	Db	69	TTCACAAGAAGATTGGTCTGTTTGTTCAGAGAGCTGCCACAGGGGCACACTGGAAG	128
Db	498	TGCCCTACGAGACACCTGTGGAGCTGTCCAGAGCGCTGCGCGCTGTCTGTGGCTGGAGG	557	QY	41	AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe	60

RESULT 3	
AW268610	
LOCUS	632 bp mRNA linear EST 03-JAN-2000
DEFINITION	xv4lb12.x1 Soares_NFL_T_GBC_S1 Homo sapiens CDNA clone IMAGE:2815679.3' similar to SW:WSL1_HUMAN Q93038 WSL-1 PROTEIN PRECURSOR ;, mRNA sequence.

SOURCE ORGANISM	human. Homo sapiens
REFERENCE AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE	1 (bases 1 to 632) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap . National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

JOURNAL COMMENT

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov

This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Possible reversed clone: similarity on wrong strand

Possible reversed clone: polyT not found

Seq primer: -40UP from G1bco

High quality sequence stop: 455.

FEATURES	Location/Qualifiers
source	1. .632

```

1. .632
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2815679"
/clone_11b="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NbHL19W, testis NHT, and B-cell
NCI-CGAP-GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driven

```

QY	121	GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg	140
Db	369	CAACCATGCTAGACTGGGGGGCTGCACCGCCACACACGGCTACTCTCTTCCCCGACA	428
QY	141	AspThrAspCysGlyThrCysLeuProGlyPheTyrgLuHisGlyAspGlyCysValSer	160
Db	429	GATACTGACTGTGGGACCTGCCTGCCTTCTATGAACATGGCGATGGCTGTGTCTCC	488
QY	161	CysProThrSerThrIleuGlySerCysProGluArgCysAlaAlaValCysGlyTyrParg	180
Db	489	TGGCCACGAGCACNCNTGGGGAGCTGTGCAGAGCGCTGTGCCGCTGTCTGTGGCTGGAGG	548
QY	181	GlnMetPheTrpValGln	186
Db	549	CAGATGTTCTTGCTCCAG	566

RESULT 4				
AI424936				
LOCUS				
DEFINITION	AI424936	688 bp	mRNA	linear
	tg19b08.x1			EST 30-MAR-1999
	similar to TR:000276	000276	LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH	
	2. i, mRNA			sequence.

ORGANISM	REFERENCE AUTHORS
Homo sapiens	
Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;	
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
1 (bases 1 to 688)	
NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap .	

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
M.D., Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.lnl.gov/db/imap/image.html
Insert Length: 2028 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 445.

location/Qualifiers
1. 688
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2109207"
/clone_lib="NCI-CGAP_CL11"
/tissue_type="B-cell, chronic lymphocytic leukemia"
/lab_host="DH10B"
/note="Vector: p7T73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTACCAATCTGAAGTGGAGCGCGCATCTTTTCTTTTCTTTTCTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified p7T73 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."

FEATURES
source

BASE COUNT 113 a 208 c 229 g 138 t
ORIGIN

Alignment Scores:

Pred. No.: 3.79e-90 Length: 688
Score: 1049.00 Matches: 178
Percent Similarity: 97.28% Conservative: 1
Best Local Similarity: 96.74% Mismatches: 5
Query Match: 95.28% Indels: 0
DB: 9 Gaps: 0

US-09-993-234-6_COPY_19_204 (1-186) x A1424936 (1-688)

QY 1 LeuLeuGlyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
|||||
Db 47 CTGCTGGGGCGCGGGGGGGGGCGGCGACTCGTAGCCCCAGGTGTGACTGTGCCGGTGCAC 106
QY 21 PheHisLysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLys 40
|||||
Db 107 TTCACACAGAAGATGGTCTGTTTGTTCAGAGAGCTGCCACAGCGGGGCACTAAGTGAAG 166
QY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
|||||
Db 167 GCCCTTGACAGGAGCGCTCGGCAACTCCACTGCTGTGTGTCCCAAGACACCTTC 226
QY 61 LeuAlaTyrGluAsnHisHisAsnSerGlyCysAlaArgCysGlnAlaCysAspGluGln 80
|||||
Db 227 TTGGCTGGGAGAACACCATATTTCTGAATGTGCCCGCTGCCAGCGCTGTGATGAGCAG 286
QY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
|||||
Db 287 GCCTCCAGGTGGCGCTGGAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGGCTGAAG 346
QY 101 ProGlyTyrPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCys 120
|||||
Db 347 CCAGGCTGGTGTGGAGTGCAGGTCAGCCAATGTGTCAAGAGTTTCACTTCTACTGC 406
QY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg 140
|||||
Db 407 CAACCATGCTTAGACTGCGGGGCGCTGCACCGCCACACACAGGCTACTGTGTCCCGCAGA 466

QY 141 AspThrAspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSer 160
|||||
Db 467 GGTAAGTACTGTGGGACCTGCTGCTGCTGTCTATGACATGGCATGGCTGCTGCC 526
QY 161 CysProThrSerThrLeuGlySerCysProGluArgCysAlaAlaValCysGlyTyrParg 180
|||||
Db 527 TGGCCCAACGACGACCCCTGGGAGCTGTCCAGAGAGCGCTGTGCTGTGGCTGAGG 586
QY 181 GlnMetPheTyr 184
|||
Db 587 CAGAGTAAGTGG 598

RESULT 5 562 bp mRNA linear EST 13-APR-1999
A1140043
LOCUS
DEFINITION
A1140043
qas7a04.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone
IMAGE:1693710 3' similar to SW:WSL1_HUMAN Q93038 WSL-1 PROTEIN
PRECURSOR ;, mRNA sequence.

ACCESSION A1140043.1 GI:3647500
VERSION A1140043
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 562)
TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NATIONAL Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL
COMMENT Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov

This clone is available royalty-free through LINL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Insert Length: 1640 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 494.

FEATURES
source Location/Qualifiers
1. 562

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1693710"
/clone_lib="Soares_fetal_heart_NbHH19W"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"

/note="Organ: heart; Vector: p7T73D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5',
TGTACCAATCTGAAGTGGAGCGCGCATCTTTTCTTTTCTTTTCTTTT
T 3']; double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified p7T73 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by
M.Fatima Bonaldo. This library was constructed from the
same fetus as the fetal lung library, Soares fetal lung
NbHH19W."

BASE COUNT 88 a 182 c 180 g 111 t 1 others
ORIGIN

Alignment Scores:

Pred. No.: 3.58e-86 Length: 562
Score: 1006.00 Matches: 171
Percent Similarity: 99.42% Conservative: 0
Best Local Similarity: 99.42% Mismatches: 1
Query Match: 91.37% Indels: 0
DB: 9 Gaps: 0

US-09-993-234-6_COPY_19_204 (1-186) x A1140043 (1-562)

QY 1 LeuLeuGlyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAsp 20

|||||
Db 47 CTGCTGGGGGGCCGGCCAGGGGGGCACTGCTAGCCCGAGGTGTGACTGTGCCGGTGAC 106
Qy 21 PheHISLysLysILEGlyLeuPheCysCysArgGLYcysProAlaGlyHISLysTyrLeuLys 40
|||||
Db 107 TTCCACAGAGAAGATTGCTGTGTTGTTGTCAGAGGCTGCCAGCGGGCAGCTACCTGAAG 166
Qy 41 AlaProCysThrGluProCysGLYAsnSerThrCysLeuValCysProGlnAspThrPhe 60
|||||
Db 167 GCCCTTGCAAGGAGACCCCTGCGGCACTCCACCTGCCCTGTGTGCCCAAGACACCTTC 226
Qy 61 LeuAlaTrpGluAsnHISHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80
|||||
Db 227 TTGGCCTGGGAGAACACCATTAATTCGATGTGCCCGCTGCCAGGCTGTGATGAGCAG 286
Qy 81 AlaSerGlnValAlaLeuGluAsnCysSeraAlaValAlaAspThrArgCysGLYcysLys 100
|||||
Db 287 GCCTCCAGGTGGCGCTGGAGAACTGTTCAAGCAGTGCGCCGACACCCGCTGTGCTGTAA 346
Qy 101 ProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCys 120
|||||
Db 347 CCAGGCTGGTTGTGGAGTGCAGGTCACCAATGTGTACAGCAGTTCACCTTCTACTGC 406
Qy 121 GlnProCysLeuAspCysGLYAlaLeuHISArgHISLThrArgLeuLysCysSeraArg 140
|||||
Db 407 CAACCATGCTAGACTGCGGGCCCTGCACCGCACACAGCGCTACTCTGTGCCGACAGA 466
Qy 141 AspThrAspCysGLYThrCysLeuProGlyPheTyrGluHISGlyAspGlyCysValSer 160
|||||
Db 467 GATACGTACTGTGGACCTGCCTGCTGCTTATGAACATGGCATGGCTGCTGTCC 526
Qy 161 CysProThrSerThrLeuGlySerCysProGluArg 172
|||||
Db 527 TGCCCCACGAGCACCTCTGNGAGCTGTCCAGAGCGC 562
RESULT 6
BM783972 552 bp mRNA linear EST 05-MAR-2002
LOCUS K-EST0062019 S6SNU620 Homo sapiens cDNA clone S6SNU620-31-H06 5',
DEFINITION mRNA sequence.
ACCESSION BM783972
VERSION BM783972
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 552)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@email.kr.ibm.re.kr
Plate: 31 row: H column: 06
High quality sequence stop: 552.
FEATURES
source
1..552
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="S6SNU620-31-H06"
/clone_lib="S6SNU620"
/sex="F"
/tissue_type="Ascites"
/cell_type="Scattering floating"
/cell_line="SNU-620"
/lab_host="Top10F"

/note="Organ: Stomach; Vector: pcNS; Site_1: EcoRI;
Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tabacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dT-selected mRNA by
priming with dT-tailed vector. The dT-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F' by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."
BASE COUNT 92 a 172 c 173 g 115 t
ORIGIN
Alignment Scores:
Pred. No.: 1,32e-83 Length: 552
Score: 979.00 Matches: 169
Percent Similarity: 93.92% Conservative: 1
Best Local Similarity: 93.37% Mismatches: 3
Query Match: 88.92% Indels: 8
DB: 14 Gaps: 1
US-09-993-234-6_COPY_19_204 (1-186) x BM783972 (1-552)
Qy 1 LeuLeuGlyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
|||||
Db 20 CTGCTGGGGGGCCGGCCAGGGCGGCACTGCTAGCCCGAGTGTGACTGTGCCGGTGAC 79
Qy 21 PheHISLysLysILEGlyLeuPheCysCysArgGLYcysProAlaGlyHISLysTyrLeuLys 40
|||||
Db 80 TTCCACAGAGAAGATTGCTGTGTTGTTGTCAGAGGCTGCCAGCGGGGCACTACCTGAAG 139
Qy 41 AlaProCysThrGluProCysGLYAsnSerThrCysLeuValCysProGlnAspThrPhe 60
|||||
Db 140 GCCCCTTGCAAGGAGCCCTGCGGCACTCCACCTGCTGTGTGCCCAAGACACCTTC 199
Qy 61 LeuAlaTrpGluAsnHISHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80
|||||
Db 200 TTGGCCTGGGAGAACCATTAATTCGATGTGCCCGCTGCCAGGCTGTGATGAGCAG 259
Qy 81 AlaSerGlnValAlaLeuGluAsnCysSeraAlaValAlaAspThrArgCysGLYcysLys 100
|||||
Db 260 GCCTCCAGGTGGCGCTGGAGAACTGTTCAAGATGGCGGACACCCGCTGTGCTGAAG 319
Qy 101 ProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCys 120
|||||
Db 320 CCAGGCTGGTTGTGGAGTGCAGGTCAGCAATGTGTACAGCAGTTCACCTTCTACTGC 379
Qy 121 GlnProCysLeuAspCysGLYAlaLeuHISArgHISLThrArgLeuLysSeraArg 140
|||||
Db 380 CAACCATGCTAGACTGCGGGCCCTGCACCGCCACACAGGCTACTGTGCCGACAGA 439
Qy 141 AspThrAspCysGLYThrCysLeuProGlyPheTyrGluHISGlyAspGlyCysValSer 160
|||||
Db 440 GATACGTACTGGGAGACCTGCCTGCTCTATGAACATGGCGATGCTGCTGCC 499
Qy 161 CysProThrSerThrLeuGlySerCysProGluArgCysAlaValCysGLYTrpArg 180
|||||
Db 500 TGCCCCACGTAATTCCTA-----GCTGTGCTGGGATGAGAG 535
Qy 181 Gln 181
Db 536 GAA 538
RESULT 7
AW517358 585 bp mRNA linear EST 03-MAR-2000
LOCUS AW517358
DEFINITION xp93g02.x1 Soares_NHCE_cervix Homo sapiens cDNA clone IMAGE:2747954

ORIGIN

Alignment Scores:
Pred. No.: 9.88e-83 Length: 565
Score: 970.00 Matches: 168
Percent Similarity: 93.37% Conservative: 1
Best Local Similarity: 92.82% Mismatches: 4
Query Match: 88.10% Indels: 8
DB: 14 Gaps: 1
US-09-993-234-6_COPY_19_204 (1-186) x BM744307 (1-565)

QY 1 LeuLeuGlyAlaArgAlaGlnGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
Db 20 CTGCTGGGGGCCCGGGCCAGTGGCGGACTGTAGCCCGAGGTGTGACTGTGCCGGTGAC 79
QY 21 PheHisLysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLys 40
Db 80 TTCCACAGAGAAGATTGCTGTGTTGTCAGAGGCTGCCACAGCGGGCAGCTACCTGAAG 139
QY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
Db 140 GCCCTTGCACGAGAGCCCTCGCGGCACTCCAGCTGTGTGTGTCCTCCCAAGACACCTTC 199
QY 61 LeuAlaTrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80
Db 200 TTGGCCTGGAGAACACCATTAATTCGATGTGCCCGCTGCAGGCTGTGATGAGCAG 259
QY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
Db 260 GCCTCCAGGTGGCGCTGGAGAACGTTCAGACAGTGGCCGACACCCGCTGTGGCTGAAG 319
QY 101 ProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCys 120
Db 320 CCAGGCTGGTTGTGAGTGTCCAGGTCAGCAATGTGTACAGAGTCAACCTTCTACTGC 379
QY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg 140
Db 380 CAACCATGGCTAGACTGGCGGGCCCTGCACCGCCACACACGGCTACTGTTCGCCGAGA 439
QY 141 AspThrAspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSer 160
Db 440 GATACTGACTGTGGAGACCTGCTGCTGCTTCTATGAACATGGCGATGGCTGCGTGC 499
QY 161 CysProThrSerThrLeuGlySerCysProGluArgCysAlaValAlaCysGlyTyrParg 180
Db 500 TGCCCCACGTAATTCCTA-----GCTGCTGGGATGAGG 535
QY 181 Gln 181
Db 536 GAA 538
RESULT 9
BM756372 514 bp mRNA linear EST 04-MAR-2002
LOCUS K-EST0034666 S6SNU620 Homo sapiens cDNA clone S6SNU620-27-G03 5',
DEFINITION mRNA sequence.
ACCESSION BM756372
VERSION BM756372.1 GI:19085987
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 514)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology

52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 27 row: G column: 03
High quality sequence stop: 514.
location/Qualifiers
1. 514

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="S6SNU620-27-G03"
/clone_lib="S6SNU620"
/sex="F"
/tissue_type="Ascites"
/cell_type="Scattering floating"
/cell_line="SNU-620"
/lab_host="Top10F"

/note="Organ: Stomach; Vector: pcNS; Site_1: EcoRI;
Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tobacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F' by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."

BASE COUNT 86 a 166 c 153 g 109 t
ORIGIN

Alignment Scores:
Pred. No.: 3.21e-82 Length: 514
Score: 964.00 Matches: 163
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 87.56% Indels: 0
DB: 14 Gaps: 0

US-09-993-234-6_COPY_19_204 (1-186) x BM756372 (1-514)
QY 1 LeuLeuGlyAlaArgAlaGlnGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
Db 20 CTGCTGGGGGCCCGGGCCAGGCGGCGACATGAGCCCGAGGTGTGACTGTGCCGGTGAC 79
QY 21 PheHisLysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLys 40
Db 80 TTCCACAGAGAAGATTGCTGTGTTGTCAGAGGCTGCCACAGCGGGCAGCTACCTGAAG 139
QY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
Db 140 GCCCTTGCACGAGAGCCCTCGCGGCACTCCAGCTGTGTGTGTCCTCCCAAGACACCTTC 199
QY 61 LeuAlaTrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80
Db 200 TTGGCCTGGAGAACACCATTAATTCGATGTGCCCGCTGCAGGCTGTGATGAGCAG 259
QY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
Db 260 GCCTCCAGGTGGCGCTGGAGAACGTTCAGACAGTGGCCGACACCCGCTGTGGCTGAAG 319
QY 101 ProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCys 120
Db 320 CCAGGCTGGTTGTGAGTGTCCAGGTCAGCAATGTGTACAGAGTCAACCTTCTACTGC 379
QY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg 140
Db 380 CAACCATGGCTAGACTGGCGGGCCCTGCACCGCCACACACGGCTACTGTTCGCCGAGA 439

QY 141 AspThrAspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSer 160
|||||
Db 440 GATACTGACTGTGGACCTGCCTGCCTGTCTATGACATGCGGATGGCTGCCTGTCC 499
QY 161 CysProThr 163
|||||
Db 500 TGCCCCACG 508

RESULT 10
BM783979

LOCUS
DEFINITION BM783979 514 bp mRNA linear EST 05-MAR-2002
K-EST0062030 S6SNU620 Homo sapiens cDNA clone S6SNU620-32-A05 5',
mRNA sequence.
BM783979
BM783979.1 GI:19132211

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 514)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@email.kribb.re.kr
Plate: 32 row: A column: 05
High quality sequence stop: 514.
Location/Qualifiers

FEATURES
source
1. 514
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="S6SNU620-32-A05"
/clone_lib="S6SNU620"
/sex="F"
/tissue_type="Ascites"
/cell_type="Scattering floating"
/cell_line="SNU-620"
/lab_host="Top10F"
/note="Organ: Stomach; Vector: pcNS; Site_1: EcoRI;
Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tobacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F' by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."

BASE COUNT 86 a 166 c 153 g 109 t

ORIGIN

Alignment Scores:
Pred. No.: 3.21e-82 Length: 514
Score: 964.00 Matches: 163
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 87.56% Indels: 0
DB: 14 Gaps: 0

US-09-993-234-6_COPY_19_204 (1-186) x BM783979 (1-514)

QY 1 LeuLeuGlyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
|||||
Db 20 CTGCTGGGGGGCCCCGAGGGCCGCGACACTGCTAGCCCAAGGTGTACTGTGCGGTGAC 79

QY 21 PheHisLysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlyHisTyrLeuLys 40
|||||
Db 80 TTCACACAAGAAATGTGTCTTTTGTGTGCAGAGGCTGCCACGCGGGCAGCTACTGAAG 139

QY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
|||||
Db 140 GCCCCTTGACACGAGCCCTGCGGCAACTCCACCTGCTGTGTGTCCCAAGACACCTTC 199

QY 61 LeuAlaTrpGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGln 80
|||||
Db 200 TTGGCCTGGAGAACCAACATAATTCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAG 259

QY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
|||||
Db 260 GCCTCCACAGGTGGCGCTGGAGAAGCTGTTCAGCAGATGGCCGACACCCGCTGTGCTGAAG 319

QY 101 ProGlyTrpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCys 120
|||||
Db 320 CCAGGCTGTTTGTGAGTGCAGGTCAGGCCAATGTGTACAGAGTTACACCTTCTACTGC 379

QY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg 140
|||||
Db 380 CAACCATGCTAGACTGCGGGGCCCTGCACCGCCACACACGCGTACTGTGTCCGACAGA 439

QY 141 AspThrAspCysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSer 160
|||||
Db 440 GATACTGACTGTGGACCTGCCTGCCTGCTGTATGAAACATGGCGATGGCTGCGTGTCC 499

QY 161 CysProThr 163
|||||
Db 500 TGCCCCACG 508

RESULT 11
AI203624

LOCUS
DEFINITION AI203624 508 bp mRNA linear EST 29-OCT-1998
ge75f02.x1 Soares-fetal_lung_NbHL19W Homo sapiens cDNA clone
IMAGE:1744827 3' similar to SW:WSL1_HUMAN Q93038 WSL-1 PROTEIN
PRECUSOR ; , mRNA sequence.
AI203624
AI203624.1 GI:3756230

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 508)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1699 Std Error: 0.00
Seq primer: -40UP from Glibco
High quality sequence stop: 442.
Location/Qualifiers

FEATURES
source
1. 508
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1744827"
/clone_lib="Soares_fetal_lung_NbHL19W"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: lung; Vector: pT7T3D (Pharmacia) with a

modified polylinker; site_1: Not I; site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAGTGGAGCGCGCAATTTTCTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares fetal heart NDH19W."

BASE COUNT 82 a 161 c 159 g 106 t
ORIGIN

Alignment Scores:
Pred. No.: 3.19e-80 Length: 508
Score: 943.00 Matches: 160
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 85.65% Indels: 0
DB: 9 Gaps: 0

US-09-993-234-6_COPY_19_204 (1-186) x A1203624 (1-508)

OY 1 LeuLeuGlyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
DB 29 CTGCTGGGGGGCCGGGGCCAGGCGGCACTGCTAGCCCAAGTGACTGTGCCGGTGAC 88
OY 21 PheHisLysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlnHisTyrLeuLys 40
DB 89 TTCCACAGAGAATTGGTCTGTTTGTGCAGAGGCTGCCAGCGGGCACTACCTGAAG 148
OY 41 AlaProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPhe 60
DB 149 GCCCCTGCACGGAGGCCCTGGGCACTCCACCTGCTGTGTGCCCAAGACACCTTC 208
OY 61 LeuAlaTirpGluAsnHisHisAsnSerGlnCysAlaArgCysGlnAlaCysAspGluGln 80
DB 209 TTGGCCTGGGAGAACCAACCATTAATTCGAATGTGCCCGCTGCCAGGCTGTGATGAGCAG 268
OY 81 AlaSerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLys 100
DB 269 GCCCTCCAGGTGGCGCTGGAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGCTGAAG 328
OY 101 ProGlyTirpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCys 120
DB 329 CCAGGCTGTGTGGAGTGCACGTCACCAATGTGTACAGCAGTTCACCTTCTACTGC 388
OY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg 140
DB 389 CAACCATGCTAGACTGCGGGCCCTGCACCGCACACACGGCTACTCTGTCCCGCAGA 448
OY 141 AspThrAspCysGlyThrCysLeuProGlyPheTyrGlnHisGlyAspGlyCysValSer 160
DB 449 GATACCTGACTGTGGGACCTGCGCTGCTTATGACATGGCGATGGCTGCGTGTCC 508

RESULT 12
BM741016

LOCUS BM741016 492 bp mRNA linear EST 01-MAR-2002
DEFINITION K-EST0013376 S6SNU620 Homo sapiens cDNA clone S6SNU620-2-C03 5',
mRNA sequence.
ACCESSION BM741016
VERSION .BM741016.1 GI:19062345

KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 492)

AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001

JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 2 row: C column: 03
High quality sequence stop: 492.
location/Qualifiers

FEATURES
source 1. 492
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="S6SNU620-2-C03"
/clone_lib="S6SNU620"
/sex="F"
/tissue_type="Ascites"
/cell_type="Scattering floating"
/cell_line="SNU-620"
/lab_host="Top10F"
/note="Organ: Stomach; Vector: pcNS; Site_1: EcoRI;
Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tabacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dT-selected mRNA by
priming with dT-tailed vector. The dT-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F' by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."

BASE COUNT 85 a 157 c 146 g 104 t
ORIGIN

Alignment Scores:
Pred. No.: 1.77e-79 Length: 492
Score: 935.00 Matches: 161
Percent Similarity: 99.38% Conservative: 0
Best Local Similarity: 99.38% Mismatches: 1
Query Match: 84.92% Indels: 1
DB: 14 Gaps: 0

US-09-993-234-6_COPY_19_204 (1-186) x BM741016' (1-492)

OY 2 LeuGlyAlaArgAlaGlnGlyGlyThrArgSerProArgCysAspCysAlaGlyAspPhe 21
DB 2 CTGGGGGGCCGGGCCA-GGGGGCACTGCTAGCCCCAGGTGTGACTGTGCCGGTGACTTC 60
OY 22 HisLysLysIleGlyLeuPheCysCysArgGlyCysProAlaGlnHisTyrLeuLysAla 41
DB 61 CACAAGAAGATTGCTGTTTGTGTGCAGAGGCTGCCAGCGGGGCACCTGAAGGCC 120
OY 42 ProCysThrGluProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeu 61
DB 121 CCTTGACAGGAGCCCTGCGCACTCCACCTGCTGTGTGTCCCAAGACACCTTCTTG 180
OY 62 AlaTirpGluAsnHisHisAsnSerGlnCysAlaArgCysGlnAlaCysAspGluGlnAla 81
DB 181 GCCTGGAGAACCAACCATTAATTCGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCC 240
OY 82 SerGlnValAlaLeuGluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysPro 101
DB 241 TCCAGAGTGGCGCTGGAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGCTGAAGCCA 300
OY 102 GlyTirpPheValGluCysGlnValSerGlnCysValSerSerProPheTyrCysGln 121
DB 301 GGCTGTGTGTGAGTGCACGTCAGCCCAATGTGTACAGCAGTTCACCCCTTCTACTGCCAA 360

DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
<http://image.lnl.gov>
Plate: LAM12833 row: n column: 03
High quality sequence stop: 689.

FEATURES

source
1.1010
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5770562"
/clone_lib="NIH_MGC_121"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
fetal brains, female age 20 weeks, female age 24 weeks,
and male age 26 weeks. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
0.7-3.5 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 017. Note:
this is a NIH_MGC Library."

BASE COUNT 179 a 353 c 287 g 191 t
ORIGIN

Alignment Scores:

Pred. No.: 1.58e-72 Length: 1010
Score: 867.00 Matches: 146
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 78.75% Indels: 0
DB: 14 Gaps: 0

US-09-993-234-6_COPY_19_204 (1-186) x BQ068309 (1-1010)

QY 36 GLYHISTYRLEULYSALAPROCYSTHRLUPROCYSGLYASNSErThrcysleuValcys 55
|||||
Db 50 GGGACACTACCTGAAGGCCCCCTTGACCGAGCCCTCGCGCACTCCACCTGCTGTGTGT 109
QY 56 ProGlnAsPThrPheLeuAlATrPGLuASnHISASnSergLucysAlaArgCysGln 75
|||||
Db 110 CCCCAAGACACCTCTTGCGCTGGGAGAACCAACCATATCTGAATGTGCCCGCTGCCAG 169
QY 76 AlaCysASpGLuGlnAlaSerGlnValAlaLeuGluASnCysSeraAlaValAlaAspThr 95
|||||
Db 170 GCGTGTGATGAGCAGGCGCTCCAGGTGGCGCTGGAGAAGCTGTTACAGCAGTGGCCGACACC 229
QY 96 ArgCysGlyCysLysProGlyTrpPheValGluCysGlnValSergLucysValSerSer 115
|||||
Db 230 CGCTGTGCGCTGTAAGCAGGCGTGTGTGGAGTGCCAGGTCCACCAATGTGTACAGCAGT 289
QY 116 SerProPheTyrCysGlnProCysLeuAspCysGlyAlaLeuHISArgHISThrArgLeu 135
|||||
Db 290 TCACCTTCTACTGCCACCAATGCTAGACTGGGGGGCCCTGCACACCGCGCTA 349
QY 136 LeuCysSerArgArgAspThrAspCysGlyThrCysLeuProGlyPheTyrGluHISGly 155
|||||
Db 350 CTCTGTTCCTCCGACAGATACTGACTGTGGACCTGCGCTGCTTCTATGAACATGGC 409
QY 156 AspGlyCysValSerCysProThrSerThrLeuGlySerCysProGluArgCysAlaAla 175
|||||
Db 410 GATGGCTGCGTGTCTGCCCCCAGACACCCCTGGGAGAGCTGTCCAGACGCGTGTGCGCT 469
QY 176 ValCysGlyTrpArgGln 181
|||||
Db 470 GTCGTGGCTGGAGGACAG 487

RESULT 15
LOCUS AM002222 478 bp mRNA linear EST 09-MAR-2000
DEFINITION wt85c09.x1 Soares_thymus_NHFTth Homo sapiens cDNA clone
IMAGE:2514256 3' similar to TR:014866 014866. SOLUBLE DEATH RECEPTOR

3 BETA. ;, mRNA sequence.

ACCESSION AW002222
VERSION AW002222.1 GI:5849138

KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 478)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITILE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgaps-remail.nih.gov

This clone is available royalty-free through LINL ; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.

Insert length: 1648 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 410.

Location/Qualifiers

FEATURES

source

1.478
/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2514256"

/clone_lib="Soares_thymus_NHFTth"

/dev_stage="fetal"

/lab_host="DH10B (phage-resistant)"

/note="Organ: thymus, pooled; Vector: pT7T3D-Pac

(Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; 1st strand cDNA was primed with a Not I -

oligo(dT) primer [5',

TGTTACCAATCTGACAGTGGGAGCGGCCGCAACGTTTCTTTTCTTTTCTTTT 3'],

double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of the modified pT7T3 vector. Library

went through one round of normalization. Library

constructed by Bento Soares and M. Fatima Bonaldo.

"

BASE COUNT 76 a 152 c 150 g 100 t

ORIGIN

Alignment Scores:

Pred. No.: 4.82e-69 Length: 478
Score: 825.50 Matches: 148
Percent Similarity: 98.01% Conservative: 0
Best Local Similarity: 98.01% Mismatches: 3
Query Match: 74.98% Indels: 3
DB: 10 Gaps: 0

US-09-993-234-6_COPY_19_204 (1-186) x AW002222 (1-478)

QY 1 LeuLeuGlyAlaArgAlaGlnGlyThrArgSerProArgCysAspCysAlaGlyAsp 20
|||||
Db 29 CTGCTGGGGGCCCCGGCCAGGGGGCACTCGTAGCCCCAGGTGTGACTGTGCCGCTGAC 88
QY 21 PheHISLysLysIleGlyLeuPheCysArgGlyCysProAlaGlyHISLysLeuLys 40
|||||
Db 89 TTCACACAGAAGATTGCTGTGTTGTTCAGAGGCTGCCACGGGGGCACTACTGAAG 148
QY 41 AlaProCysThrGluProCysGlyAsnSerThrcysleuValCysProGlnAsPThrPhe 60
|||||
Db 149 GCGCCCTTGACAGGAGCCCTGCGGCACTCCACCTGCTGTGTGTCCCAAGACACCTTC 208
QY 61 LeuAlATrPGLuASnHISASnSergLucysAlaArgCysGlnAlaCysAspGluGln 80
|||||
Db 209 TTGGCTGGGAGAACACCATATCTGAAATGTGCCCGCTGCGCAGCTGTGATGAGCAG 268
QY 81 AlaSergInValAlaLeuGluASnCysSeraAlaValAlaAspThrArgCysGlyCysLys 100
|||||
Db 269 GCCTCCAGGTGGCGCTGGAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGCTGTAAG 328
QY 101'ProGlyTrpPheValGluCysGlnValSergLucysValSerSerProPheTyrCys 120
|||||

Db 329 CCAGGCTGGTTGTGAGTGCAGGTCAGCCAATGTGTACAGCAGTTCAACCCCTTCTACTGC 388
QY 121 GlnProCysLeuAspCysGlyAlaLeuHisArgHisThrArgLeuLeuCysSerArgArg 140
Db 389 CAACCATGCTAGACTGGGGGCCCTGCACCGCCACAA-CGGCTACTCTGTTC-CGCAGA 446
QY 141 AspThrAspCysGlyThrCysLeuProGlyPhe 151
Db 447 GATCT-GACTGTGGGACCTGCCCTGCCCTGCTT 478

Search completed: April 6, 2003, 23:25:29
Job time : 1167.45 secs

GenCore version 5.1.4-p5-4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 6, 2003, 15:35:34 ; Search time 825.126 Seconds

(without alignments)
2504.221 Million cell updates/sec

Title: US-09-993-234-6_COPY_339_409
Perfect score: 368
Sequence: 1 MDAVPARRWKEFVRTLGIRE.....LGAVYALLERMGLDGCVEDL 71

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+p2n.model -DEV=xlh
-Q=/cgn2.1/USPTO_spool/US09993234/runat_27032003.115455_15349/app_query.fasta_1.2346
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09993234_eCGN_1_1_8534_eRunat_27032003.115455_15349 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*

29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	368	100.0	705	9 HSU94508	U94508 Human lymph
2	368	100.0	838	9 HSU94507	U94507 Human lymph
3	368	100.0	952	9 HSU94506	U94506 Human lymph
4	368	100.0	1087	9 HSU94505	U94505 Human lymph
5	368	100.0	1119	9 HSU94509	U94509 Human lymph
6	368	100.0	1143	9 HSU94510	U94510 Human lymph
7	368	100.0	1198	9 HSU94504	U94504 Human lymph
8	368	100.0	1250	6 AX150176	AX150176 Sequence
9	368	100.0	1254	6 AR119657	AR119657 Sequence
10	368	100.0	1254	9 HSU72763	U72763 Human death
11	368	100.0	1254	9 HSU78029	U78029 Human aopto
12	368	100.0	1257	9 HSU94501	U94501 Human lymph
13	368	100.0	1257	9 HSU94502	U94502 Human lymph
14	368	100.0	1355	9 HSU94503	U94503 Human lymph
15	368	100.0	1528	9 HSU83597	U83597 Human death
16	368	100.0	1557	9 HSU75380	U75380 Human apopt
17	368	100.0	1581	9 AK094463	AK094463 Homo sapi
18	368	100.0	1634	9 HSU74611	U74611 Human Apo-3
19	368	100.0	1662	6 AX055442	AX055442 Sequence
20	368	100.0	1662	6 AX201344	AX201344 Sequence
21	368	100.0	1783	6 AR119656	AR119656 Sequence
22	368	100.0	2053	9 AK094488	AK094488 Homo sapi
23	368	100.0	4811	9 AB051851	AB051851 Homo sapi
24	368	100.0	4825	9 AB051850	AB051850 Homo sapi
25	368	100.0	53982	9 AL158217	AL158217 Homo sapi
26	356	96.7	1669	9 AF026070	AF026070 Homo sapi
27	356	96.7	1743	6 AX331947	AX331947 Sequence
28	356	96.7	1743	9 HSN5L1	Y09392 H.sapiens m
29	350	96.7	1763	9 AF026071	AF026071 Homo sapi
30	350	95.1	1619	10 BC017526	BC017526 Mus muscu
31	350	95.1	97483	2 AC118359	AC118359 Rattus no
32	350	95.1	196368	2 AL772240	AL772240 Mus muscu
33	344	93.5	1665	10 AF329969	AF329969 Mus muscu
34	309	84.0	18015	10 AF134858	AF134858 Mus muscu
35	278	75.5	523	11 G37503	G37503 SHGC-57889
36	161	43.8	1956	10 MUSTNER2	M59377 Murine tumo
37	161	43.8	2004	4 SSU19994	U19994 Sus scrofa
38	161	43.8	2048	10 M0SMTNFR1	M60468 Mouse tumor
39	161	43.8	2063	10 M0P55R	X59238 Murine mRNA
40	161	43.8	2086	10 BC004599	BC004599 Mus muscu
41	161	43.8	2154	10 MUSTNFX	L26349 Mus musculu
42	161	43.8	2179	10 MMTNERES	X57796 Mouse mRNA
43	161	43.8	52858	2 AC115960	AC115960 Mus muscu
44	159	43.2	2171	4 AB051103	AB051103 Felis cat
45	157	42.7	2115	10 AF329976	AF329976 Rattus no

ALIGNMENTS

RESULT 1

HSU94508 LOCUS HSU94508 705 bp mRNA linear PRI 15-MAY-1997
DEFINITION Human lymphocyte associated receptor of death 7 mRNA, alternatively
spliced, complete cds.
ACCESSION U94508
VERSION U94508.1 GI:2071962
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 705)
AUTHORS Sreaton,G.R., Xu,X.N., Olsen,A.L., Cowper,A.E., Tan,R.,
McMichael,A.J. and Bell,J.I.
TITLE LARD: a new lymphoid-specific death domain containing receptor
regulated by alternative pre-mRNA splicing
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)
MEDLINE 97272273
PUBMED 9114039
REFERENCE 2 (bases 1 to 705)
AUTHORS Sreaton,G.R.
TITLE Direct Submission
JOURNAL Submitted (19-MAR-1997) Molecular Immunology Group, Institute of
Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3
9DU, UK
FEATURES
source location/Qualifiers
1. 705
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Hela"
/cell_type="lymphocyte"
1. 705
/function="mediates apoptosis"
/note="similar to Fas and TNF-R1; lacks transmembrane
domain; possibly soluble; LARD-6; LARD-7; NGFR family
member"
/codon_start=1
/product="lymphocyte associated receptor of death 7"
/protein_id="AAC51313.1"
/db_xref="GI:2071963"
/translation="MEQRPRGCAVAALLLVLGARAQGTRSPRCDCAGDFHKKIG
LFCRCGPADAGMEALTPPATLSPIDSAHTLAPDSEKICTVOLGNSWTGYP
PETOALCPQVTSWDLPSRALGPAAPTLSPESPAQSPAMMLQPGPOLYDMDAVP
ARRWKEFVRTIGLREAEIEAVEVEIGFRDQYEMLKRWKQQQPAIGAVYAALEKRG
LDGVEDLRSRLQRCGP"
misc_feature 160..161
/note="deletion compared to LARD 1a, deposited in GenBank
Accession Number U94501, probable skipping of putative
exons 3, 4, 5, 6 and 7"
BASE COUNT 112 a 236 c 248 g 109 t
ORIGIN
Alignment Scores:
Pred. No.: 6.17e-32 Length: 705
Score: 368.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-09-993-234-6_COPY_339_409 (1-71) x HSU94508 (1-705)
QY 1 MetaspalaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGlu 20
Db 466 ATGACGCGGTCCACAGCGCGGTGGAAGAGTTCTGTCGCGCAGCTGGCGGAG 525
QY 21 AlagluileGluAlaValGluValGluileGlyArgPheArgAspGlnIntyrglumet 40
Db 526 GCAGAGATCGAAGCCGTGAGGTGAGATCGCGCTTCGAGACCAAGCAGTACGAGATG 585
QY 41 LeuysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGlu 60
Db 586 CTCAGCGGTGGCGCAGCAGACCCCGCGGCTCTGAGCGCTTACGGCGCCTGAG 645

QY 61 ArgMetGlyLeuAspGlyCysValGluAspLeu 71
Db 646 CGCATGGGGCTGGACGCGCTGCGTGAAGACTTG 678
RESULT 2
LOCUS HSU94507
DEFINITION HSU94507 838 bp mRNA linear PRI 15-MAY-1997
Human lymphocyte associated receptor of death 6 mRNA, alternatively
spliced, complete cds.
ACCESSION U94507
VERSION U94507.1 GI:2071960
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 838)
AUTHORS Sreaton,G.R., Xu,X.N., Olsen,A.L., Cowper,A.E., Tan,R.,
McMichael,A.J. and Bell,J.I.
TITLE LARD: a new lymphoid-specific death domain containing receptor
regulated by alternative pre-mRNA splicing
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)
MEDLINE 97272273
PUBMED 9114039
REFERENCE 2 (bases 1 to 838)
AUTHORS Sreaton,G.R.
TITLE Direct Submission
JOURNAL Submitted (19-MAR-1997) Molecular Immunology Group, Institute of
Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3
9DU, UK
FEATURES
source location/Qualifiers
1. 838
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Hela"
/cell_type="lymphocyte"
1. 381
/function="mediates apoptosis"
/note="similar to Fas and TNF-R1; truncated before the
transmembrane domain; possibly soluble; LARD-6"
/codon_start=1
/product="lymphocyte associated receptor of death 6"
/protein_id="AAC51312.1"
/db_xref="GI:2071961"
/translation="MEQRPRGCAVAALLLVLGARAQGTRSPRCDCAGDFHKKIG
LFCRCGPAAISOVALKNCASAVADTRCGCKPGWFVEQVSOVSSSPFYCQPLDCGAL
HRHTRLCHPSVTILGRRPHPSSTS"
misc_feature 160..161
/note="deletion compared to LARD 1a, deposited in GenBank
Accession Number U94501, probable skipping of putative
exon 3"
misc_feature 328..329
/note="deletion compared to LARD-1a, deposited in GenBank
Accession Number U94501, probably due to skipping of
putative exons 5, 6 and 7, leading to premature
transcriptional termination"
BASE COUNT 134 a 281 c 285 g 138 t
ORIGIN
Alignment Scores:
Pred. No.: 7.38e-32 Length: 838
Score: 368.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-09-993-234-6_COPY_339_409 (1-71) x HSU94507 (1-838)
QY 1 MetaspalaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGlu 20
Db 599 ATGACGCGGTCCACAGCGCGCTGGAAGAGTTCTGTCGCGCAGCTGGCGGAG 658

QY 21 AlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGluMet 40
Db 659 GCAGAGATCGAAGCCGCTGGAGGTGGAGATCGGCCCTTCCGAGACCAGCAGTACGAGATG 718
QY 41 LeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGlu 60
Db 719 CTCAGACGCTGGCGCCAGCAGACGCCCGGGCCTCGAGCCGTTTACGCGGCCCTGGAG 778
QY 61 ArgMetGlyLeuAspGlyCysValGluAspLeu 71
Db 779 CGCATGGGGCTGGACGCGCTGCGGAAGACTTG 811
RESULT 3
HSU94506 952 bp mRNA linear PRI 15-MAY-1997
LOCUS Human lymphocyte associated receptor of death 5 mRNA, alternatively
DEFINITION spliced, complete cds.
ACCESSION U94506
VERSION U94506.1 GI:2071958
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 952)
.AUTHORS Screaton,G.R., Xu,X.N., Olsen,A.L., Cowper,A.E., Tan,R.,
McMichael,A.J. and Bell,J.I.
TITLE LARD: a new lymphoid-specific death domain containing receptor
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)
MEDLINE 97272273
PUBMED 9114039
REFERENCE 2 (bases 1 to 952)
.AUTHORS Screaton,G.R.
TITLE Direct Submission
JOURNAL Submitted (19-MAR-1997) Molecular Immunology Group, Institute of
Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3
9DU, UK
FEATURES
source location/Qualifiers
1.952 /organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Hela"
/cell_type="lymphocyte"
1.411 /function="mediates apoptosis"
/note="LARD-5; similar to Fas and TNF-R1; possibly
soluble; truncated before the transmembrane domain"
/codon_start=1
/product="lymphocyte associated receptor of death 5"
/protein_id="AAC51311.1"
/db_xref="GI:2071959"
/translation="MEQRPFGCAVAALLLVILGARAQGGTRSPRCDCAGDFHKKIG
LFCRCGCPASQVALENCASAVADTRCGKPGWFEVCQVSQCVSSSPFYCQPLDCGAL
HRHRLICSRDITDCGTCLPGFYEHDGCVSCTP"
160.161 /note="deletion compared to LARD 1a, deposited in GenBank
Accession Number U94501, probable skipping of putative
exon 3"
misc_feature 407.408
/note="deletion compared to LARD-1a, deposited in GenBank
Accession Number U94501, probably due to skipping of
putative exons 6 and 7, leading to premature
transcriptional termination"
BASE COUNT 154 a 317 c 319 g 162 t
ORIGIN
Alignment Scores:
Pred. No.: 8.42e-32 length: 952
Score: 368.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-09-993-234-6_copy_339_409 (1-71) x HSU94506 (1-952)
QY 1 MetaSpAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGlu 20
Db 713 ATGACAGCGGTCCACGCGCGCTGGAAGAGATTGTCGCGCACGCTGGGGCTGGCGAG 772
QY 21 AlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGluMet 40
Db 773 GCAGAGATCGAAGCCGCTGGAGGTGGAGATCGGCCCTTCCGAGACCAGCAGTACGAGATG 832
QY 41 LeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGlu 60
Db 833 CTCAGACGCTGGCGCCAGCAGACGCCCGGGCCTCGAGCCGTTTACGCGGCCCTGGAG 892
QY 61 ArgMetGlyLeuAspGlyCysValGluAspLeu 71
Db 893 CGCATGGGGCTGGACGCGCTGCGGAAGACTTG 925

RESULT 4
HSU94505 1087 bp mRNA linear PRI 15-MAY-1997
LOCUS Human lymphocyte associated receptor of death 4 mRNA, alternatively
DEFINITION spliced, complete cds.
ACCESSION U94505
VERSION U94505.1 GI:2071956
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1087)
.AUTHORS Screaton,G.R., Xu,X.N., Olsen,A.L., Cowper,A.E., Tan,R.,
McMichael,A.J. and Bell,J.I.
TITLE LARD: a new lymphoid-specific death domain containing receptor
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)
MEDLINE 97272273
PUBMED 9114039
REFERENCE 2 (bases 1 to 1087)
.AUTHORS Screaton,G.R.
TITLE Direct Submission
JOURNAL Submitted (19-MAR-1997) Molecular Immunology Group, Institute of
Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3
9DU, UK
FEATURES
source location/Qualifiers
1.1087 /organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Hela"
/cell_type="lymphocyte"
1.546 /function="mediates apoptosis"
/note="LARD-4; similar to Fas and TNF-R1; possibly
soluble; truncated before the transmembrane domain"
/codon_start=1
/product="lymphocyte associated receptor of death 4"
/protein_id="AAC51310.1"
/db_xref="GI:2071957"
/translation="MEQRPFGCAVAALLLVILGARAQGGTRSPRCDCAGDFHKKIG
LFCRCGCPAGHYLRAPCTEPCGNSITCLVCPDPTFLAMENHNSSECARCOQDQASQV
ALENCASAVADTRCGKPGWFEVCQVSQCVSSSPFYCQPLDCGALHRHRLICSRDIT
DCGTCLPGFYEHDGCVSCTP"
542.543 /note="deletion compared to LARD 1a, deposited in GenBank
Accession Number U94501, probable skipping of putative
exons 6 and 7 leading to premature transcriptional
termination"
BASE COUNT 180 a 363 c 355 g 189 t
ORIGIN

Alignment Scores:

Pred. No.: 9.65e-32 Length: 1087
Score: 368.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-993-234-6_COPY_339_409 (1-71) x HSU94505 (1-1087)

OY 1 MetaspalavalProalaArgArGTTrPLysGluPheValArgThrLeuGlyLeuArgGlu 20
|||||
Db 848 ATGACGCGGTCCAGCGCGCGCTGGAAGAGTTCTGCGCACGCTGGGGCTGCGGAG 907
OY 21 AlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrgluMet 40
|||||
Db 908 GCAGAGATCGAAGCGCTGAGGTGAGATCGCGCTTCCGAGACCAGCAGTACGAGATG 967
OY 41 LeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGlu 60
|||||
Db 968 CTCAGCGCTGCGCCAGACAGACCCCGCGGCTCGGAGCCGTTACGCGGCCCTGGAG 1027
OY 61 ArgMetGlyLeuAspGlyCysValGluAspLeu 71
|||||
Db 1028 CGCATGGGGCTGACGCGCTGCTGGAAGACTTG 1060

RESULT 5 HSU94509 1119 bp mRNA linear PRI 15-MAY-1997
LOCUS Human lymphocyte associated receptor of death 8 mRNA, alternatively
spliced, complete cds.
ACCESSION U94509
VERSION U94509.1 GI:2071964
KEYWORDS
SOURCE
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1119)
AUTHORS Sreaton,G.R., Xu,X.N., Olsen,A.L., Cowper,A.E., Tan,R.,
McMichael,A.J. and Bell,J.I.
TITLE LARD: a new lymphoid-specific death domain containing receptor
regulated by alternative pre-mRNA splicing
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)
MEDLINE 97272273
PUBMED 9114039
REFERENCE 2 (bases 1 to 1119)
AUTHORS Sreaton,G.R.
TITLE Direct Submission
JOURNAL Submitted (19-MAR-1997) Molecular Immunology Group, Institute of
Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3
9DU, UK

FEATURES
source
1. 1119 location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Hela"
/cell_type="lymphocyte"
1. 1119
/function="mediates apoptosis"
/note="LARD-8; NGFR family member; similar to Fas and
TNF-R1"
/codon_start=1
/product="lymphocyte associated receptor of death 8"
/protein_id="AAC51314.1"
/db_xref="GI:2071965"

CDS
/translation="MEQRPRGCAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIG
LFCRCGPAAASQVALENCASAVADTRCGCKPGWFEVCQYSCVSSPFYCQPCLDGAL
HRHTRLICSRKRDTCGTCLEPGFEHGDGCVSPTSLGSCPERCAAVCGWRQMFVVOY
LLAGLVVPLLGATLTYTYRHCHWPKPLVTADAGMALTPRPATHLSPIDSAHTLLA
PPDSSEKICTVOLVGNSTWPGYPTQALCPQVTMSWDQLPSRALGPAAAPTLSPEP
AGSPAMMLQPGPOLYVDADAVPARRWKEFVRTLGLREAEIEAVEVEIGRFRDOYEML
KRWROQOPAGIGAIVYALERMGLDGCVEDLRSLQKGP"

misc_feature

160. .161
/note="deletion compared to LARD 1a, deposited in GenBank
Accession Number U94501, probable skipping of putative
exon 3"
BASE COUNT 175 a 374 c 371 g 199 t
ORIGIN

Alignment Scores:

Pred. No.: 9.94e-32 Length: 1119
Score: 368.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-993-234-6_COPY_339_409 (1-71) x HSU94509 (1-1119)

OY 1 MetaspalavalProalaArgArGTTrPLysGluPheValArgThrLeuGlyLeuArgGlu 20
|||||
Db 880 ATGACGCGGTCCAGCGCGCGCTGGAAGAGTTCTGCGCACGCTGGGGCTGCGGAG 939
OY 21 AlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrgluMet 40
|||||
Db 940 GCAGAGATCGAAGCGCTGAGGTGAGATCGCGCTTCCGAGACCAGCAGTACGAGATG 999
OY 41 LeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGlu 60
|||||
Db 1000 CTCAGCGCTGCGCCAGACAGACCCCGCGGCTCGGAGCCGTTACGCGGCCCTGGAG 1059
OY 61 ArgMetGlyLeuAspGlyCysValGluAspLeu 71
|||||
Db 1060 CGCATGGGGCTGACGCGCTGCTGGAAGACTTG 1092

RESULT 6 HSU94510 1143 bp mRNA linear PRI 15-MAY-1997
LOCUS Human lymphocyte associated receptor of death 9 mRNA, alternatively
spliced, complete cds.
ACCESSION U94510
VERSION U94510.1 GI:2071966
KEYWORDS
SOURCE
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1143)
AUTHORS Sreaton,G.R., Xu,X.N., Olsen,A.L., Cowper,A.E., Tan,R.,
McMichael,A.J. and Bell,J.I.
TITLE LARD: a new lymphoid-specific death domain containing receptor
regulated by alternative pre-mRNA splicing
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)
MEDLINE 97272273
PUBMED 9114039
REFERENCE 2 (bases 1 to 1143)
AUTHORS Sreaton,G.R.
TITLE Direct Submission
JOURNAL Submitted (19-MAR-1997) Molecular Immunology Group, Institute of
Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3
9DU, UK

FEATURES
source
1. 1143 location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Hela"
/cell_type="lymphocyte"
1. 1143
/function="mediates apoptosis"
/note="LARD-9; NGFR family member; similar to Fas and
TNF-R1"
/codon_start=1
/product="lymphocyte associated receptor of death 9"
/protein_id="AAC51315.1"
/db_xref="GI:2071967"

CDS

/translation="MEQRPRGCAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIG
LFCRCGPAAASQVALENCASAVADTRCGCKPGWFEVCQYSCVSSPFYCQPCLDGAL
HRHTRLICSRKRDTCGTCLEPGFEHGDGCVSPTSLGSCPERCAAVCGWRQMFVVOY
LLAGLVVPLLGATLTYTYRHCHWPKPLVTADAGMALTPRPATHLSPIDSAHTLLA
PPDSSEKICTVOLVGNSTWPGYPTQALCPQVTMSWDQLPSRALGPAAAPTLSPEP
AGSPAMMLQPGPOLYVDADAVPARRWKEFVRTLGLREAEIEAVEVEIGRFRDOYEML
KRWROQOPAGIGAIVYALERMGLDGCVEDLRSLQKGP"

misc_feature 598.599 /note="deletion compared to LARD 1a, deposited in GenBank Accession Number U94501, probable skipping of putative exon 7 encoding the transmembrane domain"

BASE COUNT 188 a 378 c 378 g 199 t

ORIGIN

Alignment Scores:

Pred. No.:	1.02e-31	Length:	1143
Score:	368.00	Matches:	71
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-993-234-6_COPY_339_409 (1-71) x HSU94510 (1-1143)

OY 1 MetaspalaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGlu 20
|||||
DB 904 ATGGACGGCGTCCACAGCGCGCTGGAAGAGATTCTGCGCACGCTGGGGCTGGCGAG 963

OY 21 AlaGluIleGluAlaValAlaGluValIleGlyArgPheArgAspGlnGlnTyrGluMet 40
|||||
DB 964 GCAGAGATCGAAGCCGTGAGGTGAGATCGCGCTTCCGAGACAGACAGTACGAGATG 1023

OY 41 LeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGlu 60
|||||
DB 1024 CTCAGCGCTGGCGCCAGACAGCCCGCGGCTCGAGCCGTTTACGCGGCTGGAG 1083

OY 61 ArgMetGlyLeuAspGlyCysValGluAspLeu 71
|||||
DB 1084 CGCATGGGGCTGGACGCGCTGCGTGAAGACTTG 1116

RESULT 7
HSU94504 1198 bp mRNA linear PRI 15-MAY-1997
LOCUS Human lymphocyte associated receptor of death 3 mRNA, alternatively spliced, complete cds.

DEFINITION

ACCESSION U94504
VERSION U94504.1 GI:2071954

KEYWORDS

SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE 1 (bases 1 to 1198)
AUTHORS MCMichael,A.J. and Bell,J.I.
TITLE LARD: a new lymphoid-specific death domain containing receptor regulated by alternative pre-mRNA splicing
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)
MEDLINE 97272273
PUBMED 9114039
REFERENCE 2 (bases 1 to 1198)
AUTHORS Screation,G.R.
TITLE Direct Submission
JOURNAL Submitted (19-MAR-1997) Molecular Immunology Group, Institute of Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3 9DU, UK

FEATURES
source 1.1198
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Hela"
/cell_type="lymphocyte"
1.657

CDS

/function="mediates apoptosis"
/note="LARD-3; similar to Fas and TNF-R1; possibly soluble; truncated before the transmembrane domain"
/codon_start=1
/product="lymphocyte associated receptor of death 3"
/protein_id="AAC51309.1"
/db_xref="GI:2071955"
/translation="MEORPRGCAVAALLLVLGARAOGGTRSPRCDACDDEHKKIG LFCRCGPAGHYLKAPCTEPCGNSTCLVCPDPTFLAWENHNHNSCARCQACDEQASOV ALENCASAVADTRCGCKPGWFEVCQVSSSPFYCQPLDCGALHHRTRLCSRDTCGTCLPGFYEHGDCVSCPTLGGPAGWPCGPPAWGHPDLHIPPLASQAPGYCR"

misc_feature 542.543 /note="deletion compared to LARD 1a, deposited in GenBank Accession Number U94501, probable skipping of putative exon 6 leading to premature transcriptional termination"

BASE COUNT 193 a 405 c 384 g 216 t

ORIGIN

Alignment Scores:

Pred. No.:	1.07e-31	Length:	1198
Score:	368.00	Matches:	71
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-993-234-6_COPY_339_409 (1-71) x HSU94504 (1-1198)

OY 1 MetaspalaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGlu 20
|||||
DB 959 ATGGACGGCGTCCACAGCGCGCTGGAAGAGATTCTGCGCACGCTGGGGCTGGCGAG 1018

OY 21 AlaGluIleGluAlaValAlaGluValIleGlyArgPheArgAspGlnGlnTyrGluMet 40
|||||
DB 1019 GCAGAGATCGAAGCCGTGAGGTGAGATCGCGCTTCCGAGACAGACAGTACGAGATG 1078

OY 41 LeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGlu 60
|||||
DB 1079 CTCAGCGCTGGCGCCAGACAGCCCGCGGCTCGAGCCGTTTACGCGGCTGGAG 1138

OY 61 ArgMetGlyLeuAspGlyCysValGluAspLeu 71
|||||
DB 1139 CGCATGGGGCTGGACGCGCTGCGTGAAGACTTG 1171

RESULT 8
AX150176 1250 bp DNA linear PAT 08-JUN-2001
LOCUS Sequence 1 from Patent WO0135995.
DEFINITION AX150176
ACCESSION AX150176
VERSION AX150176.1 GI:14348204

KEYWORDS human.

SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE 1 (bases 1 to 1250)
AUTHORS Tittle,T.V. and Wegmann,K.W.
TITLE Tr3-specific binding agents and methods for their use
JOURNAL Patent: WO 0135995-A 1 25-MAY-2001;
TITLE, Thomas V. (US); Wegmann, Keith W. (US)

FEATURES
source 1.1250
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 201 a 420 c 406 g 223 t

ORIGIN

Alignment Scores:

Pred. No.:	1.11e-31	Length:	1250
Score:	368.00	Matches:	71
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0

Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-993-234-6_COPY_339_409 (1-71) x AX150176 (1-1250)
QY 1 MetaspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGlu 20
DB 1011 ATGGACGGCGGTCCAGCGCGCGCTGGAAGAGATTCTGCACACGCTGGGGCTGCGCGAG 1070
QY 21 AlaGluIleGluAlaValAlaGluValGluIleGlyArgPheArgAspGlnGlnTyrgluMet 40
DB 1071 GCAGAGATCGAAGCCGCTGGAGGTGAGATCGGCCGCTTCCGAGACCAGCAGTACGAGATG 1130
QY 41 LeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGlu 60
DB 1131 CTCAGCGCTGGCGCCAGCAGCAGCCCGCGGCTCGAGCCGTTACCGCGCGCTGGAG 1190
QY 61 ArgMetGlyLeuAspGlyCysValGluAspLeu 71
DB 1191 CGCATGGGGCTGGACGGCTCGCTGGAAGACTTG 1223
RESULT 9
AR119657 1254 bp DNA linear PAT 16-MAY-2001
LOCUS AR119657
DEFINITION Sequence 3 from patent US 6153402.
ACCESSION AR119657
VERSION AR119657.1 GI:14102356
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
BASE COUNT 201 a 420 c 407 g 226 t
ORIGIN
Alignment Scores:
Pred. No.: 1.12e-31 Length: 1254
Score: 368.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-993-234-6_COPY_339_409 (1-71) x AR119657 (1-1254)
QY 1 MetaspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGlu 20
DB 1015 ATGGACGGCGGTCCAGCGCGCGCTGGAAGAGATTCTGCACACGCTGGGGCTGCGCGAG 1074
QY 21 AlaGluIleGluAlaValAlaGluValGluIleGlyArgPheArgAspGlnGlnTyrgluMet 40
DB 1075 GCAGAGATCGAAGCCGCTGGAGGTGAGATCGGCCGCTTCCGAGACCAGCAGTACGAGATG 1134
QY 41 LeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGlu 60
DB 1135 CTCAGCGCTGGCGCCAGCAGCAGCCCGCGGCTCGGAGCCGTTACGCGCGCTGGAG 1194
QY 61 ArgMetGlyLeuAspGlyCysValGluAspLeu 71
DB 1195 CGCATGGGGCTGGACGGCTCGCTGGAAGACTTG 1227
RESULT 10
HSU72763 1254 bp mRNA linear PRI 15-NOV-1996
LOCUS HSU72763
DEFINITION Human death receptor 3 (DR3) mRNA, complete cds.
ACCESSION U72763.1 GI:1669511
VERSION

KEYWORDS Homo sapiens.
SOURCE Homo sapiens
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
gene
CDS
BASE COUNT 201 a 420 c 407 g 226 t
ORIGIN
Alignment Scores:
Pred. No.: 1.12e-31 Length: 1254
Score: 368.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-09-993-234-6_COPY_339_409 (1-71) x HSU72763 (1-1254)
QY 1 MetaspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGlu 20
DB 1015 ATGGACGGCGGTCCAGCGCGCGCTGGAAGAGATTCTGCACACGCTGGGGCTGCGCGAG 1074
QY 21 AlaGluIleGluAlaValAlaGluValGluIleGlyArgPheArgAspGlnGlnTyrgluMet 40
DB 1075 GCAGAGATCGAAGCCGCTGGAGGTGAGATCGGCCGCTTCCGAGACCAGCAGTACGAGATG 1134
QY 41 LeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGlu 60
DB 1135 CTCAGCGCTGGCGCCAGCAGCAGCCCGCGGCTCGGAGCCGTTACGCGCGCTGGAG 1194
QY 61 ArgMetGlyLeuAspGlyCysValGluAspLeu 71
DB 1195 CGCATGGGGCTGGACGGCTCGCTGGAAGACTTG 1227
RESULT 11
HSU78029 1254 bp mRNA linear PRI 15-JAN-1997
LOCUS HSU78029
DEFINITION Human apoptosis inducing receptor AIR mRNA, complete cds.
ACCESSION U78029

VERSION U78029.1 GI:1778763
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS 1 (bases 1 to 1254)
Degli-Esposti,M.A., Din,W.S., Cosman,D., Smith,C.A. and Goodwin,R.G.
TITLE AIR, A Novel Member of the TNF Receptor Family, Is a Strong Inducer of Apoptosis
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1254)
AUTHORS Degli-Esposti,M.A. and Goodwin,R.G.
TITLE Direct Submission
JOURNAL Submitted (12-NOV-1996) Biochemistry, Immunex Corporation, 51 University St., Seattle, WA 98101, USA
FEATURES
source
1.1254
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/map="1pter"
/cell_type="peripheral blood T-cells"
1.1254
/codon_start=1
/product="apoptosis inducing receptor AIR"
/protein_id="AAB40918.1"
/db_xref="GI:1778764"
/translation="MEQRPRGCAVAALLLVLGARAQGTSPRCDCAGDFHKKIG
LFCCRGCPAGHYLKAPCTEPCGNSTCLVCPDFTFLAMENHNHNSCARCQACDEQASOV
ALENCASAVADTRCGCKPGWFEQVSCVSSPFYCQPCLDGALHRTLRILCSRRDT
DCGTCLPGFEYEHGDCVSCPTSTLGSCPERCAVCGWQMFVQVLLAGLVVPLLLGA
TLTYTYRHWCWPHKPLVTADAGMEALTPPATHTLSPLDSAHHTLAPDSSSEKICTVOL
VGNSTPGYPERQELALCPQVTSWMDQLPSRALGPAAPTLSPESPAGSPAMMLQPGPO
LYDVMADVAPARRMKEFVRTLGLREAIEAVEVEIGRRDQOYEMLKRWQOQPAIGLA
VYALERMGLDGCVEEDLRSRLQRP"
BASE COUNT 201 a 420 c 407 g 226 t
ORIGIN
Alignment Scores:
Pred. No.: 1.12e-31 Length: 1254
Score: 368.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-09-993-234-6_COPY_339_409 (1-71) x HSU78029 (1-1254)
QY 1 MetaspalavalProalaArgarGtrplysGluPhevalArgThrleuGlyleuArgGlu 20
Db 1015 ATGGACGGCGTCCACGCGCGCGTGAAGAGTTCGTGCGCACGCTGGGGCTGCGCGAG 1074
QY 21 AlagluileglualavalgluValgluileglyArgpheaArgaspGlnGlnTyrgluMet 40
Db 1075 GCAGAGATCGAAGCCGTGAGGTGAGATCGGCCGCTTCCGAGACCAAGAGTACGAGATG 1134
QY 41 LeuLysArgTrpArgGlnGlnProAlaGlyLeuGlyAlaValTyraAlaLeuGlu 60
Db 1135 CTCAGCGCTGGCGCCAGCAGACGCCCGGGCTCGGAGCCGTTTACGGCGCCCTGGAG 1194
QY 61 ArgmetGlyLeuAspGlyCysValGluAspLeu 71
Db 1195 CGCATGGGGCTGGACGCGCTGCGTGAAGACTTG 1227
RESULT 12
LOCUS HSU94501 1254 bp mRNA linear PRI 15-MAY-1997
DEFINITION Human lymphocyte associated receptor of death 1a mRNA, complete cds.
ACCESSION U94501
VERSION U94501.1 GI:2071948

KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS 1 (bases 1 to 1254)
McMichael,A.J., Xu,X.N., Olsen,A.L., Cowper,A.E., Tan,R., LARD: a new lymphoid-specific death domain containing receptor regulated by alternative pre-mRNA splicing
Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)
JOURNAL MEDLINE
PUBMED 97272273
REFERENCE 2 (bases 1 to 1254)
AUTHORS Sreaton,G.R.
TITLE Direct Submission
JOURNAL Submitted (19-MAR-1997) Molecular Immunology Group, Institute of Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3 9DU, UK
FEATURES
source
1.1254
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Hela"
/cell_type="lymphocyte"
1.1254
/function="mediates apoptosis"
/note="LARD-1a; membrane protein; similar to Fas and TNF-R1; contains a death domain"
/codon_start=1
/product="lymphocyte associated receptor of death 1a"
/protein_id="AAC51306.1"
/db_xref="GI:2071949"
/translation="MEQRPRGCAVAALLLVLGARAQGTSPRCDCAGDFHKKIG
LFCCRGCPAGHYLKAPCTEPCGNSTCLVCPDFTFLAMENHNHNSCARCQACDEQASOV
ALENCASAVADTRCGCKPGWFEQVSCVSSPFYCQPCLDGALHRTLRILCSRRDT
DCGTCLPGFEYEHGDCVSCPTSTLGSCPERCAVCGWQMFVQVLLAGLVVPLLLGA
TLTYTYRHWCWPHKPLVTADAGMEALTPPATHTLSPLDSAHHTLAPDSSSEKICTVOL
VGNSTPGYPERQELALCPQVTSWMDQLPSRALGPAAPTLSPESPAGSPAMMLQPGPO
LYDVMADVAPARRMKEFVRTLGLREAIEAVEVEIGRRDQOYEMLKRWQOQPAIGLA
VYALERMGLDGCVEEDLRSRLQRP"
BASE COUNT 201 a 420 c 407 g 226 t
ORIGIN
Alignment Scores:
Pred. No.: 1.12e-31 Length: 1254
Score: 368.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-09-993-234-6_COPY_339_409 (1-71) x HSU94501 (1-1254)
QY 1 MetaspalavalProalaArgarGtrplysGluPhevalArgThrleuGlyleuArgGlu 20
Db 1015 ATGGACGGCGTCCACGCGCGCGTGAAGAGTTCGTGCGCACGCTGGGGCTGCGCGAG 1074
QY 21 AlagluileglualavalgluValgluileglyArgpheaArgaspGlnGlnTyrgluMet 40
Db 1075 GCAGAGATCGAAGCCGTGAGGTGAGATCGGCCGCTTCCGAGACCAAGAGTACGAGATG 1134
QY 41 LeuLysArgTrpArgGlnGlnProAlaGlyLeuGlyAlaValTyraAlaLeuGlu 60
Db 1135 CTCAGCGCTGGCGCCAGCAGACGCCCGGGCTCGGAGCCGTTTACGGCGCCCTGGAG 1194
QY 61 ArgmetGlyLeuAspGlyCysValGluAspLeu 71
Db 1195 CGCATGGGGCTGGACGCGCTGCGTGAAGACTTG 1227
RESULT 13
LOCUS HSU94502 1257 bp mRNA linear PRI 15-MAY-1997

DEFINITION Human lymphocyte associated receptor of death 1b mRNA,
alternatively spliced, complete cds.
ACCESSION U94502
VERSION U94502.1 GI:2071950
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1257)
AUTHORS Screation,G.R., Xu,X.N., Olsen,A.L., Cowper,A.E., Tan,R.,
McMichael,A.J. and Bell,J.I.
TITLE LARD: a new lymphoid-specific death domain containing receptor
regulated by alternative pre-mRNA splicing
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)
MEDLINE 97272273
PUBMED 9114039
REFERENCE 2 (bases 1 to 1257)
AUTHORS Screation,G.R.
TITLE Direct Submission
JOURNAL Submitted (19-MAR-1997) Molecular Immunology Group, Institute of
Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3
9DU, UK
FEATURES
source
1.1257
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Hela"
/cell_type="lymphocyte"
1.1257
/function="mediates apoptosis"
/note="LARD-1b; membrane protein; similar to Fas and
TNF-R1; contains a death domain"
/codon_start=1
/product="lymphocyte associated receptor of death 1b"
/protein_id="AAC51307.1"
/db_xref="GI:2071951"
/translation="MEQRPRGCAVAALLLVLLGARAOGGTRSPRCDCAGDFHKKIG
LFCCRGCPAGHYLKAPCTEPCGNSCLVCPDPTFLAWENHNHNSCARCOACDEQASQV
ALENCASAVADTRCGCKPGWFEVCQVSSSPFYCQPCLDGALHRTLRILCSRRDT
DCGTCLPGEYEHGDGCVSCTSTIGSCPERRCAVCGWRFVQVLLAGLVPLLGA
TLTYTRHGWPHKPLVTADEAGMALTPPATHLSPIDSAHTLLAPDSSEKICTVQ
LVGNSWTPPGYPTQDALCPQVWSDQLPSRALGPAAPTLSPESPAGSPAMLOPGP
QLVDVADAVPARRWKEFVRTLGLREAIEAVEVEIGRFDDQYEMLKRWROQOPAGLG
AVYALERMGLDGCVEDLRSRLQKGP"
708.711
/note="insertion compared to LARD-1a, deposited in GenBank
Accession Number U94501, probably represents alternative
3' splice site"
BASE COUNT 202 a 421 c 408 g 226 t
ORIGIN
misc_feature
Alignment Scores:
Pred. No.: 1.12e-31 Length: 1257
Score: 368.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-09-993-234-6_COPY_339_409 (1-71) x HSU94502 (1-1257)
QY 1 MetaspalaValProAlaArgArgTrrplySglupheValArgThrleuglyLeuArgGlu 20
Db 1018 ATGACGCGGTCCAGCGCGCTGGAAGAGTTCGTGCGCACGCTGGGCTGCGCGAG 1077
QY 21 AlagluilegluaAlaValgluValgluileglYArgpheArgaspIngtYrglumet 40
Db 1078 GCAGAGATCGAAGCCGTGAGGTGAGATCGGCCCTCCGAGACACGACAGTACGAGATG 1137
QY 41 LeuLysArgTrrpArgInglngInlProAlaglYleuGlYAlaValTrrAlaAlaLeuGlu 60
Db 1138 CTCAGCGCTGGCCGACGACGACGCCCGGCTCGAGCGCTTACGCGGCCCTGGAG 1197

QY 61 ArgmetcylLeuAspGlyCysValGluAspLeu 71
Db 1198 CGCATGGGGCTGACGCGCTCGTGAAGACTTG 1230
RESULT 14
HSU94503
LOCUS
DEFINITION HSU94503 1355 bp mRNA linear PRI 15-MAY-1997
Human lymphocyte associated receptor of death 2 mRNA, alternatively
spliced, complete cds.
ACCESSION U94503
VERSION U94503.1 GI:2071952
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1355)
AUTHORS Screation,G.R., Xu,X.N., Olsen,A.L., Cowper,A.E., Tan,R.,
McMichael,A.J. and Bell,J.I.
TITLE LARD: a new lymphoid-specific death domain containing receptor
regulated by alternative pre-mRNA splicing
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)
MEDLINE 97272273
PUBMED 9114039
REFERENCE 2 (bases 1 to 1355)
AUTHORS Screation,G.R.
TITLE Direct Submission
JOURNAL Submitted (19-MAR-1997) Molecular Immunology Group, Institute of
Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3
9DU, UK
FEATURES
source
1.1355
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Hela"
/cell_type="lymphocyte"
1.762
/function="mediates apoptosis"
/note="LARD-2; similar to Fas and TNF-R1; possibly
soluble; truncated before the transmembrane domain"
/codon_start=1
/product="lymphocyte associated receptor of death 2"
/protein_id="AAC51308.1"
/db_xref="GI:2071953"
/translation="MEQRPRGCAVAALLLVLLGARAOGGTRSPRCDCAGDFHKKIG
LFCCRGCPAGHYLKAPCTEPCGNSCLVCPDPTFLAWENHNHNSCARCOACDEQASQV
ALENCASAVADTRCGCKPGWFEVCQVSSSPFYCQPCLDGALHRTLRILCSRRDT
DCGTCLPGEYEHGDGCVSCTSTIGSCPERRCAVCGWRFVQVLLAGLVPLLGA
GERGNNHPTPTSCFQCSGSRCSWLALWSPSCLGPP"
599.700
/note="insertion compared to LARD 1a, deposited in GenBank
Accession Number U94501, probable retained intron leading
to premature transcriptional termination"
BASE COUNT 223 a 441 c 451 g 240 t
ORIGIN
misc_feature
Alignment Scores:
Pred. No.: 1.21e-31 Length: 1355
Score: 368.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-09-993-234-6_COPY_339_409 (1-71) x HSU94503 (1-1355)
QY 1 MetaspalaValProAlaArgArgTrrplySglupheValArgThrleuglyLeuArgGlu 20
Db 1116 ATGACGCGGTCCAGCGCGCTGGAAGAGTTCGTGCGCACGCTGGGCTGCGCGAG 1175
QY 21 AlagluilegluaAlaValgluValgluileglYArgpheArgaspIngtYrglumet 40

Db 1176 GCAGAGATCGAAGCCGTGGAGGTGAGATCGGCCGCTTCGAGACCAGCAGTACGAGATG 1235

QY 41 LeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGlu 60
|||||
Db 1236 CTCAGCGCGTGGCGCCAGCAGCAGCAGCCCGGGGCTCGGAGCCGTTTACGGCGCCCTGGAG 1295

QY 61 ArgMetGlyLeuAspGlyCysValGluAspLeu 71
|||||
Db 1296 CGCATGGGCGCTGGACGGCTGCTGGAAGACTTG 1328

RESULT 15
HSU83597 1528 bp mRNA linear PRI 27-JAN-1997
LOCUS Human death domain receptor 3 (DDR3) mRNA, partial cds.

DEFINITION
U83597
ACCESSION
VERSION
U83597.1 GI:1800292

KEYWORDS
U83597.1 GI:1800292

SOURCE
Homo sapiens.
ORGANISM Homo sapiens.

REFERENCE
1 (bases 1 to 1528)
Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.

AUTHORS
Chaudhary, P.M. and Hood, L.E.

TITLE
Direct Submission
JOURNAL Submitted (03-JAN-1997) Molecular Biotechnology, University of Washington, 1705 NE Pacific Street, HSB-K360, Seattle, WA 98195, USA

FEATURES
source location/Qualifiers

1..1528
/organism="Homo sapiens"
/db_xref="taxon:9606"

/chromosome="1"
/map="1p36"

1..1528
/gene="DDR3"

<1..1238
/gene="DDR3"

CDS
/gene="DDR3"

/function="mediates apoptosis when cross-linked"

/note="A TNFR1-related death-domain containing receptor; DR3, WSL-LR, Apo-3, TRAMP; transmembrane form; similar to human EST clone 298913, GenBank Accession Number N71143"

/codon_start=3
/product="death domain receptor 3"

/protein_id="AAB41432.1"

/db_xref="GI:1800293"

/translation="GCAVAALLLVLLGARAQGGTRSPRCDACAGDFHKKIGLEPCRG
CPAGHYLKAPCTEPCGNSCTICVPODTFLAWENHNSCARCOACDEOASOVALENC
AVADTRCGCKPGWFEVCOVSQCVSSPFYCQPCLDGALHRHTRLILCSRRDPTDCTCL
LGFEYHGDGCVSCPSTLGSCEPERCAAVCGWROMFVQVLLGLVVPILIGATLTYTY
RHCWPHKPLVTADAEAMEALTPPATLHSLPLDSAHTLAPDSEKICTVQLVNSWT
PGYPETQEALCPQVTFWSMDQLPSRALGPAAPTLSPESPAGSPAMMLQPGPOLYVMD
AVPARWKEFVRTILGLREAEIAVEVEIGRFDDQYEMLKRWRQQQPAGLGAVYAALE
RMGLDGCVEDLRSRLRGPR"

BASE COUNT 280 a 496 c 470 g 282 t

ORIGIN

Alignment Scores:

Pred. No.: 1.37e-31 Length: 1528

Score: 368.00 Matches: 71

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 9 Gaps: 0

US-09-993-234-6_COPY_339_409 (1-71) x HSU83597 (1-1528)

QY 1 MetAspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGlu 20
|||||

Db 999 ATGAGCGCGGTCCAGCGCGCGGTGAAGAGATTGTCGCGCACGCTGGGGCTGCGCGAG 1058,
QY 21 AlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnIntYrGluMet 40
|||||

Db 1059 GCAGAGATCGAAGCCGTGGAGGTGAGATCGCCGCTTCGAGACCAGCAGTACGAGATG 1118

QY 41 LeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGlu 60
|||||
Db 1119 CTCAGCGCGTGGCGCCAGCAGCAGCAGCCCGGGGCTCGGAGCCGTTTACGGCGCCCTGGAG 1178

QY 61 ArgMetGlyLeuAspGlyCysValGluAspLeu 71
|||||
Db 1179 CGCATGGGCGCTGGACGGCTGCTGGAAGACTTG 1211

Search completed: April 6, 2003, 21:08:13
Job time : 829.126 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 6, 2003, 15:33:09 ; Search time 66.109 Seconds
(without alignments)
2418.610 Million cell updates/sec

Title: US-09-993-234-6_COPY_339_409
Perfect score: 368
Sequence: 1 MDAVPAARKWEKRTVLGLRE.....LGAVYAALERMGLDGCVEDL 71

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2185239 segs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO/spool/US0993234/runat_27032003_115454_15312/app_query.fasta_1.2346
-DB=N_Geneseq_101002 -QFMT=fastap -SUFFIX=ring -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US0993234_@CGN_1_1.660 @runat_27032003_115454_15312 -NCPU=6 -ICPU=3
-NO_XLPHY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMECUT=120
-WARN_TIMECUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_101002: *
1: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT: *
2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT: *
3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT: *
4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT: *
5: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT: *
6: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT: *
7: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT: *
8: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT: *
9: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT: *
10: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT: *
11: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT: *
12: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT: *
13: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT: *
14: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT: *
15: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT: *
16: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT: *
17: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT: *
18: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT: *
19: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT: *
20: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT: *
21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT: *
22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT: *
23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT: *
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	368	100.0	1250	22	AAF83770	Nucleotide sequenc
2	368	100.0	1254	18	AAT89427	Death domain conta
3	368	100.0	1254	20	AAK00925	Death domain conta
4	368	100.0	1254	21	AAC68777	Human death domain
5	368	100.0	1634	18	AAT91180	Human apoptosis pr
6	368	100.0	1634	22	AAH27782	Human genomic DNA
7	368	100.0	1634	24	AAL47186	Human rheumatoid a
8	368	100.0	1662	22	AAC91477	Human PRO779 cDNA.
9	368	100.0	1662	24	ABK40265	cDNA encoding huma
10	368	100.0	1783	18	AAT89426	Death domain conta
11	368	100.0	1783	20	AAK00924	Death domain conta
12	368	100.0	1783	21	AAC68776	Human death domain
13	368	100.0	1847	19	AAV28700	Human apoptosis in
14	368	100.0	4825	24	AAL47185	Human DR3 gene ass
15	368	100.0	10797	23	ABK42690	Genomic sequence #
16	356	96.7	1743	24	ABL64119	Breast cancer rela
17	350	95.1	1251	19	AAV28701	Mouse apoptosis in
18	278	75.5	511	24	ABQ47530	Oligonucleotide fo
19	278	75.5	511	24	ABQ47531	Oligonucleotide fo
20	205	55.7	511	24	ABQ47532	Oligonucleotide fo
21	205	55.7	511	24	ABQ47533	Oligonucleotide fo
22	157	42.7	2130	24	ABK63694	Rat sequence diffe
23	157	42.7	2173	11	AAQ06284	Rat Tumour Necrosi
24	151	41.0	1368	14	AAQ49932	Lambda-derived TNF
25	151	41.0	1368	21	AAA95105	Human TNFR1 coding
26	151	41.0	2062	13	AAQ20973	TNF-alpha binding
27	151	41.0	2062	13	AAQ24440	Encodes TNF-alpha
28	151	41.0	2088	12	AAQ10883	30kD TNF inhibitor
29	151	41.0	2088	22	AAC83946	Human 30 kDa TNF i
30	151	41.0	2111	12	AAQ10955	Encodes human 55kD
31	151	41.0	2111	20	AAZ09170	Human tumour necro
32	151	41.0	2111	22	AAH48859	Human TNFBP-associ
33	151	41.0	2111	24	ABK84039	Human cDNA differe
34	151	41.0	2111	24	ABN95862	Gene #2360 used to
35	151	41.0	2141	11	AAQ06285	Human Tumour Necro
36	151	41.0	2161	21	AAZ48475	Human tumour necro
37	151	41.0	2161	24	ABK13194	Human tumour necro
38	151	41.0	2170	14	AAQ50870	p55 Tumour necrosi
39	151	41.0	2175	16	AAQ90513	p55 TNF-R gene. H
40	151	41.0	2176	12	AAQ12215	Type I TNF recepto
41	151	41.0	2254	21	AAA95104	Partial human TNFR
42	98	26.6	441	22	AAI88626	Human polynucleoti
43	94	25.5	1062	19	AAV63095	Human TR6 partial
44	94	25.5	1062	22	AAC84744	Partial nucleotide
45	94	25.5	1236	20	AAK23721	Human killer adria

ALIGNMENTS

RESULT 1	
AAF83770	standard; DNA; 1250 BP.
AAAF83770;	
AC	06-AUG-2001 (first entry)
XX	
DT	Nucleotide sequence of human TR3 gene.
XX	
DE	TR3; cell proliferation; leukemia; immunosuppressive; cytostatic;
XX	dermatological; antiarthritic; antidiabetic; neuroprotective; cardiant;
KW	antithyroid; antiinflammatory; antiallergic; T-cell-inhibitor; ds.
KW	
XX	
OS	Homo sapiens.
XX	
FT	Key Location/Qualifiers
FT	1..1250

FT FT /*tag= a
FT FT /transl_except= "(pos:481..482, aa:Asp)"
FT FT /note= "this codon has an apparent 1 nucleotide
FT FT deletion which alters the reading frame"
FT FT /transl_except= "(pos:558..559, aa:Cys)"
FT FT /note= "this codon has an apparent 1 nucleotide
FT FT deletion which alters the reading frame"
FT FT /transl_except= "(pos:638..639, aa:Leu)"
FT FT /note= "this codon has an apparent 1 nucleotide
FT FT deletion which alters the reading frame"
FT FT /transl_except= "(pos:718..719, aa:Met)"
FT FT /note= "this codon has an apparent 1 nucleotide
FT FT deletion which alters the reading frame"
FT FT sig_peptide 1..72
FT FT /*tag= b
FT FT mat_peptide 73..1247
FT FT /*tag= c
XX XX
PN WO200135995-A2.
XX XX
PD 25-MAY-2001.
XX XX
PF 17-NOV-2000; 2000MO-US31692.
XX XX
PR 19-NOV-1999; 99US-0166583.
XX XX
PA (TITT/) TITTLE T V.
PA (WEGM/) WEGMANN K W.
XX XX
PI Tittle TV, Wegmann KW;
XX XX
DR WPI; 2001-343711/36.
DR P-PSDB; AAB84941.
XX XX
PT Composition for treatment of T-cell mediated disease e.g. arthritis,
PT cancer comprises a biologically active TR3-specific binding agent
PT especially a monoclonal antibody -
XX XX
PS Disclosure; Page 72; 77pp; English.
XX XX
CC The invention relates to a composition comprising a biologically active
CC TR3-specific binding agent (I) that binds to TR3 and inhibits the
CC proliferation of cells expressing TR3. (I) identified by the methods are
CC useful for treating a subject suspected of having a disease associated
CC with a proliferation of cells expressing TR3 especially leukemias or
CC lymphomas or a T-cell mediated disease especially autoimmune diseases
CC such as myasthenia gravis, systemic lupus erythematosis, rheumatoid
CC arthritis, diabetes, multiple sclerosis, sarcoidosis, myocarditis,
CC thyroiditis and tumours. (I) is also useful for treating a subject
CC suspected of having graft-versus-host disease, rejection of a
CC transplanted organ such as heart, liver, lung, kidney, pancreas, bowel,
CC skin or an appendage, or inflammatory diseases, allergies and contact
CC dermatitis. The present sequence represents the nucleotide sequence of
CC human TR3 gene.
XX XX
SQ Sequence 1250 BP; 201 A; 419 C; 406 G; 224 T; 0 other;

Alignment Scores:
Pred. No.: 2.23e-40 Length: 1250
Score: 368.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0

US-09-993-234-6_COPY_339_409 (1-71) x AAF83770 (1-1250)

QY 1 MetaspalaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGlu 20
Db 1011 ATGGACGGGTCCACAGCGCGCTGGAGAGGAGTTCGTGCGCACGCTGGGGCTGCGCGAG 1070

QY 21 AlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrgLumet 40
|||||

Db 1071 GCAGAGATCGAAGCCGTGAGGTGAGATCGGCCGCTTCCGAGACCAGCAGTACGAGATG 1130

QY 41 LeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrrAlaAlaLeuGlu 60
Db 1131 CTCAGCGCTGGCGCCAGACAGACGCCCGCGGCTTCGAGACCGTTTACGCGGCCCTGGAG 1190

QY 61 ArgMetGlyLeuAspGlyCysValGluAspLeu 71
Db 1191 CGCATGGGGCTGAGCGGCTGCGTGAAGACTTG 1223

RESULT 2
AAT89427
ID AAT89427 standard; cDNA; 1254 BP.
XX XX
AC AAT89427;
XX XX
DT 02-MAR-1998 (first entry)
XX XX
DE Death domain containing receptor DR3 cDNA.
XX XX
KW Death domain containing receptor; DR3; human; apoptosis;
XX KW inflammation; NF-kappaB; ds.
OS Homo sapiens.
XX XX
FH Key Location/Qualifiers
FT sig_peptide 1..72
FT /*tag= a
FT mat_peptide 73..1251
FT /*tag= b
XX XX
PN WO9733904-A1.
XX XX
PD 18-SEP-1997.
XX XX
PF 17-OCT-1996; 96WO-US16849.
XX PF
PR 12-MAR-1996; 96US-0013285.
XX PR
PA (HUMA-) HUMAN GENOME SCI INC.
PA (UNMI) UNIV MICHIGAN.
XX PA
PI Dillon PJ, Dixit VM, Gentz RL, Ni J, Yu G;
XX PI
DR WPI; 1997-470812/43.
DR P-PSDB; AAW31517.
XX DR
XX PT Death domain containing receptor polypeptide(s) DR3 and DR3-V1 -
PT for activation of apoptosis and NF-kappaB, antagonists can be used
PT to treat inflammatory diseases
XX PT
XX PS Claim 6; Page 75-77; 108pp; English.
XX PS
XX CC This cDNA clone codes for human death domain containing receptor
CC DR3 (see AAW31517), a novel member of the tumour necrosis factor
CC receptor family. It was isolated from a HUVEC cDNA library.
CC Related death domain containing receptor DR3-V1 cDNA (see AAT89426)
CC was isolated from a human testis tumour cDNA library. The genes
CC have also been identified in cDNA libraries of foetal liver,
CC foetal brain, tonsil and leukocyte. Nucleic acids encoding full-
CC length or mature DR3, or the extracellular, transmembrane,
CC intracellular or especially the death domain of DR3, can be used to
CC produce recombinant polypeptides in transformed host cells. These
CC polypeptides can be used to treat diseases and disorders associated
CC with the inhibition of apoptosis. Antagonists can be used to treat
CC diseases and disorders associated with increased apoptosis and for
CC treating inflammatory diseases and disorders.
XX CC
SQ Sequence 1254 BP; 201 A; 420 C; 407 G; 226 T; 0 other;

Alignment Scores:
Pred. No.: 2.24e-40 Length: 1254
Score: 368.00 Matches: 71

Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-09-993-234-6_COPY_339_409 (1-71) x AAT89427 (1-1254)

OY 1 MetaspalaValProAlaArgTrpLysGluPheValArgThrLeuGlyLeuArgGlu 20
|||||
DB 1015 ATGACGCGGTCCACGCGCGCTGGAAGAGTTCGTGCGCACGCTGGGCTGCCGAG 1074,
OY 21 AlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGluMet 40
|||||
DB 1075 GCAGAGATCGAAGCCGCTGGAGGTGAGATCGCCGCTTCGAGACCAAGCAGTACGAGATG 1134
OY 41 LeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGlu 60
|||||
DB 1135 CTCAGCGCGTGGCGCCAGCAGCAGCCCGCGGCTCGGAGCCGTTTACGCGGCCCTGGAG 1194
OY 61 ArgMetGlyLeuAspGlyCysValGluAspLeu 71
|||||
DB 1195 CGCATGGGCGCTGGACGCGCTGCTGGAAGACTTG 1227

RESULT 3
AAK00925
ID AAK00925 standard; cDNA; 1254 BP.

AC AAK00925;

DT 25-MAR-1999 (first entry)

DE Death domain containing receptor polypeptide (DR3) encoding cDNA.

KW Death domain; receptor; DR3-V1; DR3; recombinant; ds.

OS Homo sapiens.

FH Key Location/Qualifiers
FT CDS 1..1254

FT sig_peptide 1..72 /product= "Death domain containing receptor DR3"

FT mat_peptide 73..1251 /tag= b

FT /tag= c

PN JP11000170-A.

PD 06-JAN-1999.

PE 12-MAR-1997; 97JP-0057503.

PR 06-FEB-1997; 97US-0037341.

PR 12-MAR-1996; 96US-0013285.

PR 17-OCT-1996; 96US-0028711.

PA (HUMA-) HUMAN GENOME SCI INC.

PA (UNMI) UNIV MICHIGAN.

DR WPI: 1999-124390/11.

DR P-PSDB; AAW95538.

XX New death domain containing receptor and recombinant vector -
optionally comprising leader sequence

PS Claim 6; Fig 3; 50pp; Japanese.

CC The invention provides nucleotide sequences encoding death domain
containing receptor polypeptides DR3-V1 and DR3. The DR3-V1 cDNA clone
is contained in ATCC deposition No. 97456 and the DR3 cDNA clone is
contained in ATCC deposition No. 97757. Recombinant vectors comprising
the nucleic acid sequences and optionally the leader sequences are
used for the recombinant production of the proteins. The present

CC sequence represents a cDNA encoding the death domain containing
receptor polypeptide (DR3).

XX Sequence 1254 BP; 201 A; 420 C; 407 G; 226 T; 0 other;

SO Alignment Scores:

Pred. No.: 2.24e-40 Length: 1254
Score: 368.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 20 Gaps: 0

US-09-993-234-6_COPY_339_409 (1-71) x AAK00925 (1-1254)

OY 1 MetaspalaValProAlaArgTrpLysGluPheValArgThrLeuGlyLeuArgGlu 20
|||||
DB 1015 ATGACGCGGTCCACGCGCGCTGGAAGAGTTCGTGCGCACGCTGGGCTGCCGAG 1074
OY 21 AlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGluMet 40
|||||
DB 1075 GCAGAGATCGAAGCCGCTGGAGGTGAGATCGCCGCTTCGAGACCAAGCAGTACGAGATG 1134
OY 41 LeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGlu 60
|||||
DB 1135 CTCAGCGCGTGGCGCCAGCAGCAGCCCGCGGCTCGGAGCCGTTTACGCGGCCCTGGAG 1194
OY 61 ArgMetGlyLeuAspGlyCysValGluAspLeu 71
|||||
DB 1195 CGCATGGGCGCTGGACGCGCTGCTGGAAGACTTG 1227

RESULT 4
AAC68777
ID AAC68777 standard; cDNA; 1254 BP.

AC AAC68777;

DT 20-FEB-2001 (first entry)

DE Human death domain containing receptor DR3 coding sequence.

KW Human; death domain containing receptor; DR3; cancer;

KW autoimmune disorder; inflammation; cardiovascular disorder; infection;

KW neurodegenerative disease; angiogenesis; ss.

OS Homo sapiens.

PN WO200064465-A1.

PD 02-NOV-2000.

PE 21-APR-2000; 2000WO-US10741.

PR 22-APR-1999; 99US-0130488.

PR 28-MAY-1999; 99US-0136741.

PA (HUMA-) HUMAN GENOME SCI INC.

PA (UNMI) UNIV MICHIGAN.

PA (YUGG/) YU G.

PA (NIJ/) NI J.

PA (GENT/) GENTZ R L.

PA (DILL/) DILLON P J.

PA (DIXI/) DIXIT V M.

PI Yu G, Ni J, Gentz RL, Dillon PJ, Dixit VM;

DR WPI: 2000-687263/67.

DR P-PSDB; AAB36265.

PT Treating graft-versus-host disease, cancer, immunodeficiency or an
autoimmune disease comprising administering an antibody to Death Domain
Containing Receptor proteins and a second therapeutic agent -

```
PS      Example 2B; Fig 2; 273pp; English.
XX
CC      The present invention provides the protein and coding sequences for two
CC      death domain containing receptors, designated DR3 and DR3-V1. These
CC      receptors are involved in apoptosis, and the sequences given can be used
CC      in the treatment of cancers, infections, cardiovascular disorders such as
CC      arrhythmias, ischaemia, aneurysms, arterial occlusive diseases, embolisms
CC      and congenital heart defects, neurodegenerative diseases including
CC      Alzheimer's and Parkinson's diseases, autoimmune disease such as multiple
CC      sclerosis, arthritis, diabetes, Graves' disease, asthma and psoriasis,
CC      and to promote angiogenesis and wound healing.
XX
SQ      Sequence 1254 BP; 201 A; 420 C; 407 G; 226 T; 0 other;

Alignment Scores:
Pred. No.:      2.24e-40      Length:      1254
Score:          368.00      Matches:      71
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:            21      Gaps:        0

US-09-993-234-6_COPY_339_409 (1-71) x AAC68777 (1-1254)

QY      1 MetAspAlaValProAlaAArgArGTTrPlySGluPheValArgThrLeuGlyLeuArgGlu 20
      |||||||
DB      1015 ATGGACGCGGTCCACGCGCGCGCTGGAAGAGATTCTGCGCACGCTGGGGCTGCGCGAG 1074

QY      21 AlaGluIleGluAlaValAlaGluValIleGlyArgPheArgAspGlnGlnIleTyrGluMet 40
      |||||||
DB      1075 GCAGAGATCGAAGCGCTGGAGGTGGAGATCGCGCTTCCGAGACCAGACGATCGAGATG 1134

QY      41 LeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGlu 60
      |||||||
DB      1135 CTCAAGCGCTGGCGCCAGACAGCCCCGCGGCTCGGAGCCGTTACGGCGGCTGGAG 1194

QY      61 ArgMetGlyLeuAspGlyCysValGluAspLeu 71
      |||||||
DB      1195 CGCATGGGCTGGACGCGCTGCGTGAAGACTTG 1227

RESULT 5
AAT91180
ID      AAT91180 standard; cDNA; 1634 BP.
XX
AC      AAT91180;
XX
DT      14-APR-1998 (first entry)
XX
DE      Human apoptosis protein Apo-3 cDNA clone FH20.57.
XX
KW      Apo-3; apoptosis; human; therapy; drug screening; ss.
XX
OS      Homo sapiens.
XX
FH      Key      Location/Qualifiers
FH      CDS      89..1342
FH              /*tag= a
FH              sig_peptide 89..160
FH              /*tag= b
FH              mat_peptide /note= "determined by hydropathy analysis"
FH              161..1339
FH              /*tag= c
XX
XX      WO9737020-A1.
XX
XX      09-OCT-1997.
XX
XX      31-MAR-1997; 97WO-US05230.
XX
XX      23-SEP-1996; 96US-0710802.
XX      01-APR-1996; 96US-0625328.
XX
XX      (GETH ) GENENTECH INC.
```

```
XX      Ashkenazi AJ;
XX
XX      WPT; 1997-503105/46.
XX
PT      Polypeptide(s) Apo-3 and Apo-2LI - useful for regulating apoptosis
PT      in mammalian cells
XX
PS      Example 1; Page 45-46; 70pp; English.
XX
CC      cDNA clone FH20.57 (ATCC 55820) codes for a novel polypeptide (see
CC      W26709), designated Apo-3, that stimulates or induces apoptotic
CC      activity in mammalian cells. It was isolated from a human foetal
CC      heart cDNA library by screening with probes (see T91183-84) based
CC      on an EST sequence (Genbank locus W71984) that showed homology to
CC      the intracellular domain of human TNFR1 and CD95. Amino acid
CC      residues 1-181 of Apo-3 are identical to another novel apoptosis
CC      polypeptide, Apo-2LI (see W26708). Nucleic acids encoding Apo-3
CC      can be used diagnostically for tissue-specific typing and to
CC      produce recombinant Apo-3 polypeptides, especially the
CC      extracellular domain (amino acids 1-198) or death domain (amino
CC      acids 338-417). Apo-3 can be used to induce apoptosis or
CC      NF-kappa-N- or JNK-mediated gene expression for therapeutic
CC      purposes. Non-human transgenic animals containing cells that
CC      express Apo-3 nucleic acid, and knockout animals containing
CC      cells that have an altered Apo-3 gene, can be used in drug
CC      screening and development.
XX
SQ      Sequence 1634 BP; 300 A; 528 C; 519 G; 287 T; 0 other;

Alignment Scores:
Pred. No.:      3.11e-40      Length:      1634
Score:          368.00      Matches:      71
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:            18      Gaps:        0

US-09-993-234-6_COPY_339_409 (1-71) x AAT91180 (1-1634)

QY      1 MetAspAlaValProAlaAArgArGTTrPlySGluPheValArgThrLeuGlyLeuArgGlu 20
      |||||||
DB      1103 ATGGACGCGGTCCACGCGCGCGCTGGAAGAGATTCTGCGCACGCTGGCGCTGCGAG 1162

QY      21 AlaGluIleGluAlaValAlaGluValIleGlyArgPheArgAspGlnGlnIleTyrGluMet 40
      |||||||
DB      1163 GCAGAGATCGAAGCGCTGGAGGTGGAGATCGCGCTTCCGAGACCAGACGATGAGATG 1222

QY      41 LeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGlu 60
      |||||||
DB      1223 CTCAAGCGCTGGCGCCAGACAGCCCCGCGGCTCGGAGCCGTTACGGCGGCTGGAG 1282

QY      61 ArgMetGlyLeuAspGlyCysValGluAspLeu 71
      |||||||
DB      1283 CGCATGGGCTGGACGCGCTGCGTGAAGACTTG 1315

RESULT 6
AAH27782
ID      AAH27782 standard; DNA; 1634 BP.
XX
AC      AAH27782;
XX
DT      15-AUG-2001 (first entry)
XX
DE      Human genomic DNA encoding a rheumatoid arthritis associated protein.
XX
KW      Rheumatoid arthritis; transmembrane protein; human; ds.
XX
OS      Homo sapiens.
XX
FH      Key      Location/Qualifiers
FH      CDS      89..1342
FH              /*tag= a
```



```
FT /product= "Rheumatoid arthritis associated protein"
XX
PN WO200132921-A2.
XX
PD 10-MAY-2001.
XX
PF 01-NOV-2000; 2000WO-JP07690.
XX
PR 01-NOV-1999; 99JP-0310805.
XX
PA (SHIO/) SHIOZAWA S.
XX
PI Shiozawa S, Konishi Y;
XX
DR WPI; 2001-308750/32.
XX
DR P-PSDB; AAB97370.
XX
PT Diagnosing rheumatoid arthritis by probing digested human genomic DNA
PT or comparing expression of mRNA or polypeptide of a region of
PT transmembrane protein
XX
PS Claim 1; Page 14-18; 21pp; Japanese.
XX
CC This invention relates to a method of diagnosing chronic rheumatoid
CC arthritis by digesting human genomic DNA with EcoRI and hybridizing it
CC with a probe containing a fragment of the present sequence which
CC represents DNA encoding a transmembrane protein. The method is used for
CC the diagnosis of chronic rheumatoid arthritis, and for developing new
CC treatments.
XX
SQ Sequence 1634 BP; 300 A; 528 C; 519 G; 287 T; 0 other;

Alignment Scores:
Pred. No.: 3.11e-40 Length: 1634
Score: 368.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0

US-09-993-234-6_COPY_339_409 (1-71) x AAH27782 (1-1634)
QY 1 MetAspAlaValProAlaArgTrpLysGluPheValArgThrLeuGlyLeuArgGlu 20
DB 1103 ATGGACGGCGTCCAGCGCGCGCTGGAAGAGTTCGTGCGCACGCTGGCGCTGCGGAG 1162
QY 21 AlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGluMet 40
DB 1163 GCAGAGATCGAAGCCGTGAGGTGAGATCGGCCGCTCCGAGACCAAGTACGAGATG 1222
QY 41 LeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGlu 60
DB 1223 CTCAGCGCTGGCGCCAGCAGACCCCGCGGCTCCGAGCCGTTTACGGCGCCCTGGAG 1282
QY 61 ArgMetGlyLeuAspGlyCysValGluAspLeu 71
DB 1283 CGCATGGGGCTGGACGGCTGCTGGAAGACTTG 1315
RESULT 7
AAL47186
ID AAL47186 standard; cDNA; 1634 BP.
XX
AC AAL47186;
XX
DT 22-AUG-2002 (first entry)
XX
DE Human rheumatoid arthritis associated DR3 gene related cDNA #1.
XX
KW Human; DR3; rheumatoid arthritis; antirheumatic; antiarthritic;
XX gene therapy; gene; ss.
OS Homo sapiens.
XX
```

```

FH Key Location/Qualifiers
FT CDS 89..1342
FT /tag= a
FT /product= "AA017879"
XX
PN WO200234912-A1.
XX
PD 02-MAY-2002.
XX
PF 24-OCT-2001; 2001WO-JP09313.
XX
PR 24-OCT-2000; 2000JP-0324296.
PR 27-MAR-2001; 2001JP-0090546.
PR 30-MAR-2001; 2001JP-0099990.
XX
PA (NEWI-) NEW IND RES ORG.
PA (SHIO/) SHIOZAWA S.
XX
PI Shiozawa S, Konishi Y;
XX
DR WPI; 2002-417132/44.
DR P-PSDB; AA017879.
XX
CC Genomes, particularly DR3 genomic DNA, participating in rheumatoid
CC arthritis via mutation, useful in evaluating disease onset and its
CC possibility and providing therapy and remedies
XX
PS Example 1; Page 66-69; 84pp; Japanese.
XX
CC The present invention relates to the human DR3 gene, which is associated
CC with rheumatoid arthritis. Certain mutations in the gene can be linked to
CC the disease. The sequences can be used to evaluate disease onset and its
CC possibility and to provide therapy and remedies. The present sequence is
CC a coding sequence described in the exemplification of the invention.
XX
SQ Sequence 1634 BP; 300 A; 528 C; 519 G; 287 T; 0 other;

Alignment Scores:
Pred. No.: 3.11e-40 Length: 1634
Score: 368.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 24 Gaps: 0

US-09-993-234-6_COPY_339_409 (1-71) x AAL47186 (1-1634)
QY 1 MetAspAlaValProAlaArgTrpLysGluPheValArgThrLeuGlyLeuArgGlu 20
DB 1103 ATGGACGGCGTCCAGCGCGCGCTGGAAGAGTTCGTGCGCACGCTGGCGCTGCGGAG 1162
QY 21 AlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGluMet 40
DB 1163 GCAGAGATCGAAGCCGTGAGGTGAGATCGGCCGCTCCGAGACCAAGTACGAGATG 1222
QY 41 LeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGlu 60
DB 1223 CTCAGCGCTGGCGCCAGCAGACCCCGCGGCTCCGAGCCGTTTACGGCGCCCTGGAG 1282
QY 61 ArgMetGlyLeuAspGlyCysValGluAspLeu 71
DB 1283 CGCATGGGGCTGGACGGCTGCTGGAAGACTTG 1315
RESULT 8
AAC91477
ID AAC91477 standard; cDNA; 1662 BP.
XX
AC AAC91477;
XX
DT 21-MAR-2001 (first entry)
XX
DE Human PRO779 cDNA.
XX
```

KW Human; PRO; antiinflammatory; dermatological; antiarthritic;
KW antirheumatic; cardiant; antianaemic; immunosuppressive; antithyroid;
KW antidiabetic; nootropic; neuroprotective; hepatotropic; virucide;
KW antiallergic; antiasthmatic; immune related disorder;
KW hepatobiliary disease; autoimmune disease; allergy; ss.
OS Homo sapiens.
XX
PN WO200073452-A2.
XX
PD 07-DEC-2000.
XX
PF 02-JUN-2000; 2000WO-US15264.
XX
PR 02-JUN-1999; 99WO-US12252.
PR 20-JUL-1999; 99US-0144732.
PR 20-JUL-1999; 99US-0144758.
PR 28-JUL-1999; 99US-0146222.
PR 01-SEP-1999; 99WO-US20111.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 29-OCT-1999; 99US-0162506.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28634.
PR 09-DEC-1999; 99US-0170262.
PR 20-DEC-1999; 99WO-US30911.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Chan B, Goddard A, Godowski PJ, Gurney AL;
PI Hebert C, Henzel W, Kabakoff RC, Shelton DL, Tumas D, Watanabe CK;
PI Wood WI;
XX
DR WPI; 2001-025253/03.
DR P-PSDB; AAB50918.
XX
PT Thirty three nucleic acids encoding PRO polypeptides which are useful
PT in the diagnosis and treatment of immune related disorders, e.g.
PT systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
PT thyroiditis and diabetes mellitus -
XX
PS Claim 48; Fig 33; 218pp; English.
XX
CC The present sequence is one of thirty three nucleic acids encoding PRO
CC polypeptides. The PRO polypeptides, anti-PRO antibodies, agonists and
CC antagonists are useful for treating and diagnosing immune related
CC disorders such as systemic lupus erythematosus, rheumatoid arthritis,
CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
CC anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,
CC immune-mediated renal disease, demyelinating diseases of the central
CC and peripheral nervous systems (such as multiple sclerosis, idiopathic
CC demyelinating polyneuropathy or Guillain-Barre syndrome, and chronic
CC inflammatory demyelinating polyneuropathy), hepatobiliary diseases
CC (such as infectious, autoimmune chronic active hepatitis, primary
CC biliary cirrhosis, granulomatous hepatitis and sclerosing cholangitis),
CC inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's
CC disease, autoimmune or immune-mediated skin diseases (such as bullous
CC skin diseases, erythema multiforme, contact dermatitis, psoriasis),

CC allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,
CC food hypersensitivity and urticaria), immunological diseases of the
CC lung (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis
CC and hypersensitivity pneumonitis), transplantation associated diseases
CC including graft rejection and graft-versus-host diseases.
XX
SQ Sequence 1662 BP; 302 A; 540 C; 531 G; 289 T; 0 other;
SQ
Alignment Scores:
Pred. No.: 3.18e-40 Length: 1662
Score: 368.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0
US-09-993-234-6_COPY_339_409 (1-71) x AAC91477 (1-1662)
QY 1 Metaspalavalprolaaargatrpplysgluphevalargthrleuglyleuarglu 20
DB 1117 ATGACGCGGTCCACGCGCGCGCTGGAAGAGATTGTCGCACAGCTGGGCTGCCGAG 1176
QY 21 Alagiutleglualavalgluvalgluileglyarpheargasplnglntyrglumet 40
DB 1177 GCAGAGATCGAAGCCGTGAGGTGAGATGCGCGCTCCGAGACCAGCAGTACGAGATG 1236
QY 41 Leulysargtrparglncglnglnproalaglyleuglyalavaltyralaalaleuglu 60
DB 1237 CTCAAGCGCTGGCGCCAGACAGACGCCCGCGCGCTCGGAGCCGTTACGCGCCCTGGAG 1296
QY 61 Argmetglyleuaspglycysvalgluaspleu 71
DB 1297 CGCATGGGCTGGACGCGCTGCGTGAAGACTTG 1329
RESULT 9
ABK40265
ID ABK40265 standard; cDNA; 1662 BP.
XX
AC ABK40265;
XX
DT 15-JUL-2002 (first entry)
XX
DE cDNA encoding human PRO779 polypeptide.
XX
KW Human; PRO; benign tumour; malignant tumour; lymphoid malignancy;
KW leukaemia; neuronal disorder; stromal disorder; blastocoeleic disorder;
KW inflammatory disorder; immune disorder; angiogenic disorder;
KW gene therapy; cytostatic; neuroprotective; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200153486-A1.
XX
PD 26-JUL-2001.
XX
PF 11-FEB-2000; 2000WO-US03565.
XX
PR 08-MAR-1999; 99WO-US05028.
PR 11-MAR-1999; 99US-123972P.
PR 11-MAY-1999; 99US-133459P.
PR 02-JUN-1999; 99WO-US12252.
PR 22-JUN-1999; 99US-140650P.
PR 22-JUN-1999; 99US-140653P.
PR 20-JUL-1999; 99US-144758P.
PR 26-JUL-1999; 99US-145698P.
PR 28-JUL-1999; 99US-146222P.
PR 17-AUG-1999; 99US-149395P.
PR 31-AUG-1999; 99US-151689P.
PR 01-SEP-1999; 99WO-US20111.
PR 15-SEP-1999; 99WO-US21090.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.

PR 05-JAN-2000; 2000WO-US00219.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL, Hillan KJ;
PI Marsters SA, Pan J, Pitti RM, Roy MA, Smith V, Stone DM;
PI Watanabe CK, Wood WI;
XX
DR WPI; 2002-205567/26.
DR P-PSDB; AAW86139.
XX
PT Thirty five nucleic acids encoding PRO polypeptides, useful for
PT treating benign or malignant tumours, leukaemias and lymphoid
PT malignancies, inflammatory, angiogenic and immunologic disorders -
XX
PS Claim 50; Fig 23; 302pp; English.
XX
CC The present invention relates to the isolation of novel human PRO
CC polypeptides and the polynucleotide sequences encoding them. The
CC PRO polypeptides, agonists, antagonists or anti-PRO antibodies are
CC useful for treating benign or malignant tumours (e.g. renal, kidney,
CC bladder, breast, etc), leukaemias and lymphoid malignancies, other
CC disorders such as neuronal, glial, astrocytal, hypothalamic, glandular,
CC macrophagal, stromal and blastocoelec disorders, inflammatory, immune
CC and angiogenic disorders. The polynucleotide sequences are also
CC useful in gene therapy. ABK40254-ABK40288 encode for the human PRO
CC polypeptides of the invention.
XX
SQ Sequence 1662 BP; 302 A; 540 C; 531 G; 289 T; 0 other;

Alignment Scores:
Pred. No.: 3.18e-40 Length: 1662
Score: 368.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 24 Gaps: 0

US-09-993-234-6_COPY_339_409 (1-71) x ABK40265 (1-1662)
QY 1 MetAspAlaValProAlaArgTrpIlySGluPheValArgThrLeuGlyLeuArgGlu 20
DB 1117 ATGCAGCGCGTCCACAGCGCGCGCTGGAAGAGATTCTGCGCACGCTGGGGCTGCGCGAG 1176
QY 21 AlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGluMet 40
DB 1177 GCAGAGATCGAAGCCGTGAGGTGAGATCGCGCTCCGAGACACAGATAGATG 1236
QY 41 LeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGlu 60
DB 1237 CTCAGCGCTGGCGCCAGCAGCAGACCCCGGGGCTCGAGCCGTTACGGCGGCTGAG 1296
QY 61 ArgMetGlyLeuAspGlyCysValGluAspLeu 71
DB 1297 CGCATGGGCTGGACGCGCTGCTGGAAGACTTG 1329

RESULT 10
AAT89426
ID AAT89426 standard; cDNA; 1783 BP.
XX
AC AAT89426;
XX
DT 02-MAR-1998 (first entry)
XX
DE Death domain containing receptor DR3-V1 cDNA.
XX
KW Death domain containing receptor; DR3-V1; human; apoptosis;
KW inflammation; NF-kappaB; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 198..1484

FT FT /*tag= a
FT sig_peptide 198..302
FT /*tag= b
FT mat_peptide 304..1481
FT /*tag= c
XX
PN WO9733904-A1.
XX
PD 18-SEP-1997.
XX
PF 17-OCT-1996; 96WO-US16849.
XX
PR 12-MAR-1996; 96US-0013285.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (UNMI) UNIV MICHIGAN.
XX
PI Dillon PJ, Dixit VM, Gentz RL, Ni J, Yu G;
XX
DR WPI; 1997-470812/43.
DR P-PSDB; AAW31516.
XX
PT Death domain containing receptor polypeptide(s) DR3 and DR3-V1 -
PT for activation of apoptosis and NF-kappaB, antagonists can be used
PT to treat inflammatory diseases
XX
PS Claim 2; Page 71-73; 108pp; English.
XX
CC This cDNA clone, deposited as ATCC 97456, codes for human death
CC domain containing receptor DR3-V1 (see AAW31516), a novel member of
CC the tumour necrosis factor receptor family. It was isolated from a
CC cDNA library derived from cells of a human testis tumour. Related
CC death domain containing receptor DR3 cDNA (see AAT89427) was isolated
CC from a HUVEC cDNA library. The genes have also been identified in
CC cDNA libraries of foetal liver, foetal brain, tonsil and leukocyte.
CC Nucleic acids encoding full-length or mature DR3-V1 can be used to
CC produce recombinant polypeptides in transformed host cells. These
CC polypeptides can be used to treat diseases and disorders associated
CC with the inhibition of apoptosis. Antagonists, such as antibodies
CC raised against DR3-V1, can be used to treat diseases and disorders
CC associated with increased apoptosis and for treating inflammatory
CC diseases and disorders.
XX
SQ Sequence 1783 BP; 330 A; 562 C; 564 G; 327 T; 0 other;

Alignment Scores:
Pred. No.: 3.47e-40 Length: 1783
Score: 368.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-09-993-234-6_COPY_339_409 (1-71) x AAT89426 (1-1783)
QY 1 MetAspAlaValProAlaArgTrpIlySGluPheValArgThrLeuGlyLeuArgGlu 20
DB 1245 ATGCAGCGCGTCCACAGCGCGCTGGAAGAGATTCTGCGCACGCTGGGGCTGCGCGAG 1304
QY 21 AlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGluMet 40
DB 1305 GCAGAGATCGAAGCCGTGAGGTGAGATCGCGCTTCCGAGACACAGATACGAGATG 1364
QY 41 LeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGlu 60
DB 1365 CTCAGCGCTGGCGCCAGCAGCAGACCCCGGGGCTCGAGCCGTTACCGCGGCTGAG 1424
QY 61 ArgMetGlyLeuAspGlyCysValGluAspLeu 71
DB 1425 CGCATGGGCTGGACGCGCTGCTGGAAGACTTG 1457

RESULT 11
AAX00924

ID AAX00924 standard; cDNA; 1783 BP.
XX
AC AAX00924;
XX
DT 25-MAR-1999 (first entry)
XX
DE Death domain containing receptor polypeptide (DR3-V1) encoding cDNA.
XX
KM Death domain; receptor; DR3-V1; DR3; recombinant; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 198..1484
FT sig_peptide /tag= a
FT mat_peptide /product= "Death domain containing receptor DR3-V1"
FT 198..300
FT 301..1481 /tag= b
FT /*tag= c
XX
XX JP11000170-A.
XX
XX 06-JAN-1999.
XX
XX 12-MAR-1997; 97JP-0057503.
XX
XX 06-FEB-1997; 97US-0037341.
XX 12-MAR-1996; 96US-0013285.
XX 17-OCT-1996; 96US-0028711.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX (UNMI) UNIV MICHIGAN.
XX
XX WPI: 1999-124390/11.
XX DR P-PSDB; AAW95537.
XX
XX New death domain containing receptor and recombinant vector -
XX PT optionally comprising leader sequence
XX
XX
XX Claim 2; Fig 1, 2; 50pp; Japanese.
XX
XX The invention provides nucleotide sequences encoding death domain
XX CC containing receptor polypeptides DR3-V1 and DR3. The DR3-V1 cDNA clone
XX CC is contained in ATCC deposition No. 97456 and the DR3 cDNA clone is
XX CC contained in ATCC deposition No. 97757. Recombinant vectors comprising
XX CC the nucleic acid sequences and optionally the leader sequences are
XX CC used for the recombinant production of the proteins. The present
XX CC sequence represents a cDNA encoding the death domain containing
XX CC receptor polypeptide (DR3-V1).
XX
XX SQ Sequence 1783 BP; 330 A; 562 C; 564 G; 327 T; 0 other;
XX
XX Alignment Scores:
XX Pred. No.: 3.47e-40 Length: 1783
XX Score: 368.00 Matches: 71
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 100.00% Indels: 0
XX DB: 20 Gaps: 0
XX
XX US-09-993-234-6_COPY_339_409 (1-71) x AAX00924 (1-1783)
XX
OY 1 MetAspAlaValProAlaArgArgTrrpLysGluPheValArgThrLeuGlyLeuArgGlu 20
DB 1245 ATGGACGGCGGTCCACAGCGCGGCTGGAAGAGATTCGTGCGCACGCTGGGGCTGCGCGAG 1304
OY 21 AlaGluIleGluAlaValAlaGluValAlaGluIleGlyArgPheArgAspGlnGlnTyrGluMet 40
DB 1305 GCAGAGATCGAAGCCGTGAGGTGAGATCGGCCCTTCCGAGACCAGCAGTACGAGATG 1364
OY 41 LeuLysArgTrrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGlu 60
|||||

DB 1365 CTCAGCGCTGGCCGACAGCAGCCCGGGGCTCGGAGCCGTTTACGGCGCCCTGAG 1424
OY 61 ArgMetGlyLeuAspGlyCysValGluAspLeu 71
DB 1425 CGCATGGGGCTGACGGCTGCTGGAAGACTTG 1457
RESULT 12
AAC68776
ID AAC68776 standard; cDNA; 1783 BP.
XX
XX AAC68776;
XX
XX 20-FEB-2001 (first entry)
XX
XX Human death domain containing receptor DR3-V1 coding sequence.
XX
XX Human; death domain containing receptor; DR3-V1; cancer;
XX KM autoimmune disorder; inflammation; cardiovascular disorder; infection;
XX KW neurodegenerative disease; angiogenesis; ss.
XX
XX Homo sapiens.
XX
XX WO200064465-A1.
XX
XX 02-NOV-2000.
XX
XX 21-APR-2000; 2000WO-US10741.
XX
XX 22-APR-1999; 99US-0130488.
XX 28-MAY-1999; 99US-0136741.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX (UNMI) UNIV MICHIGAN.
XX
XX (YUGG/) YU G.
XX PA (NIJ/) NI J.
XX PA (GENT/) GENTZ R L.
XX PA (DILL/) DILLON P J.
XX PA (DIXI/) DIXIT V M.
XX
XX Yu G, Ni J, Gentz RL, Dillon PJ, Dixit VM;
XX
XX
XX WPI: 2000-687263/67.
XX DR P-PSDB; AAB36264.
XX
XX Treating graft-versus-host disease, cancer, immunodeficiency or an
XX PT autoimmune disease comprising administering an antibody to Death Domain
XX PT Containing Receptor proteins and a second therapeutic agent -
XX
XX Example 1; Fig 1; 273pp; English.
XX
XX The present invention provides the protein and coding sequences for two
XX CC death domain containing receptors, designated DR3 and DR3-V1. These
XX CC receptors are involved in apoptosis, and the sequences given can be used
XX CC in the treatment of cancers, infections, cardiovascular disorders such as
XX CC arrhythmias, ischemia, aneurysms, arterial occlusive diseases, embolisms
XX CC and congenital heart defects, neurodegenerative diseases including
XX CC Alzheimer's and Parkinson's diseases, autoimmune disease such as multiple
XX CC sclerosis, arthritis, diabetes, Graves' disease, asthma and psoriasis,
XX CC and to promote angiogenesis and wound healing.
XX
XX SQ Sequence 1783 BP; 330 A; 562 C; 564 G; 327 T; 0 other;
XX
XX Alignment Scores:
XX Pred. No.: 3.47e-40 Length: 1783
XX Score: 368.00 Matches: 71
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 100.00% Indels: 0
XX DB: 21 Gaps: 0
XX
XX US-09-993-234-6_COPY_339_409 (1-71) x AAC68776 (1-1783)
XX
OY 1 MetAspAlaValProAlaArgArgTrrpLysGluPheValArgThrLeuGlyLeuArgGlu 20
|||||

Db 1245 ATGACGCGGCTCCAGCGCGCGCTGAGAGATTCTGCGCACGCTGGGCTGCGCAG 1304
 QY 21 AlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGluMet 40
 Db 1305 GCAGAGATCGAAGCCGTGAGAGTGGAGATCGCGCCTCCGAGACCAGCAGTACGAGATG 1364
 QY 41 LeuLysArgTrpArgGlnGlnGlnInProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGlu 60
 Db 1365 CTCACGCGCTGGCGCCAGCAGCAGCCCGCGGCTCGAGCCGTTACGCGCGCCCTGAG 1424
 QY 61 ArgMetGlyLeuAspGlyCysValGluAspLeu 71
 Db 1425 CGCATGGGGCTGGACGCGCTGCCGTGGAGACTTG 1457
 RESULT 13
 AAV28700
 ID AAV28700 standard; cDNA; 1847 BP.
 XX
 AC AAV28700;
 XX
 DT 20-AUG-1998 (first entry)
 XX
 DE Human apoptosis inducing receptor coding sequence.
 XX
 KW Apoptosis inducing receptor; AIR protein; human; cell death regulator;
 KW Type I transmembrane protein; tumour cell death; autoimmune disease;
 KW therapy; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 236..1489
 FT /**tag= a
 FT /product= AIR
 XX
 PN WO9814565-A1.
 XX
 PD 09-APR-1998.
 XX
 PF 03-OCT-1997; 97WO-US17876.
 XX
 PR 04-OCT-1996; 96US-0044456.
 XX
 PA (IMMV) IMMUNEX CORP.
 XX
 PI Perkins PA;
 XX
 DR WPI: 1998-240077/21.
 DR P-PSDB; AAW57045.
 XX
 PT DNA encoding apoptosis inducing receptor - which is Type I
 PT transmembrane protein, useful for regulating cell death
 XX
 PS Claim 2; Page 28-30; 45pp; English.
 CC
 CC This sequence encodes the human apoptosis inducing receptor (AIR) of the
 CC invention. AIR is a Type I transmembrane protein, soluble forms of which
 CC can be used to regulate cell death in a therapeutic setting. Soluble AIR
 CC can also be used in vitro to block apoptosis or AIR-expressing cells, or
 CC to screen agonists or antagonists of AIR activity. The cytoplasmic domain
 CC of AIR can be used to develop assays for inhibitors of AIR-induced cell
 CC death, which is useful to regulate cell death in a therapeutic setting as
 CC well as in vitro. Agonists of AIR activity can be used to kill tumour
 CC cells that express AIR, or T cells expressing AIR in autoimmune diseases.
 SO Sequence 1847 BP; 316 A; 605 C; 579 G; 347 T; 0 other;

Alignment Scores:	
Pred. No.:	3.63e-40
Score:	368.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
	Length: 1847
	Matches: 71
	Conservative: 0
	Mismatches: 0

Query Match:	100.00%	Indels:	0
DB:	19	Gaps:	0
US-09-993-234-6_COPY_339_409 (1-71) x AAV28700 (1-1847)			
QY 1 MetaspAlaValProAlaArgArgTrPlySgluPheValArgThrLeuGlyLeuArgGlu 20			
Db 1250 ATGGACGGCGTCCACGCGCGCTGGAAGAGATTCTGCGCACGCTGGGCTGCGGAG 1309			
QY 21 AlagiulIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGluMet 40			
Db 1310 GCAGAGATCGAAGCCGTGTGAGGTGAGATCGGCCGCTTCCGAGACCAGCAGTACGAGATG 1369			
QY 41 LeulysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGlu 60			
Db 1370 CTCACGGCGCTGGCGCCACGACGACGCCCGCGGCGCTCGGACCGCTTACGGCGCCCTGGAG 1429			
QY 61 ArgMetGlyLeuAspGlyCysValGluAspLeu 71			
Db 1430 CGCATGGGGCTGGACCGGCTCGTGGAGAAGACTTG 1462			

RESULT 14	ID	AAI47185	standard; DNA; 4825 BP.
XX	AC	AAI47185;	
XX	DT	22-AUG-2002	(first entry)
XX	DE	Human DR3 gene associated with rheumatoid arthritis.	
XX	KW	Human; DR3; rheumatoid arthritis; anti-rheumatic; antiarthritic	
XX	KW	gene therapy; gene; ds.	
XX	OS	Homo sapiens.	
XX	FH	Key	
FT	FT	CDS	
FT	FT	Location/Qualifiers	
FT	FT	1..4825	
FT	FT	/tag= a	
FT	FT	/product= "DR3"	
FT	FT	/note= "this sequence contains introns"	
FT	FT	1..127	
FT	FT	/tag= b	
FT	FT	/number= 1	
FT	FT	128..635	
FT	FT	/tag= c	
FT	FT	/number= 1	
FT	FT	636..756	
FT	FT	/tag= d	
FT	FT	/number= 2	
FT	FT	757..973	
FT	FT	/tag= e	
FT	FT	/number= 2	
FT	FT	974..1108	
FT	FT	/tag= f	
FT	FT	/number= 3	
FT	FT	1109..1476	
FT	FT	/tag= g	
FT	FT	/number= 3	
FT	FT	1477..1644	
FT	FT	/tag= h	
FT	FT	/number= 4	
FT	FT	1645..1742	
FT	FT	/tag= i	
FT	FT	/number= 4	
FT	FT	1743..1821	
FT	FT	/tag= j	
FT	FT	/number= 5	
FT	FT	1822..3068	
FT	FT	/tag= k	
FT	FT	/number= 5	
FT	FT	3069..3124	
FT	FT	/tag= l	

FT /number= 6
FT Intron 3125..3225
FT /tag= m
FT /number= 6
FT exon 3226..3333
FT /tag= n
FT /number= 7
FT Intron 3334..3529
FT /tag= o
FT /number= 7
FT exon 3530..3577
FT /tag= p
FT /number= 8
FT Intron 3578..4021
FT /tag= q
FT /number= 8
FT exon 4022..4202
FT /tag= r
FT /number= 9
FT Intron 4203..4433
FT /tag= s
FT /number= 9
FT exon 4434..4825
FT /tag= t
FT /number= 10

WO200234912-A1.

02-MAY-2002.

24-OCT-2001; 2001WO-JP09313.

24-OCT-2000; 2000JP-0324296.
27-MAR-2001; 2001JP-0090546.
30-MAR-2001; 2001JP-0099990.

(NEWI-) NEW IND RES ORG.
(SHIO/) SHIOZAWA S.

Shiozawa S, Konishi Y;

WPI; 2002-417132/44.

Genomes, particularly DR3 genomic DNA, participating in rheumatoid arthritis via mutation, useful in evaluating disease onset and its possibility and providing therapy and remedies -

Claim 1; Page 64-66; 84pp; Japanese.

The present invention relates to the human DR3 gene, which is associated with rheumatoid arthritis. Certain mutations in the gene can be linked to the disease. The sequences can be used to evaluate disease onset and its possibility and to provide therapy and remedies. The present sequence is the gene of the invention.

Sequence 4825 BP; 921 A; 1378 C; 1521 G; 1005 T; 0 other;

Alignment Scores:

Pred. No.: 1.21e-39 Length: 4825
Score: 368.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 24 Gaps: 0

US-09-993-234-6_COPY_339_409 (1-71) x AAL47185 (1-4825)

QY 1 MetAspAlaValProAlaArgTTrpLysGluPheValArgThrLeuGlyLeuArgGlu 20
Db 4523 ATGACCGCGCTCCACGCGCGCTGCAAGAGTTCGTCCGCGCAGCTGGGGCTGCGCGAG 4582
QY 21 AlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGluMet 40

Db 4583 GCAGAGATCGAAGCCGTGGAGGTGGAGATCGCCGCTTCGAGACCAGCAGTACGAGATG 4642
QY 41 LeuLysArgTTrpArgGlnGlnInProAlaGlyLeuGlyAlaValTyrAlaLeuGlu 60
Db 4643 CTCACGCGCTGGCGCCACGACGACGACCCCGCGGCTTCGAGCCGTTACGCGGCCCTGAG 4702
QY 61 ArgMetGlyLeuAspGlyCysValGluAspLeu 71
Db 4703 CGCATGGGCGTGGACGCGCTGCGTGAAGACTTG 4735
RESULT 15
ABK42690
ID ABK42690 standard; DNA; 10797 BP.
XX
AC ABK42690;
XX
DT 21-MAY-2002 (first entry)
XX
DE Genomic sequence #589 encoding novel human connective tissue polypeptide.
XX
KW Human; connective tissue related disorder; cancer; gene therapy;
XX cyostatic; gene; ds.
OS Homo sapiens.
XX
PN WO200155343-A1.
XX
PD 02-AUG-2001.
XX
PE 17-JAN-2001; 2001WO-US01322.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.

PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.

PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX
PI Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-565190/63.
DR
XX
XX
PT Nucleic acid encoding novel connective tissue associated polypeptides,
PT used in diagnosing, preventing, treating or ameliorating a disorder
PT such as cancer or rheumatoid arthritis -
XX
XX
PS Disclosure; SEQ ID No 1577; 673pp; English.
XX
CC The present invention relates to the isolation of novel human connective
CC tissue related polypeptides (AAU86435-AAU86923) and the polynucleotide
CC (cDNA and genomic) sequences encoding them. The sequences of the
CC invention are useful in the diagnosis, treatment, prevention and/or
CC prognosis of diseases associated with connective tissue(s), including
CC cancer. The polynucleotide sequences of the invention are also useful
CC in gene therapy. ABK42102-ABK43116 represent genomic sequences encoding
CC the novel human connective tissue related polypeptides.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 10797 BP; 2003 A; 3215 C; 3378 G; 2201 T; 0 other;

Alignment Scores:
Pred. No.: 3,31e-39 Length: 10797
Score: 368.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 23 Gaps: 0

US-09-993-234-6_COPY_339_409 (1-71) x ABK42690 (1-10797)
QY 1 MetaspalavalProalaArgArGTrPlySclupheValArgThrleuGlyLeuArgGlu 20
Db 9122 ATGGACGGCGTCCACAGCGCGGCTGGAAGAGTTCGTGCGCACGCTGGGGCTGCGGAG 9181
QY 21 AlaGluIleGluAlaValGluValGluIleGlyArgPheArgaspGlnIntTyrglumet 40
Db 9182 GCAGAGATCGAAGCCGTGAGGTGAGATCGGCCGCTCCGAGACGACAGTACGAGATG 9241
QY 41 LeuIysArgTrpArgGlnGlnGlnProalaGlyLeuGlyAlaValTyraIalaLeuGlu 60
Db 9242 CTCAGCGCGTGGCCACAGCAGACGCCCGCGCTCGAGGCCGTTACGGCGCCCTGAG 9301
QY 61 ArgmetGlyLeuAspGlyCysValGluAspLeu 71
Db 9302 CGCATGGGGCTGGAACGGCTGCGTGAAGACTTG 9334

Search completed: April 6, 2003, 16:53:36
Job time : 75.109 secs

Gencore version 5.1.4-p5-4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 6, 2003, 16:28:24 ; Search time 11.9856 Seconds
(without alignments)
1816.682 Million cell updates/sec

Title: US-09-993-234-6_COPY_339_409
Perfect score: 368
Sequence: 1 MDAVPARRRKEFEVRLGLRE.....LGAVYALERMGLDGCVEDL 71

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US09993234/runat_27032003_115457_15378/app_query.fasta_1.2346
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rn1 -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09993234.ecgn1_1_116.ernat.27032003_115457_15378 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA: *
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq: *
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq: *
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	368	100.0	1254	3	US-08-815-469-3 Sequence 3, Applt
2	368	100.0	1634	4	US-08-928-069-11 Sequence 11, Applt
3	368	100.0	1634	4	US-08-828-683A-9 Sequence 9, Applt
4	368	100.0	1783	3	US-08-815-469-1 Sequence 1, Applt
5	161	43.8	1956	2	US-08-762-308-10 Sequence 10, Applt
6	156	42.4	2440	4	US-09-513-007-1 Sequence 1, Applt
7	151	41.0	427	4	US-09-397-787-236 Sequence 236, App
8	151	41.0	2062	1	US-08-050-319B-24 Sequence 24, Appl
9	151	41.0	2062	2	US-08-465-982-24 Sequence 24, Appl
10	151	41.0	2161	3	US-09-106-038A-1 Sequence 1, Applt
11	151	41.0	2161	4	US-09-505-250-3 Sequence 3, Applt
12	151	41.0	2175	1	US-08-321-668-1 Sequence 1, Applt

13	151	41.0	2175	1	US-08-837-941-1	Sequence 1, Applt
14	151	41.0	2175	1	US-08-126-016-1	Sequence 1, Applt
15	151	41.0	2175	4	US-08-054-970-1	Sequence 1, Applt
16	94	25.5	1062	4	US-09-333-593A-3	Sequence 3, Applt
17	94	25.5	1236	4	US-09-134-618-1	Sequence 1, Applt
18	94	25.5	1323	3	US-08-883-036A-1	Sequence 1, Applt
19	94	25.5	1799	4	US-09-329-633A-1	Sequence 1, Applt
20	94	25.5	1799	4	US-09-079-029-2	Sequence 2, Applt
21	94	25.5	3881	4	US-09-333-593A-1	Sequence 1, Applt
22	90	24.5	2413	2	US-08-651-579-1	Sequence 1, Applt
23	78.5	21.3	2268	1	US-08-444-005-14	Sequence 14, Appl
24	76	20.7	2040	2	US-08-533-669A-5	Sequence 5, Applt
25	76	20.7	2040	4	US-09-183-861-5	Sequence 5, Applt
26	76	20.7	2040	4	US-09-022-765-5	Sequence 5, Applt
27	74	20.1	1407	4	US-09-505-250-2	Sequence 2, Applt
28	74	20.1	2152	4	US-09-013-895A-1	Sequence 1, Applt
29	74	20.1	2152	4	US-09-565-918-1	Sequence 1, Applt
30	74	20.1	2152	4	US-09-448-868-1	Sequence 1, Applt
31	70.5	19.2	606	4	US-09-328-111-495	Sequence 495, App
32	70.5	19.2	2016	4	US-09-132-118-1	Sequence 1, Applt
33	70.5	19.2	2137	1	US-08-444-005-16	Sequence 16, Appl
34	70.5	19.2	2617	3	US-09-161-443-1	Sequence 1, Applt
35	70.5	19.2	9687	4	US-09-133-944-2	Sequence 2, Applt
36	70.5	19.2	9687	4	US-09-208-827-2	Sequence 2, Applt
37	67	18.2	157	3	US-08-883-036A-3	Sequence 3, Applt
38	65	17.7	2808	3	US-08-870-126-7	Sequence 7, Applt
39	65	17.7	2808	4	US-09-445-247-7	Sequence 7, Applt
40	63	17.1	1868	4	US-09-739-455-1	Sequence 1, Applt
41	63	17.1	1878	4	US-09-732-025-1	Sequence 1, Applt
42	62.5	17.0	5118	4	US-08-669-785-3	Sequence 3, Applt
43	62	16.8	35060	3	US-08-814-095-7	Sequence 7, Applt
44	61.5	16.7	12127	3	US-08-444-644-32	Sequence 32, Appl
45	61.5	16.7	12127	4	US-08-232-246A-32	Sequence 32, Appl

ALIGNMENTS

RESULT 1
US-08-815-469-3
: Sequence 3, Application US/08815469
: Patent No. 6153402
: GENERAL INFORMATION:
: APPLICANT: Yu, Guo-Liang
: APPLICANT: Ni, Jian
: APPLICANT: Dixit, Vishva
: APPLICANT: Gentz, Reiner L.
: APPLICANT: Dillon, Patrick J.
: TITLE OF INVENTION: Death Domain Containing Receptors
: NUMBER OF SEQUENCES: 17
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
: STREET: 1100 New York Ave., NW, Suite 600
: CITY: Washington
: STATE: DC
: COUNTRY: USA
: ZIP: 20005-3934
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/815,469
: FILING DATE: HERewith
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: No. 6153402 Yet Assigned
: FILING DATE: 06-FEB-1997
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/028,711
: FILING DATE: 17-OCT-1996
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/013,285

FILING DATE: 12-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1254 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1251
US-08-815-469-3

Alignment Scores:
Pred. No.: 3.63e-43 Length: 1254
Score: 368.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-993-234-6_COPY_339_409 (1-71) x US-08-815-469-3 (1-1254)

OY 1 MetaspAlaValProAlaArGArGTTrpLysGluPheValArGThrLeuGlyLeuArGlu 20
|||||
DB 1015 ATGACGCGGTCCAGCGCGCGCTGGAAGAGATTCTGCGCACGCTGGGCTGCGCGAG 1074
OY 21 AlaGluIleGluAlaValGluValGluIleGlyArGpHeArGAspGlnGlnTyrgluMet 40
|||||
DB 1075 GCAGAGATCGAAGCGCTGGAGGTGAGATCGCGCTTCCGAGACCAGCAGTACGAGATG 1134
OY 41 LeuLysArGTTrpArGlnGlnGlnProAlaGlyLeuGlyAlaValTyraAlaLeuGlu 60
|||||
DB 1135 CTCAGCGCTGGCGCCAGCAGACGCCCGGCGCTCGAGCCGTTTACGCGCCCTGGAG 1194
OY 61 ArgMetGlyLeuAspGlyCysValGluAspLeu 71
|||||
DB 1195 CGCATGGGGCTGGACGGCTGCGTGAAGACTTG 1227

RESULT 2

US-08-928-069-11
Sequence 11, Application US/08928069
Patent No. 6462176
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-3 POLYPEPTIDE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,069
FILING DATE: 11-Sep-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/026943
FILING DATE: 09/23/1996

ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1052R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1634 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-928-069-11

Alignment Scores:
Pred. No.: 5.16e-43 Length: 1634
Score: 368.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-993-234-6_COPY_339_409 (1-71) x US-08-928-069-11 (1-1634)

OY 1 MetaspAlaValProAlaArGArGTTrpLysGluPheValArGThrLeuGlyLeuArGlu 20
|||||
DB 1103 ATGACGCGGTCCAGCGCGCGCTGGAAGAGATTCTGCGCACGCTGGGCTGCGCGAG 1162
OY 21 AlaGluIleGluAlaValGluValGluIleGlyArGpHeArGAspGlnGlnTyrgluMet 40
|||||
DB 1163 GCAGAGATCGAAGCGCTGGAGGTGAGATCGCGCTTCCGAGACCAGCAGTACGAGATG 1222
OY 41 LeuLysArGTTrpArGlnGlnGlnProAlaGlyLeuGlyAlaValTyraAlaLeuGlu 60
|||||
DB 1223 CTCAGCGCTGGCGCCAGCAGACGCCCGGCGCTCGAGCCGTTTACGCGCCCTGGAG 1282
OY 61 ArgMetGlyLeuAspGlyCysValGluAspLeu 71
|||||
DB 1283 CGCATGGGGCTGGACGGCTGCGTGAAGACTTG 1315

RESULT 3

US-08-828-683A-9
Sequence 9, Application US/08828683A
Patent No. 6469144
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,683A
FILING DATE: 31-Mar-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/625328
FILING DATE: 1-Apr-1996
APPLICATION NUMBER: 08/710802
FILING DATE: 23-Sep-1996
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600

REFERENCE/DOCKET NUMBER: P1007P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1634 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-08-828-683A-9

Alignment Scores:
Pred. No.: 5.16e-43 Length: 1634
Score: 368.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-993-234-6_COPY_339_409 (1-71) x US-08-828-683A-9 (1-1634)

QY 1 MetaspAlaValProAlaArgTrpLysGluPheValArgThrLeuGlyLeuArgGlu 20
|||||
Db 1103 ATGACGCGGTCCACGCGCGCTGGAAGAGTTCGTCCGACGCTGGGCTGGCGAG 1162
QY 21 AlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGluMet 40
|||||
Db 1163 GCAGAGATCGAAGCCGTGAGGTGAGATCGGCCCTTCGAGACACAGCATGAGATG 1222
QY 41 LeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGlu 60
|||||
Db 1223 CTCAGCGCTGGCGCCACAGCAGCCCGGGCTCGGAGCGCTTACGGCGCCCTGAG 1282
QY 61 ArgMetGlyLeuAspGlyCysValGluAspLeu 71
|||||
Db 1283 CGCATGGGCTGACGCGCTGCTGGAAGACTTG 1315

RESULT 4
US-08-815-469-1
Sequence 1, Application US/08815469
Patent No. 6153402
GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang
APPLICANT: Ni, Jian
APPLICANT: Dixit, Vishva
APPLICANT: Gentz, Reiner L.
APPLICANT: Dillon, Patrick J.
TITLE OF INVENTION: Death Domain Containing Receptors
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/815,469
FILING DATE: HERewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: No. 6153402 yet Assigned
FILING DATE: 06-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,711
FILING DATE: 17-OCT-1996

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,285
FILING DATE: 12-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1783 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 198..1481
US-08-815-469-1

Alignment Scores:
Pred. No.: 5.79e-43 Length: 1783
Score: 368.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-993-234-6_COPY_339_409 (1-71) x US-08-815-469-1 (1-1783)

QY 1 MetaspAlaValProAlaArgTrpLysGluPheValArgThrLeuGlyLeuArgGlu 20
|||||
Db 1245 ATGACGCGGTCCACGCGCGCTGGAAGAGTTCGTCCGACGCTGGGCTGGCGAG 1304
QY 21 AlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGluMet 40
|||||
Db 1305 GCAGAGATCGAAGCCGTGAGGTGAGATCGGCCCTTCGAGACACAGCATGAGATG 1364
QY 41 LeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGlu 60
|||||
Db 1365 CTCAGCGCTGGCGCCACAGCAGCCCGGGCTCGAGCGCTTACGCGCGCTGAG 1424
QY 61 ArgMetGlyLeuAspGlyCysValGluAspLeu 71
|||||
Db 1425 CGCATGGGCTGACGCGCTGCTGGAAGACTTG 1457

RESULT 5
US-08-762-308-10
Sequence 10, Application US/08762308
Patent No. 5925548
GENERAL INFORMATION:
APPLICANT: Beutler, Bruce A.
APPLICANT: Bazzoni, Flavia M.
TITLE OF INVENTION: MODIFIED RECEPTORS THAT CONTINUOUSLY
TITLE OF INVENTION: SIGNAL
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/762,308
FILING DATE: 09-DEC-1996


```
RESULT 8
US-08-050-319B-24
; Sequence 24, Application US/08050319B
; Patent No. 5633145
; GENERAL INFORMATION:
; APPLICANT: M.Feldmann, P.W. Gray,
; APPLICANT: M.J.C. Turner, F.M Brennan
; TITLE OF INVENTION: Modified human TNFalpha (Tumor
; TITLE OF INVENTION: Necrosis Factor alpha) Receptor
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reed & Robbins
; STREET: 635 Bryant Street
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/050,319B
; FILING DATE: 10-May-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Robbins, Roberta L.
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 5150-0030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 617-8999
; TELEFAX: (415) 327-3231
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2062 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 155..1519
; US-08-050-319B-24

Alignment Scores:
Pred. No.: 4.96e-12 Length: 2062
Score: 151.00 Matches: 34
Percent Similarity: 62.67% Conservative: 13
Best Local Similarity: 45.33% Mismatches: 24
Query Match: 41.03% Indels: 4
DB: 1 Gaps: 2

US-09-993-234-6_COPY_339_409 (1-71) x US-08-050-319B-24 (1-2062)
QY 1 MetAspAlaValProAlaArgTrpLysGluPheValArgThrLeuGlyLeuArgGlu 20
Db 1241 GTGAGAACGTGCCCGCTGGAGCTGCAAGACGATTCGTGGCGGCTAGGGCTGAGCGAC 1300
QY 21 AlaGluIleGluAlaValGluValGluIleGlyArg---PheArgAspGlnGlnIleTyrGlu 39
Db 1301 CACGAGATCGATCGCTGAGCTGCAAGACGCGCTGCTGCGCGCAGAGCGCAATACAGC 1360
QY 40 MetLeuLysArgTrpArgGlnGlnGlnPro-----AlaGlyLeuGlyAlaValTyr 56
Db 1361 ATGCTGGCGACCTGAGGCGGCGCACGCCGCGCGGCGAGGCCACGCTGAGCTGTGGGA 1420
QY 57 AlaAlaLeuGluArgMetGlyLeuAspGlyCysValGluAspLeu 71
Db 1421 CGCGTGCTCCGCGACATGACCTGCTGGGCTGCTGAGGACATC 1465
RESULT 9
US-08-465-982-24
```

```
; Sequence 24, Application US/08465982
; Patent No. 5863786
; GENERAL INFORMATION:
; APPLICANT: M.Feldmann, P.W. Gray,
; APPLICANT: M.J.C. Turner, F.M Brennan
; TITLE OF INVENTION: Modified human TNFalpha (Tumor
; TITLE OF INVENTION: Necrosis Factor alpha) Receptor
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reed & Robbins
; STREET: 635 Bryant Street
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,982
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/050,319
; FILING DATE: 10-May-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Robbins, Roberta L.
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 5150-0030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 617-8999
; TELEFAX: (415) 327-3231
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2062 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 155..1519
; US-08-465-982-24

Alignment Scores:
Pred. No.: 4.96e-12 Length: 2062
Score: 151.00 Matches: 34
Percent Similarity: 62.67% Conservative: 13
Best Local Similarity: 45.33% Mismatches: 24
Query Match: 41.03% Indels: 4
DB: 2 Gaps: 2

US-09-993-234-6_COPY_339_409 (1-71) x US-08-465-982-24 (1-2062)
QY 1 MetAspAlaValProAlaArgTrpLysGluPheValArgThrLeuGlyLeuArgGlu 20
Db 1241 GTGAGAACGTGCCCGCTGGAGCTGCAAGACGATTCGTGGCGGCTAGGGCTGAGCGAC 1300
QY 21 AlaGluIleGluAlaValGluValGluIleGlyArg---PheArgAspGlnGlnIleTyrGlu 39
Db 1301 CACGAGATCGATCGCTGAGCTGCAAGACGCGCTGCTGCGCGCAGAGCGCAATACAGC 1360
QY 40 MetLeuLysArgTrpArgGlnGlnGlnPro-----AlaGlyLeuGlyAlaValTyr 56
Db 1361 ATGCTGGCGACCTGAGGCGGCGCACGCCGCGCGGCGAGGCCACGCTGAGCTGTGGGA 1420
QY 57 AlaAlaLeuGluArgMetGlyLeuAspGlyCysValGluAspLeu 71
Db 1421 CGCGTGCTCCGCGACATGACCTGCTGGGCTGCTGAGGACATC 1465
RESULT 10
```

```
US-09-106-038A-1
; Sequence 1, Application US/09106038A
; Patent No. 6007995
; GENERAL INFORMATION:
; APPLICANT: Brenda F. Baker and Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF TNFR1
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Isis Pharmaceuticals, Inc.
; STREET: 2292 Faraday Avenue
; CITY: Carlsbad
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92008
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows NT
; SOFTWARE: Microsoft Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/106,038A
; FILING DATE: June 26, 1998
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Laurel Spear Bernstein
; REGISTRATION NUMBER: 37,280
; REFERENCE/DOCKET NUMBER: RTS-0004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (760) 931-9200
; TELEFAX: (760) 603-3820
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2161
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-106-038A-1

Alignment Scores:
Pred. No.: 5,28e-12 Length: 2161
Score: 151.00 Matches: 34
Percent Similarity: 62.67% Conservative: 13
Best Local Similarity: 45.33% Mismatches: 24
Query Match: 41.03% Indels: 4
DB: 3 Gaps: 2

US-09-993-234-6_COPY_339_409 (1-71) x US-09-106-038A-1 (1-2161)
QY 1 MetAspAlaValProAlaArgTrpLysGluPheValArgThrLeuGlyLeuArgGlu 20
; ::::: ||||| ||||| ||||| ||||| ||||| ||||| :::::
Db 1342 GTGGAGAAGCTGCCCGCTGCGCTGGAAGAAATCGTGGCGCGCTGAGCGCGAC 1401
;
QY 21 AlaGluIleGluAlaValGluValGluIleGlyArg---PheArgAspGlnGlnTyrGlu 39
; ||||| ::::: ||||| ||||| ||||| ||||| ||||| |||||
Db 1402 CACGAGATCGATCGGCTGAGCTGCAGAACGGCGCTGCGCGAGCGCGCAATACAGC 1461
;
QY 40 MetLeuLysArgTrpArgGlnGlnGlnPro-----AlaGlyLeuGlyAlaValTyr 56
; ||||| ||||| ::::: ||||| ||||| ||||| ||||| |||||
Db 1462 ATGCTGGCAGCTGGAGGGCGGCGACGCGCGCGCGAGGCCACGCTGAGCTGCTGGGA 1521
;
QY 57 AlaAlaLeuGluArgMetGlyLeuAspGlyCysValGluAspLeu 71
; || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1522 CGCGTGCTCCGCGACATGACCTGCTGGCTGCTGAGGACATC 1566
;
RESULT 11
US-09-505-250-3
; Sequence 3, Application US/09505250A
; Patent No. 6329148
; GENERAL INFORMATION:
; APPLICANT: Rosen, Glenn
; APPLICANT: Kao, Peter
; TITLE OF INVENTION: Synergistic Anti-Cancer Therapy with
```

```
; TITLE OF INVENTION: Triptolides and Death Domain Ligands
; FILE REFERENCE: SUN-109PRV2
; CURRENT APPLICATION NUMBER: US/09/505,250A
; CURRENT FILING DATE: 2000-02-15
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 2161
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (256)...(1623)
; US-09-505-250-3

Alignment Scores:
Pred. No.: 5,28e-12 Length: 2161
Score: 151.00 Matches: 34
Percent Similarity: 62.67% Conservative: 13
Best Local Similarity: 45.33% Mismatches: 24
Query Match: 41.03% Indels: 4
DB: 3 Gaps: 2

US-09-993-234-6_COPY_339_409 (1-71) x US-09-505-250-3 (1-2161)
QY 1 MetAspAlaValProAlaArgTrpLysGluPheValArgThrLeuGlyLeuArgGlu 20
; ::::: ||||| ||||| ||||| ||||| ||||| ||||| :::::
Db 1342 GTGGAGAAGCTGCCCGCTGCGCTGGAAGAAATCGTGGCGCGCTGAGCGCGAC 1401
;
QY 21 AlaGluIleGluAlaValGluValGluIleGlyArg---PheArgAspGlnGlnTyrGlu 39
; ||||| ::::: ||||| ||||| ||||| ||||| ||||| |||||
Db 1402 CACGAGATCGATCGGCTGAGCTGCAGAACGGCGCTGCGCGAGCGCGCAATACAGC 1461
;
QY 40 MetLeuLysArgTrpArgGlnGlnGlnPro-----AlaGlyLeuGlyAlaValTyr 56
; ||||| ||||| ::::: ||||| ||||| ||||| ||||| |||||
Db 1462 ATGCTGGCAGCTGGAGGGCGGCGACGCGCGCGCGAGGCCACGCTGAGCTGCTGGGA 1521
;
QY 57 AlaAlaLeuGluArgMetGlyLeuAspGlyCysValGluAspLeu 71
; || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1522 CGCGTGCTCCGCGACATGACCTGCTGGCTGCTGAGGACATC 1566
;
RESULT 12
US-08-321-668-1
; Sequence 1, Application US/08321668
; Patent No. 5665859
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: BRAKEBUSCH, Cord
; APPLICANT: VARFOLOMEV, Eugene
; APPLICANT: BATKIN, Michael
; TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF
; TITLE OF INVENTION: THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/321,668
; FILING DATE: 12-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 107268
; FILING DATE: 12-OCT-1993
; ATTORNEY/AGENT INFORMATION:
```



```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/126,016
; FILING DATE: 24-SEP-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/625668
; FILING DATE: 13-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, ROGER L
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: WALLACH4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2175 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 256..1620
; NAME/KEY: mat_peptide
; LOCATION: 319..1620
; US-08-126-016-1

Alignment Scores:
Pred. No.: 5.32e-12 Length: 2175
Score: 151.00 Matches: 34
Percent Similarity: 62.67% Conservative: 13
Best Local Similarity: 45.33% Mismatches: 24
Query Match: 41.03% Indels: 4
DB: 1 Gaps: 2

US-09-993-234-6_COPY_339_409 (1-71) x US-08-126-016-1 (1-2175)
QY 1 MetaspAlaValProAlaArgTrpLysGluPheValArgThrLeuGlyLeuArgGlu 20
; ::::: ||||| ||||| ||||| ||||| ||||| ||||| ::::
Db 1342 GTGAGAACGTGCCCGCGTGGCTGGAAGGAATTCGTGCGGCGCTAGGCGTGAAGC 1401
QY 21 AlaGluLeGluAlaValAlaGluValGluLeuGlyArg--PheArgAspGlnGlnTyrGlu 39
; ||||| ::::: ||||| ||||| ||||| ||||| |||||
Db 1402 CACGAGATCGATCGCTGAGCTGCAGAACGGCGCTGCGCGAGCGCAATACAGC 1461
QY 40 MetLeuLysArgTrpArgGlnGlnPro-----AlaGlyLeuGlyAlaValTyr 56
; ||||| ||||| ::::: ||||| ||||| ||||| |||||
Db 1462 ATGCTGGCGACCTGAGAGCGCGCCAGCGCGCGAGGCCACAGCTGAGAGCTGCGGA 1521
QY 57 AlaAlaLeuGluArgMetGlyLeuAspGlyCysValGluAspLeu 71
; ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1522 CGCGTGTCCGCGACATGACCTGCTGGGCTGCTGAGAGACATC 1566

RESULT 15
US-08-054-970-1
; Sequence 1, Application US/08054970
; Patent No. 6395267
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: BRAKEBUSCH, Cord
; TITLE OF INVENTION: TNF RECEPTOR ACTION MODULATION
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W.
; CITY: Washington
```

```

; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/054,970
; FILING DATE: 03-MAY-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, Kevin G.
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: WALLACH-9
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2175 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 256..1620
; US-08-054-970-1

Alignment Scores:
Pred. No.: 5.32e-12 Length: 2175
Score: 151.00 Matches: 34
Percent Similarity: 62.67% Conservative: 13
Best Local Similarity: 45.33% Mismatches: 24
Query Match: 41.03% Indels: 4
DB: 4 Gaps: 2

US-09-993-234-6_COPY_339_409 (1-71) x US-08-054-970-1 (1-2175)
QY 1 MetaspAlaValProAlaArgTrpLysGluPheValArgThrLeuGlyLeuArgGlu 20
; ::::: ||||| ||||| ||||| ||||| ||||| ||||| ::::
Db 1342 GTGAGAACGTGCCCGCGTGGCTGGAAGGAATTCGTGCGGCGCTAGGCGTGAAGC 1401
QY 21 AlaGluLeGluAlaValAlaGluValGluLeuGlyArg--PheArgAspGlnGlnTyrGlu 39
; ||||| ::::: ||||| ||||| ||||| ||||| |||||
Db 1402 CACGAGATCGATCGCTGAGCTGCAGAACGGCGCTGCGCGAGCGCAATACAGC 1461
QY 40 MetLeuLysArgTrpArgGlnGlnPro-----AlaGlyLeuGlyAlaValTyr 56
; ||||| ||||| ::::: ||||| ||||| ||||| |||||
Db 1462 ATGCTGGCGACCTGAGAGCGCGCCAGCGCGCGAGGCCACAGCTGAGAGCTGCGGA 1521
QY 57 AlaAlaLeuGluArgMetGlyLeuAspGlyCysValGluAspLeu 71
; ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1522 CGCGTGTCCGCGACATGACCTGCTGGGCTGCTGAGAGACATC 1566
```

Search completed: April 6, 2003, 23:30:04
Job time : 17.9856 secs

GenCore version 5.1.4-p5-4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 6, 2003, 21:08:18 ; Search time 27.0348 Seconds
(without alignments)
2303.655 Million cell updates/sec

Title: US-09-993-234-6_COPY_339_409
Perfect score: 368
Sequence: 1 MDAVPAARMKEFVRILGLRE.....LGAVYAALERMGLDGCVEDL 71

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 593429 segs, 438583890 residues

Total number of hits satisfying chosen parameters: 1186858

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_{p2n}.model -DEV=xlh
-O=/cgn2_1/USPTO_spool/US09993234/runat_27032003_115459_15466/app_query.fasta_1.2346
-DB=Published.Applications_NA -QEXT=fastap -SUFFIX=trpb -MINMATCH=0.1
-LOOPCL=0 -LOOEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCLIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09993234_@CGN_1_1_249_@runat_27032003_115459_15466
-NCPU=6 -ICPU=3 -NO_XLPHY -NO_MMAL -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAEXT=0.5 -FGAPOP=6
-FGAEXT=7 -YGAPOP=10 -YGAEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published.Applications_NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	368	100.0	1254	10	US-09-333-966-3	Sequence 3, Appl1
2	368	100.0	1634	9	US-10-081-280-9	Sequence 9, Appl1
3	368	100.0	1634	9	US-10-112-793-9	Sequence 9, Appl1
4	368	100.0	1634	9	US-10-112-193-11	Sequence 11, Appl1

5	368	100.0	1634	10	US-09-993-234-9	Sequence 9, Appl1
6	368	100.0	1783	10	US-09-333-966-1	Sequence 1, Appl1
7	368	100.0	10797	9	US-10-092-154-1577	Sequence 1577, Ap
8	368	100.0	10797	10	US-09-764-847-1577	Sequence 1577, Ap
9	356	96.7	1743	9	US-09-954-531-1389	Sequence 1389, Ap
10	157	42.7	2130	10	US-09-917-800A-1601	Sequence 1601, Ap
11	157	42.7	2173	9	US-09-898-234-14	Sequence 14, Appl
12	157	42.7	2173	9	US-09-899-429A-24	Sequence 24, Appl
13	157	42.7	2173	9	US-09-792-356-14	Sequence 14, Appl
14	157	42.7	2173	10	US-09-899-422-14	Sequence 14, Appl
15	156	42.4	2440	10	US-09-970-532-1	Sequence 1, Appl1
16	151	41.0	427	10	US-09-876-889-236	Sequence 236, App
17	151	41.0	479	9	US-10-043-487-100	Sequence 100, App
18	151	41.0	1368	9	US-09-898-234-1	Sequence 1, Appl1
19	151	41.0	1368	9	US-09-899-429A-1	Sequence 1, Appl1
20	151	41.0	1368	9	US-09-792-356-1	Sequence 1, Appl1
21	151	41.0	1368	10	US-09-899-422-1	Sequence 1, Appl1
22	151	41.0	2111	10	US-09-880-107-2360	Sequence 2360, Ap
23	151	41.0	2141	9	US-09-898-234-16	Sequence 16, Appl
24	151	41.0	2141	9	US-09-899-429A-26	Sequence 26, Appl
25	151	41.0	2141	9	US-09-792-356-16	Sequence 16, Appl
26	151	41.0	2141	10	US-09-899-422-16	Sequence 16, Appl
27	151	41.0	2175	12	US-10-120-397-1	Sequence 1, Appl1
28	94	25.5	1062	8	US-08-916-625B-3	Sequence 3, Appl1
29	94	25.5	1236	9	US-10-076-754-1	Sequence 1, Appl1
30	94	25.5	1236	9	US-10-076-773-1	Sequence 1, Appl1
31	94	25.5	1236	12	US-10-067-615-1	Sequence 1, Appl1
32	94	25.5	1600	10	US-09-874-138-1	Sequence 1, Appl1
33	94	25.5	1600	12	US-10-005-842-1	Sequence 1, Appl1
34	94	25.5	1799	9	US-09-992-964-10	Sequence 10, Appl
35	94	25.5	1799	10	US-09-828-739-1	Sequence 1, Appl1
36	94	25.5	1799	10	US-09-887-879-10	Sequence 10, Appl
37	94	25.5	1799	12	US-10-052-798-2	Sequence 2, Appl1
38	94	25.5	3881	8	US-08-916-625B-1	Sequence 1, Appl1
39	94	25.5	3964	9	US-09-811-088-5	Sequence 5, Appl1
40	94	25.5	3964	10	US-09-757-421-3	Sequence 3, Appl1
41	94	25.5	4051	9	US-09-811-088-3	Sequence 3, Appl1
42	94	25.5	4051	10	US-09-757-421-1	Sequence 1, Appl1
43	76	20.7	2040	9	US-09-991-496-5	Sequence 5, Appl1
44	76	20.7	2040	10	US-09-874-923-5	Sequence 5, Appl1
45	76	20.7	4233	9	US-09-991-496-99	Sequence 99, Appl1

ALIGNMENTS

RESULT 1
US-09-333-966-3
Sequence 3, Application US/09333966
Patent No. US20020009773A1
GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang
APPLICANT: Ni, Jian
APPLICANT: Dixit, Vishva
APPLICANT: Gentz, Reiner L.
APPLICANT: Dillon, Patrick J.
TITLE OF INVENTION: Death Domain Containing Receptors
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/333,966
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/815,469
FILING DATE:
APPLICATION NUMBER: No. US20020009773A1 yet Assigned
FILING DATE: 06-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,711
FILING DATE: 17-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,285
FILING DATE: 12-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1254 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1251
US-09-333-966-3

Alignment Scores:
Pred. No.: 3.73e-45 Length: 1254
Score: 368.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-993-234-6_COPY_339_409 (1-71) x US-09-333-966-3 (1-1254)

QY 1 MetAspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGlu 20
|||||
DB 1015 ATGACGCGGTCCACGCGCGCTGGAAGAGTTCGTGCGCACGCTGGGCTGCCGAG 1074
|||||
QY 21 AlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGluMet 40
|||||
DB 1075 GCAGAGATCGAAGCCGTGAGGTGAGATCGGCCCTTCGAGACACGACGATG 1134
|||||
QY 41 LeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGlu 60
|||||
DB 1135 CTCAGCGCTGGCGCCAGCAGCAGCCCGCGGCTCGAGCCGTTTACGCGGCCCTGAG 1194
|||||
QY 61 ArgMetGlyLeuAspGlyCysValGluAspLeu 71
|||||
DB 1195 CGCATGGGCTGGACGCGCTGCGTGAAGACTTG 1227
|||||

RESULT 2
US-10-081-280-9
Sequence 9, Application US/10081280
Patent No. US20020165157A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/081,280
FILING DATE: 21-Feb-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/829,270
FILING DATE: 31-Mar-1997
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5416
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1634 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-081-280-9

Alignment Scores:
Pred. No.: 5.15e-45 Length: 1634
Score: 368.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-993-234-6_COPY_339_409 (1-71) x US-10-081-280-9 (1-1634)

QY 1 MetAspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGlu 20
|||||
DB 1103 ATGACGCGGTCCACGCGCGCTGGAAGAGTTCGTGCGCACGCTGGGCTGCCGAG 1162
|||||
QY 21 AlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGluMet 40
|||||
DB 1163 GCAGAGATCGAAGCCGTGAGGTGAGATCGGCCCTTCGAGACACGACGATG 1222
|||||
QY 41 LeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGlu 60
|||||
DB 1223 CTCAGCGCTGGCGCCAGCAGCAGCCCGCGGCTCGGAGCCGTTTACGCGGCCCTGAG 1282
|||||
QY 61 ArgMetGlyLeuAspGlyCysValGluAspLeu 71
|||||
DB 1283 CGCATGGGCTGGACGCGCTGCGTGAAGACTTG 1315
|||||

RESULT 3
US-10-112-793-9
Sequence 9, Application US/10112793
Publication No. US20020192729A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)

```

;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/112,793
; FILING DATE: 28-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,683A
; FILING DATE: 31-Mar-1997
; APPLICATION NUMBER: 08/625328
; FILING DATE: 1-Apr-1996
; APPLICATION NUMBER: 08/710802
; FILING DATE: 23-Sep-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1007P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1634 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-112-793-9

Alignment Scores:
Pred. No.: 5.15e-45 Length: 1634
Score: 368.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-993-234-6_COPY_339_409 (1-71) x US-10-112-793-9 (1-1634)
QY 1 MetaspalavaIProalaargArGTrrplysGIuphevalArgThrleuGIyleuArgGIu 20
    |||||||
Db 1103 ATGACGCGGTCCACGCGCGCTGGAAGAGTTCGTGCGCAGCTGGGCTGCGCGAG 1162
QY 21 AlagluileglAlaValaIgluValaIleGIyArGPheArGAspGInGIIntyrGIumet 40
    |||||||
Db 1163 GCAGAGATCGAAGCCGTGAGGTGAGATCGCGCTTCCGAGACGACGAGTACGAGATG 1222
QY 41 LeulysArGTrrPArGInGIInProAlaGIyleuGIyAlaValTrrAlaAlaIleuGIu 60
    |||||||
Db 1223 CTCAGCGCTGGCGCCAGCAGACGCCCGGGCTCGGAGCCGTTTACGCGGCCCTGGAG 1282
QY 61 ArgmetGIyleuAspGIyCysValGIuaspleu 71
    |||||||
Db 1283 CGCATGGGGCTGGACGGCTGCTGGAAGACTTG 1315

RESULT 4
US-10-112-193-11
; Sequence 11, Application US/10112193
; Publication No. US20030004313A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-3 POLYPEPTIDE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; APPLICATION NUMBER: US/09/993,234
```

```

;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/112,193
; FILING DATE: 28-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/928,069
; FILING DATE: 11-Sep-1997
; APPLICATION NUMBER: 60/026943
; FILING DATE: 23-Sep-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1052R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1634 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-112-193-11

Alignment Scores:
Pred. No.: 5.15e-45 Length: 1634
Score: 368.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-993-234-6_COPY_339_409 (1-71) x US-10-112-193-11 (1-1634)
QY 1 MetaspalavaIProalaargArGTrrplysGIuphevalArgThrleuGIyleuArgGIu 20
    |||||||
Db 1103 ATGACGCGGTCCACGCGCGCTGGAAGAGTTCGTGCGCAGCTGGGCTGCGCGAG 1162
QY 21 AlagluileglAlaValaIgluValaIleGIyArGPheArGAspGInGIIntyrGIumet 40
    |||||||
Db 1163 GCAGAGATCGAAGCCGTGAGGTGAGATCGCGCTTCCGAGACGACGAGTACGAGATG 1222
QY 41 LeulysArGTrrPArGInGIInProAlaGIyleuGIyAlaValTrrAlaAlaIleuGIu 60
    |||||||
Db 1223 CTCAGCGCTGGCGCCAGCAGACGCCCGGGCTCGGAGCCGTTTACGCGGCCCTGGAG 1282
QY 61 ArgmetGIyleuAspGIyCysValGIuaspleu 71
    |||||||
Db 1283 CGCATGGGGCTGGACGGCTGCTGGAAGACTTG 1315

RESULT 5
US-09-993-234-9
; Sequence 9, Application US/09993234
; Patent No. US20020146768A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/993,234
```

;; FILING DATE: 19-NO. US20020146768A1-2001
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/828,683
;; FILING DATE: <Unknown>
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Marschang, Diane L.
;; REGISTRATION NUMBER: 35,600
;; REFERENCE/DOCKET NUMBER: P1007P1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415/225-5416
;; TELEFAX: 415/952-9881
;; TELEX: 910/371-7168
;; INFORMATION FOR SEQ ID NO: 9:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1634 base pairs
;; TYPE: Nucleic Acid
;; STRANDEDNESS: Single
;; TOPOLOGY: Linear
;; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-993-234-9

Alignment Scores:
Pred. No.: 5.15e-45 Length: 1634
Score: 368.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-993-234-6_COPY_339_409 (1-71) x US-09-993-234-9 (1-1634)

QY 1 MetaspalavalProalaargatgtrplysgluphevalargthrleuglyleuarglu 20
Db 1103 ATGACGCGGTCCAGCGCGCTGGAAGAGATTCTGCCACGCTGGGGCTGCGGAG 1162
QY 21 AlagluilegluAlaValgluValleuglyArgpheargaspnglnIntyrglumet 40
Db 1163 GCAGAGATCGAAGCCGTGAGGTGAGATCGGCCCTTCCGAGACCAGCAGTACGAGATG 1222
QY 41 LeulysargtrpargnglnglnProalagllyleuglyAlaValtyrAlaAlaleuglu 60
Db 1223 CTCAGCGCTGGCGCCAGCAGCAGCCCGGGGCTCGGAGCCGTTTACGCGGCTTGAG 1282
QY 61 ArgmetglyleuaspglyCysValgluaspleu 71
Db 1283 CGCATGGGGCTGGACGGCTGCTGTGAAGACTTG 1315

RESULT 6
US-09-333-966-1

;; Sequence 1, Application US/09333966
;; Patent No. US20020009773A1
;; GENERAL INFORMATION:
;; APPLICANT: Yu, Guo-Liang
;; APPLICANT: Ni, Jian
;; APPLICANT: Dixit, Vishva
;; APPLICANT: Gentz, Reinert L.
;; APPLICANT: Dillon, Patrick J.
;; TITLE OF INVENTION: Death Domain Containing Receptors
;; NUMBER OF SEQUENCES: 17
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
;; STREET: 1100 New York Ave., NW, Suite 600
;; CITY: Washington
;; STATE: DC
;; COUNTRY: USA
;; ZIP: 20005-3934
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/09/333,966
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/815,469
;; FILING DATE:
;; APPLICATION NUMBER: No. US20020009773A1 Yet Assigned
;; FILING DATE: 06-FEB-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 60/028,711
;; FILING DATE: 17-OCT-1996
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 60/013,285
;; FILING DATE: 12-MAR-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Steffe, Eric K.
;; REGISTRATION NUMBER: 36,688
;; REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-371-2600
;; TELEFAX: 202-371-2540
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1783 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: both
;; MOLECULE TYPE: cDNA
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 198..1481
US-09-333-966-1

Alignment Scores:
Pred. No.: 5.73e-45 Length: 1783
Score: 368.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-993-234-6_COPY_339_409 (1-71) x US-09-333-966-1 (1-1783)

QY 1 MetaspalavalProalaargatgtrplysgluphevalargthrleuglyleuarglu 20
Db 1245 ATGACGCGGTCCAGCGCGCTGGAAGAGATTCTGCCACGCTGGGGCTGCGGAG 1304
QY 21 AlagluilegluAlaValgluValleuglyArgpheargaspnglnIntyrglumet 40
Db 1305 GCAGAGATCGAAGCCGTGAGGTGAGATCGGCCCTTCCGAGACCAGCAGTACGAGATG 1364
QY 41 LeulysargtrpargnglnglnProalagllyleuglyAlaValtyrAlaAlaleuglu 60
Db 1365 CTCAGCGCTGGCGCCAGCAGCAGCCCGGGGCTCGGAGCCGTTTACGCGGCTTGAG 1424
QY 61 ArgmetglyleuaspglyCysValgluaspleu 71
Db 1425 CGCATGGGGCTGGACGGCTGCTGTGAAGACTTG 1457

RESULT 7

US-10-092-154-1577
;; Sequence 1577, Application US/10092154
;; Publication No. US20030054375A1
;; GENERAL INFORMATION:
;; APPLICANT: Rosen et al.
;; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;; FILE REFERENCE: PC009C1
;; CURRENT APPLICATION NUMBER: US/10/092,154
;; CURRENT FILING DATE: 2002-03-07
;; NUMBER OF SEQ ID NOS: 2003
;; Prior Application removed - See File Wrapper or Palm
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 1577

LENGTH: 10797
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-092-154-1577

Alignment Scores:

Pred. No.:	5.17e-44	Length:	10797
Score:	368.00	Matches:	71
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-993-234-6_COPY_339_409 (1-71) x US-10-092-154-1577 (1-10797)

OY 1 MetaspAlaValProAlaAArgTrPlySGluPheValArgThrLeuGlyLeuAArgGlu 20
|||||
DB 9122 ATGGACGGCTCCAGCGCGCGCTGGAAGAGATTCTGCGCACGCTGGGGCTGCGGAG 9181
OY 21 AlaGluIleGluAlaValAluValGluIleGlyArgPheArgAspGlnGlnTyrGluMet 40
|||||
DB 9182 GCAGAGATCGAAGCCGTGGAGGTGAGATCGGCGCTTCCGAGACGACAGTACGAGATG 9241
OY 41 LeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGlu 60
|||||
DB 9242 CTCAGCGCTGGCGCCAGCAGACGCCGCGCTCGGAGCCGTTTACGCGCCCTGGAG 9301
OY 61 ArgMetGlyLeuAspGlyCysValGluAspLeu 71
|||||
DB 9302 CGCATGGGCTGACGCGCTGCTGGAAGACTTG 9334

RESULT 8

US-09-764-847-1577
; Sequence 1577, Application US/09764847
; Patent No. US20020132767A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009
; CURRENT APPLICATION NUMBER: US/09/764,847
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2003
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1577
; LENGTH: 10797
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-847-1577

Alignment Scores:

Pred. No.:	5.17e-44	Length:	10797
Score:	368.00	Matches:	71
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-09-993-234-6_COPY_339_409 (1-71) x US-09-764-847-1577 (1-10797)

OY 1 MetaspAlaValProAlaAArgTrPlySGluPheValArgThrLeuGlyLeuAArgGlu 20
|||||
DB 9122 ATGGACGGCTCCAGCGCGCGCTGGAAGAGATTCTGCGCACGCTGGGGCTGCGGAG 9181
OY 21 AlaGluIleGluAlaValAluValGluIleGlyArgPheArgAspGlnGlnTyrGluMet 40
|||||
DB 9182 GCAGAGATCGAAGCCGTGGAGGTGAGATCGGCGCTTCCGAGACGACAGTACGAGATG 9241
OY 41 LeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGlu 60
|||||
DB 9242 CTCAGCGCTGGCGCCAGCAGACGCCGCGGCTCGGAGCCGTTTACGCGCCCTGGAG 9301
OY 61 ArgMetGlyLeuAspGlyCysValGluAspLeu 71

|||||
DB 9302 CGCATGGGCTGACGCGCTGCTGGAAGACTTG 9334

RESULT 9

US-09-954-531-1389
; Sequence 1389, Application US/09954531
; Patent No. US20020165180A1
; GENERAL INFORMATION:
; APPLICANT: Weaver, Zoe
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C
; FILE REFERENCE: 689290-77
; CURRENT APPLICATION NUMBER: US/09/954,531
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: US/60/233,133
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,009
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,034
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,509
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US/60/234,567
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 1392
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1389
; LENGTH: 1743
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-531-1389

Alignment Scores:

Pred. No.:	3.29e-43	Length:	1743
Score:	356.00	Matches:	69
Percent Similarity:	97.18%	Conservative:	0
Best Local Similarity:	97.18%	Mismatches:	2
Query Match:	96.74%	Indels:	0
DB:	9	Gaps:	0

US-09-993-234-6_COPY_339_409 (1-71) x US-09-954-531-1389 (1-1743)

OY 1 MetaspAlaValProAlaAArgTrPlySGluPheValArgThrLeuGlyLeuAArgGlu 20
|||||
DB 1184 ATGGACGGCTCCAGCGCGCGCTGGAAGAGTTCGTGCGCACGCTGGGGCTGCGGAG 1243
OY 21 AlaGluIleGluAlaValAluValGluIleGlyArgPheArgAspGlnGlnTyrGluMet 40
|||||
DB 1244 GCAGAGATCGAAGCCGTGGAGGTGAGATCGTCTTCCGAGACGACAGTACGAGATG 1303
OY 41 LeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGlu 60
|||||
DB 1304 CTCAGCACTGGCGCCAGCAGACGCCGCGGCTCGGAGCCGTTTACGCGCCCTGGAG 1363
OY 61 ArgMetGlyLeuAspGlyCysValGluAspLeu 71
|||||
DB 1364 CGCATGGGCTGACGCGCTGCTGGAAGACTTG 1396

RESULT 10

US-09-917-800A-1601
; Sequence 1601, Application US/09917800A
; Patent No. US20020119462A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5038-US
; CURRENT APPLICATION NUMBER: US/09/917,800A
; CURRENT FILING DATE: 2001-07-31

```
; PRIOR APPLICATION NUMBER: US 60/222,040
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 60/222,880
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/290,029
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/290,645
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 60/292,336
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/295,798
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/297,457
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,884
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,459
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 1740
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1601
; LENGTH: 2130
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020119462A1 NM_013091
US-09-917-800A-1601

Alignment Scores:
Pred. No.: 1.01e-13 Length: 2130
Score: 157.00 Matches: 35
Percent Similarity: 62.67% Conservative: 12
Best Local Similarity: 46.67% Mismatches: 24
Query Match: 42.66% Indels: 4
DB: 10 Gaps: 2

US-09-993-234-6_COPY_339_409 (1-71) x US-09-917-800A-1601 (1-2130)
QY 1 MetaspAlaValProAlaArgTrpLysGluPheValArgThrLeuGlyLeuArgGlu 20
Db 1345 GTGATGGCGTGCCTCCGACACGCTGGAAGAGTTCATGCGGCTCTGGGGCTGAGCGAG 1404
QY 21 AlaGluIleGluAlaValGluValGluIleGlyArg---PheArgAspGlnGlnTyrglu 39
Db 1405 CACGAGATCGAGCGGCTGAGCTGCAAGACGGCGTTGCCCTCCGACGAGCTCATTTACAGC 1464
QY 40 MetLeuLysArgTrpArgGlnGlnGlnPro-----AlaGlyLeuGlyAlaValTyr 56
Db 1465 ATGCTGGAAGCGCTGGCGCGCCGACACCGCGACACGAGGCGCAGCTGAGTAGTGGGC 1524
QY 57 AlaAlaLeuGluArgMetGlyLeuAspGlyCysValGluAspLeu 71
Db 1525 CGCGTGCCTTGGCAGACATGAACCTGCGCTGCTGAGAGACATC 1569

RESULT 11
US-09-898-234-14
; Sequence 14, Application US/09898234
; Patent No. US2002015112A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stratowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; FILE REFERENCE: 98,385-I
; CURRENT APPLICATION NUMBER: US/09/898,234
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/525,998
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
```

```
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 2173
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (245)..(1630)
; OTHER INFORMATION: Description of Artificial Sequence: ratTNF-R8
US-09-898-234-14

Alignment Scores:
Pred. No.: 1.03e-13 Length: 2173
Score: 157.00 Matches: 35
Percent Similarity: 62.67% Conservative: 12
Best Local Similarity: 46.67% Mismatches: 24
Query Match: 42.66% Indels: 4
DB: 9 Gaps: 2

US-09-993-234-6_COPY_339_409 (1-71) x US-09-898-234-14 (1-2173)
QY 1 MetaspAlaValProAlaArgTrpLysGluPheValArgThrLeuGlyLeuArgGlu 20
Db 1352 GTGATGGCGTGCCTCCGACACGCTGGAAGAGTTCATGCGGCTCTGGGGCTGAGCGAG 1411
QY 21 AlaGluIleGluAlaValGluValGluIleGlyArg---PheArgAspGlnGlnTyrglu 39
Db 1412 CACGAGATCGAGCGGCTGAGCTGCAAGACGGCGTTGCTGCCGCGAGGCTCATTTACAGC 1471
QY 40 MetLeuLysArgTrpArgGlnGlnGlnPro-----AlaGlyLeuGlyAlaValTyr 56
Db 1472 ATGCTGGAAGCCTGGCGCGCCGACACCGCGACAGAGGCGCAGCTGAGTAGTGGGC 1531
QY 57 AlaAlaLeuGluArgMetGlyLeuAspGlyCysValGluAspLeu 71
Db 1532 CGCGTGCCTTGGCAGACATGAACCTGCGGTGCTGCTGAGAGACATC 1576

RESULT 12
US-09-899-429A-24
; Sequence 24, Application US/09899429A
; Patent No. US20020169118A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stratowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; FILE REFERENCE: 98-385-J
; CURRENT APPLICATION NUMBER: US/09/899,429A
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/792,356
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 08/477,639
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 2173
```

```
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ratTNF-R8
; NAME/KEY: CDS
; LOCATION: (245)..(1627)
US-09-899-429A-24
```

```
Alignment Scores:
Pred. No.: 1.03e-13      Length: 2173
Score: 157.00           Matches: 35
Percent Similarity: 62.67%      Conservative: 12
Best Local Similarity: 46.67%   Mismatches: 24
Query Match: 42.66%           Indels: 4
DB: 9                      Gaps: 2
```

US-09-993-234-6_COPY_339_409 (1-71) x US-09-899-429A-24 (1-2173)

```
OY 1 MetAspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGlu 20
    ::||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1352 GTGATGGCGTGCCTCCGACACAGCTGGAAGAGTTCATGCGCTCCTGGGGCTGAGCGAG 1411

OY 21 AlaGluIleGluAlaValGluValGluIleGlyArg---PheArgAspGlnGlnTyrGlu 39
    ||||| ||||| ::||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1412 CACGAGATCGAGCGGTGAGCTGCAGAACGGCGCTGCCCTCCGAGGCTCATTTACAGC 1471

OY 40 MetLeuLysArgTrpArgGlnGlnGlnPro-----AlaGlyLeuGlyAlaValTyr 56
    ||||| ::||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1472 ATGCTGAAGCCTGGCGCGCGCCGACACACCGCGACAGAGCCACGCTGAGCTAGTGGGC 1531

OY 57 AlaAlaLeuGluArgMetGlyLeuAspGlyCysValGluAspLeu 71
    ||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1532 CGCGTCTTTGGCAGATGAACCTGCGTGGCTGCTGGAACAATC 1576
```

```
RESULT 13
US-09-792-356-14
; Sequence 14, Application US/09792356
; Publication No. US20020183485A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stratowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; FILE REFERENCE: 98,385-G
; CURRENT APPLICATION NUMBER: US/09/792,356
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 08/477,639
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 2173
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (245)..(1630)
; OTHER INFORMATION: Description of Artificial Sequence: ratTNF-R8
US-09-792-356-14
```

```
Alignment Scores:
Pred. No.: 1.03e-13      Length: 2173
Score: 157.00           Matches: 35
```

```
Percent Similarity: 62.67%      Conservative: 12
Best Local Similarity: 46.67%   Mismatches: 24
Query Match: 42.66%           Indels: 4
DB: 9                      Gaps: 2
```

US-09-993-234-6_COPY_339_409 (1-71) x US-09-792-356-14 (1-2173)

```
OY 1 MetAspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGlu 20
    ::||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1352 GTGATGGCGTGCCTCCGACACAGCTGGAAGAGTTCATGCGCTCCTGGGGCTGAGCGAG 1411

OY 21 AlaGluIleGluAlaValGluValGluIleGlyArg---PheArgAspGlnGlnTyrGlu 39
    ||||| ||||| ::||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1412 CACGAGATCGAGCGGTGAGCTGCAGAACGGCGTTCCTCCGAGGCTCATTTACAGC 1471

OY 40 MetLeuLysArgTrpArgGlnGlnGlnPro-----AlaGlyLeuGlyAlaValTyr 56
    ||||| ::||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1472 ATGCTGAAGCCTGGCGCGCGCCGACACACCGCGACAGAGCCACGCTGAGCTAGTGGGC 1531

OY 57 AlaAlaLeuGluArgMetGlyLeuAspGlyCysValGluAspLeu 71
    ||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1532 CGCGTCTTTGGCAGATGAACCTGCGTGGCTGCTGGAACAATC 1576
```

```
RESULT 14
US-09-899-422-14
; Sequence 14, Application US/09899422
; Patent No. US2002090676A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stratowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; FILE REFERENCE: 98,385-H
; CURRENT APPLICATION NUMBER: US/09/899,422
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 09/525,998
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 2173
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (245)..(1630)
; OTHER INFORMATION: Description of Artificial Sequence: ratTNF-R8
US-09-899-422-14
```

```
Alignment Scores:
Pred. No.: 1.03e-13      Length: 2173
Score: 157.00           Matches: 35
Percent Similarity: 62.67%      Conservative: 12
Best Local Similarity: 46.67%   Mismatches: 24
Query Match: 42.66%           Indels: 4
DB: 10                      Gaps: 2
```

US-09-993-234-6_COPY_339_409 (1-71) x US-09-899-422-14 (1-2173)

```
OY 1 MetAspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGlu 20
    ::||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1352 GTGATGGCGTGCCTCCGACACAGCTGGAAGAGTTCATGCGCTCCTGGGGCTGAGCGAG 1411
```

OY 21 AlaGluIleGluAlaValaGluValaGluIleGlyArg---PheArgAspGlnGlnIleTyrGlu 39
 ||||| :::||||| ||||| |||
Db 1412 CACGAGATCGACGGCTGTGGAGCTGCAGAACGGCGCTGCCCTCCGAGAGGCTCATTTACAGC 1471

OY 40 MetLeuLysArgTirParGlnGlnGlnPro-----AlaGlyLeuGlyAlaValTyr 56
 ||||| ||||| ||| ||| |||
Db 1472 ATGCTGGAAGCCTGGCGGCGCCGACACCGCAGACAGAGGCCACGCTGGACGTAGTGGGC 1531

OY 57 AlaAlaLeuGluArgMetGlyLeuAspGlyCysValGluAspLeu 71
 ||| ||| ||| ||||| :::
Db 1532 CGCGTGTCTTGGACATGAACCTGCGTGGCTGCTGAGAGAACATC 1576

RESULT 15

US-09-970-532-1
; Sequence 1, Application US/09970532
; Patent No. US20020076765A1
; GENERAL INFORMATION:
; APPLICANT: Taylor, J. Michael
; APPLICANT: Kehrl, Jr., Marcus
; APPLICANT: Lee, Eun-Kyung
; APPLICANT: Mwang, Simon
; TITLE OF INVENTION: BOVINE TUMOR NECROSIS FACTOR RECEPTOR-1
; FILE REFERENCE: 08411-018001
; CURRENT APPLICATION NUMBER: US/09/970,532
; CURRENT FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 09/513,007
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2440
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (294)...(1706)
US-09-970-532-1

Alignment Scores:
Pred. No.: 1.67e-13 Length: 2440
Score: 156.00 Matches: 36
Percent Similarity: 61.33% Conservative: 10
Best Local Similarity: 48.00% Mismatches: 25
Query Match: 42.39% Indels: 4
DB: 10 Gaps: 2

US-09-993-234-6_COPY_339_409 (1-71) x US-09-970-532-1 (1-2440)

OY 1 MetAspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGlu 20
 :::|||| ||||| ||||| ||||| |||
Db 1428 GTGGACGGCGTGCCTCCGCTGCCTGGAAGAGTGTGCGCGGCTGGAGCTGAGCGAG 1487

OY 21 AlaGluIleGluAlaValaGluValaGluIleGlyArg---PheArgAspGlnGlnIleTyrGlu 39
 ||||| :::||||| ||||| ||| |||
Db 1488 CACGAGATCGACGGCTGGAGCTGGAAGACGGCGCCACCTGCGGAGGCGCAGTACAGC 1547

OY 40 MetLeuLysArgTirParGlnGlnGlnPro-----AlaGlyLeuGlyAlaValTyr 56
 ||||| ||||| ||| ||| |||
Db 1548 ATGCTGCGCGCTGGCGGCGCCGACACGCGCGCCGAGGCCACGCTGGAAGCTGTGGGC 1607

OY 57 AlaAlaLeuGluArgMetGlyLeuAspGlyCysValGluAspLeu 71
 ||| ||| ||| ||||| :::
Db 1608 CGCGTGTCTCAGGAGACATGACCTGCTGGTGTGCTGGAACAAACATA 1652

Search completed: April 7, 2003, 03:59:22
Job time : 36.0348 secs

153

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 6, 2003, 14:15:43 ; Search time 1730 Seconds

(without alignments)
5195.662 Million cell updates/sec

Title: US-09-993-234-9_COPY_146_700

Perfect score: 555
Sequence: 1 CTGGGGGGCCCCGGCCAGGG.....GGCAGATGTTCTGGGTCAG 555

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estov:*
5: em_estpl:*
6: em_estro:*
7: em_estro:*
8: em_estro:*
9: gb_est1:*
10: gb_est2:*
11: gb_est3:*
12: gb_est4:*
13: gb_est5:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	547.6	98.7	632	10	AW268610 xv41b12.x
2	543.8	98.0	698	9	AI807913 wF52C03.x
3	535.6	96.5	767	13	BI909448 603065172
4	533	96.0	688	9	AI424936 tg19b08.x
5	512	92.3	562	9	AI140043 qa87a04.x
6	486.4	87.6	552	14	BM783972 K-EST0062

7	486.4	87.6	585	10	AW517358 xp93g02.x
8	486	87.6	514	14	BM756372 K-EST0034
9	486	87.6	514	14	BM783979 K-EST0062
10	484.8	87.4	565	14	BM744307 K-EST0017
11	477	85.9	508	9	AI203624 qe75f02.x
12	475	85.6	492	14	BM741016 K-EST0013
13	466	84.0	488	14	BM770798 K-EST0054
14	439.4	79.2	1010	14	BQ068309 AGENCOURT
15	413	74.4	478	10	AW002222 wL85C09.x
16	411.6	74.2	427	12	BE696572 PM4-CT040
17	362	65.2	422	9	AI700459 wQ14b11.x
18	350.6	63.2	433	14	H41522 yn90f12.s1
19	298.2	53.7	432	14	N71143 za80h09.s1
20	293	52.8	434	14	BM826048 K-EST0098
21	284	51.2	572	10	BE668836 159213 MA
22	275.8	49.7	345	9	AA934992 op33h05.s
23	233.2	42.0	322	9	AA971249 op73c01.s
24	232.6	41.9	468	14	H46374 yO12d07.r1
25	230.2	41.5	443	14	H46211 yO14h09.r1
26	223.2	40.2	330	14	N71141 za80q11.s1
27	215.6	38.8	673	13	BM251737 BOTL01000
28	200.8	36.2	775	12	BG867742 602786852
29	194	35.0	316	14	H49675 yO23d06.r1
30	186.6	33.6	755	13	BI655045 603282719
31	183.8	33.1	393	14	H41851 yO07f03.r1
32	177.4	32.0	397	14	H46378 yO12f05.r1
33	155.2	28.0	639	10	BB636341 BB636341
34	151.2	27.2	246	14	H19739 yn60h04.r1
35	150.2	27.1	418	14	H46662 yO12e12.r1
36	147.4	26.6	246	14	H46424 yO12e12.s1
37	136.4	24.6	517	14	BM692368 UI-E-CL1-
38	125.8	22.7	368	10	BB872434 BB872434
39	107	19.3	651	13	BM009354 603629813
40	106	19.1	252	14	BM695862 UI-E-CL1-
41	99.4	17.9	201	14	H22502 yn63g06.r1
42	92	16.6	681	10	BE563566 601334867
43	87.2	15.7	556	10	AV664984 AV664984
44	84.2	15.2	151	9	AA954505 on81d01.s
45	82	14.8	435	10	AV664983 AV664983

ALIGNMENTS

RESULT 1
LOCUS AW268610 632 bp mRNA linear EST 03-JAN-2000
DEFINITION xv41b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens CDNA clone
IMAGE:2815679 3' similar to SW:WSL1_HUMAN Q93038 WSL-1 PROTEIN
PRECUSOR ; mRNA sequence.

ACCESSION AW268610
VERSION AW268610
KEYWORDS AW268610.1 GI:6655640
SOURCE EST.
ORGANISM human.
Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE 1 (bases 1 to 632)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
CONTACT: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov

This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand

Seq primer: -40UP from Gibco
High quality sequence stop: 455.
Location/Qualifiers.
1..632

FEATURES
source /organism="Homo sapiens"

Query Match

Best Local Similarity

Matches

550;

Conservative

0;

Mismatches

5;

Indels

0;

Gaps

0;

98.7%;

Score 547.6;

DB 10;

Length 632;

99.1%;

Pred. No. 2.1e-135;

db_xref="taxon:9606"

/clone="IMAGE:2815679"

/lab_host="DH10B"

/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT

102 a

194 c

192 g

143 t

1 others

ORIGIN

1 CTGGGGCCCCCGCCAGGGCGGCACCTGCTAGCCCCAGGTGTGACTGTGCCGGTACTTC

60

12 CTGGGGCCCCCGCCAGGGCGGCACCTGCTAGCCCCAGGTGTGACTGTGCCGGTACTTC

71

61 CACAAGAGATGTGCTGTTTGTGTGCAGAGGCTGCCAGCGGGGCACTACTGAAGGCC

120

72 CACAAGAGATGTGCTGTTTGTGTGCAGAGGCTGCCAGCGGGGCACTACTGAAGGCC

131

121 CCTTGACGAGCGCTGCGGCACTCCACCTGCTGTGTGCCCAAGACACTTCTTG

180

132 CCTTGACGAGCGCTGCGGCACTCCACCTGCTGTGTGCCCAAGACACTTCTTG

191

181 GCCTGGAGAACCATATATTTCTGAATGTGCCGCTGCCAGGCTGTGATGAGCAGGCC

240

192 GCCTGGAGAACCATATATTTCTGAATGTGCCGCTGCCAGGCTGTGATGAGCAGGCC

251

241 TCCAGGTGGCGCTGGAGAAGTGTTCAGACAGTGGCCGACACCCGCTGTGCTGAAGCCA

300

252 TCCAGGTGGCGCTGGAGAAGTGTTCAGACAGTGGCCGACACCCGCTGTGCTGAAGCCA

311

301 GGCTGTTGTGAGTGCAGGTCAAGCAATGTTCAGAGTTACACCTTCTACTGCCAA

360

312 GGCTGTTGTGAGTGCAGGTCAAGCAATGTTCAGAGTTACACCTTCTACTGCCAA

371

361 CCATGCCCTAGACTGCGGGGCCCTGCACCGCCACACAGGCTACTCTGTCCCGCAGAGAT

420

372 CCATGCCCTAGACTGCGGGGCCCTGCACCGCCACACAGGCTACTCTGTCCCGCAGAGAT

431

421 ACTGACTGTGGAGCTGCTGCTGCTTCTATGAACATGGCGATGGCTGCTCCTGC

480

432 ACTGACTGTGGAGCTGCTGCTGCTTCTATGAACATGGCGATGGCTGCTCCTGC

491

481 CCCACGAGCACCTGGGGAGCTGTTCAGAGCGCTGTGCGCTGTGTGGCTGAGGCGC

540

492 CCCACGAGCACCTGGGGAGCTGTTCAGAGCGCTGTGCGCTGTGTGGCTGAGGCGC

551

541 ATGTTCTGGGTCAG

555

552 ATGTTCTGGTCCAG

566

LOCUS

AI807913

698 bp

mRNA

linear

EST 19-DEC-1999

DEFINITION

wf52c03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone

IMAGE:2359204 3' similar to SW:WSL1_HUMAN Q93038 WSL-1 PROTEIN

PRECURSOR ;

mRNA sequence.

ACCESSION

AI807913

VERSION

AI807913.1

GI:5394479

KEYWORDS

EST.

Source

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

human.

Homo sapiens

1 (bases 1 to 698)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgabs-r@mail.nih.gov

This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 1568 Std Error: 0.00

Seq primer: -40UP from G1bco

High quality sequence stop: 459.

FEATURES

source

1..698

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2359204"

/lab_host="DH10B"

/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT

111 a

218 c

214 g

155 t

ORIGIN

1 CTGGGGCCCCCGCCAGGGCGGCACCTGCTAGCCCCAGGTGTGACTGTGCCGGTACTTC

60

21 CTGGGGCCCCCGCCAGGGCGGCACCTGCTAGCCCCAGGTGTGACTGTGCCGGTACTTC

80

61 CACAAGAGATGTGCTGTTTGTGTGCAGAGGCTGCCAGCGGGGCACTACTGAAGGCC

120

81 CACAAGAGATGTGCTGTTTGTGTGCAGAGGCTGCCAGCGGGGCACTACTGAAGGCC

140

121 CCTTGACGAGCGCTGCGGCACTCCACCTGCTGTGTGCCCAAGACACCTTCTTG

180

141 CCTTGACGAGCGCTGCGGCACTCCACCTGCTGTGTGCCCAAGACACCTTCTTG

200

181 GCCTGGAGAACCATATATTTCTGAATGTGCCGCTGCCAGGCTGTGATGAGCAGGCC

240

201 GCCTGGAGAACCATATATTTCTGAATGTGCCGCTGCCAGGCTGTGATGAGCAGGCC

260

241 TCCAGGTGGCGCTGGAGAAGTGTTCAGACAGTGGCCGACACCCGCTGTGCTGAAGCCA

300

261 TCCAGGTGGCGCTGGAGAAGTGTTCAGACAGTGGCCGACACCCGCTGTGCTGAAGCCA

320

301 GGCTGTTGTGAGTGCAGGTCAAGCAATGTTCAGAGTTACACCTTCTACTGCCAA

360

321 GGCTGTTGTGAGTGCAGGTCAAGCAATGTTCAGAGTTACACCTTCTACTGCCAA

380

361 CCATGCCCTAGACTGCGGGGCCCTGCACCGCCACACAGGCTACTCTGTCCCGCAGAGAT

420

381 CCATGCCCTAGACTGCGGGGCCCTGCACCGCCACACAGGCTACTCTGTCCCGCAGAGAT

440

421 ACTGACTGTGGAGCTGCTGCTGCTTCTATGAACATGGCGATGGCTGCTCCTGC

480

441 ACTGACTGTGGAGCTGCTGCTGCTTCTATGAACATGGCGATGGCTGCTCCTGC

500

LOCUS

AI807913

698 bp

mRNA

linear

EST 19-DEC-1999

DEFINITION

wf52c03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone

IMAGE:2359204 3' similar to SW:WSL1_HUMAN Q93038 WSL-1 PROTEIN

PRECURSOR ;

mRNA sequence.

ACCESSION

AI807913

VERSION

AI807913.1

GI:5394479

KEYWORDS

EST.

```
OY 481 CCCACGAGACCCCTGGGAGACTGTCCAGAGCCGCTGTGCCGTGTGTGGCTGAGGCAG 540
Db 501 CTCACGAGCACCCCTGGAGACTGTCCAGAGCGCTGTGCCGTGTGTGGCTGAGGCAG 560
OY 541 ATGTTCTGGGTCCAG 555
Db 561 ATGTTCTGGGTCCAG 575

RESULT 3
BI909448
LOCUS 767 bp mRNA linear EST 16-OCT-2001
DEFINITION 603065172F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5214568 5',
mRNA sequence.
ACCESSION BI909448
VERSION BI909448.1 GI:16172666
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 767)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1538 row: 0 column: 17
High quality sequence stop: 754.
Location/Qualifiers
1. 767
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5214568"
/clone_lib="NIH_MGC_118"
/tissue_type="Leukocyte"
/lab_host="DH10B"
/note="Vector: pCMV-Sport6; site_1: NotI; site_2: EcoRV
(destroyed); RNA source leukocytes from anonymous pool of
non-activated adult donors. Library is oligo-dT primed
and directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
1.2-3.3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 027. Note:
this is a NIH_MGC Library."

BASE COUNT 122 a 243 c 241 g 161 t
ORIGIN
```

```
Query Match 96.5%; Score 535.6; DB 13; Length 767;
Best Local Similarity 99.1%; Pred. No. 3.8e-132;
Matches 549; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
```

```
OY 3 GGGGGCCCCGGCCAGCGGCGCACTCGTAGCCCCAGGTGTGACTGTGCCGTAATTCCA 62
Db 96 GGGGGCCCCGGTGCAGGCGGCGCACTGTAGCCCCAGGTGTGACTGTGCCGTAATTCCA 155
OY 63 CAAGAAGATTGCTGTTTGTGTGACAGAGCGTCCAGC-GGGGCACTACTGAAGCCC 121
Db 156 CAAGAAGATTGCTGTTTGTGTGACAGAGCGTCCAGCCTGGGCACTACTGAAGCCCC 215
OY 122 CTGACAGGAGCCCTGCGGCACTCCACCTGCTGTGTGTCCCAAGACACCTTCTTG 181
Db 216 CTGACAGGAGCCCTGCGGCACTCCACCTGCTGTGTGTCCCAAGACACCTTCTTG 275
```

```
OY 182 CTTGGAGAACCACTAATTTCTGATGTGCCCCGCTGCCAGGCCCTGTGATGACAGCCCT 241
Db 276 CTTGGAGAACCACTAATTTCTGATGTGCCCCGCTGCCAGGCCCTGTGATGACAGCCCT 335
OY 242 CCCAGGTGGCGCTGGAGACTGTTCAGCAGTGGCCGACACCCGCTGTGGCTGTAAACCAG 301
Db 336 CCCAGGTGGCGCTGGAGACTGTTCAGCAGTGGCCGACACCCGCTGTGGCTGTAAACCAG 395
OY 302 GCTGTTTGTGAGTGCAGGTCCAGCCCAATGTGTACAGATTACCCCTTACTGCCAAC 361
Db 396 GCTGTTTGTGAGTGCAGGTCCAGCCCAATGTGTACAGATTACCCCTTACTGCCAAC 455
OY 362 CATGCCCTAGACTGCGGGCCCTGCACCCGCCACACAGCGCTACTCTGTTCGCCGAGATA 421
Db 456 CATGCCCTAGACTGCGGGCCCTGCACCCGCCACACAGCGCTACTCTGTTCGCCGAGATA 515
OY 422 CTGACTGTGGACCTGCTTGCCTGGCTTCTATGAACATGGCGATGGCTGCTGCTGCC 481
Db 516 CTGACTGTGGACCTGCTTGCCTGGCTTCTATGAACATGGCGATGGCTGCTGCTGCC 575
OY 482 CCACGAGCACCCCTGGGAGCTGTCCAGAGCGCTGTGCCGCTGTGTGGCTGAGGCAGA 541
Db 576 CCACGAGCACCCCTGGGAGCTGTCCAGAGCGCTGTGCCGCTGTGTGGCTGAGGCAGA 635
OY 542 TGTCTGGGTCCAG 555
Db 636 TGTCTGGGTCCAG 649
```

```
RESULT 4
AI424936
LOCUS 688 bp mRNA linear EST 30-MAR-1999
DEFINITION tg19b08.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2109207 3',
similar to TR:00276 000276 LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH
2.; mRNA sequence.
ACCESSION AI424936
VERSION AI424936.1 GI:4270854
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 688)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
M.D., Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bdrp/image/image.html
Insert Length: 2028 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 445.
Location/Qualifiers
1. 688
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2109207"
/clone_lib="NCI_CGAP_CLL1"
/tissue_type="B-cell, chronic lymphocytic leukemia"
/lab_host="DH10B"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; site_1: Not I; site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGCCGCACTGCTTGTGTGTGTGTGTGTGTGTGTGT
T 3']; double-stranded cDNA was ligated to Eco RI
```

adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT 113 a 208 c 229 g 138 t
ORIGIN

Query Match 96.0%; Score 533; DB 9; Length 688;
Best Local Similarity 98.2%; Pred. No. 1.7e-131;
Matches 539; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 CTGGGGCCCCGGCCAGGCGGCACTGTCAGCCAGGTGTGACTGTGCCGGTACTTC 60
|||||
Db 50 CTGGGGCCCCGGGGGGGGGGGGCGGCGGCACTGTCAGCCAGGTGTGACTGTGCCGGTACTTC 109
QY 61 CACAAGAGATTGCTGTCTTTTGTGAGAGAGGCTGCCAGCGGGGCACTACCTGAAGGCC 120
|||||
Db 110 CACAAGAGATTGCTGTCTTTTGTGAGAGAGGCTGCCAGCGGGGCACTACCTGAAGGCC 169
QY 121 CCTTGACCGAGCCCTGCGGCACTCCACCTGCTGTGTGTGCCCAAGACACCTTCTTG 180
|||||
Db 170 CCTTGACCGAGCCCTGCGGCACTCCACCTGCTGTGTGTGCCCAAGACACCTTCTTG 229
QY 181 GCCTGGAGAACCACTAATTTCTGAATGTGCCCCGCTGCCAGGCTGTGATGAGCAGGCC 240
|||||
Db 230 GCCTGGAGAACCACTAATTTCTGAATGTGCCCCGCTGCCAGGCTGTGATGAGCAGGCC 289
QY 241 TCCAGGTGCGCTGGAGAACTGTTTCAGAGTGGCCGACACCCGCTGTGGCTGTAAAGCCA 300
|||||
Db 290 TCCAGGTGCGCTGGAGAACTGTTTCAGAGTGGCCGACACCCGCTGTGGCTGTAAAGCCA 349
QY 301 GGCTGTTTGTGAGTCCAGGTTCAGCAATGTGTACAGAGTTACCTTCTACTGCCAA 360
|||||
Db 350 GGCTGTTTGTGAGTCCAGGTTCAGCAATGTGTACAGAGTTACCTTCTACTGCCAA 409
QY 361 CCATGCTAGACTGCGGGCCCTGCACCGCCACACAGGCTACTCTGTTCGCCGAGAGAT 420
|||||
Db 410 CCATGCTAGACTGCGGGCCCTGCACCGCCACACAGGCTACTCTGTTCGCCGAGAGAT 469
QY 421 ACTGACTGTGGAGCTGCTGCTGCTTCTATGAACATGGCGATGGCTGCTGCTGC 480
|||||
Db 470 ACTGACTGTGGAGCTGCTGCTGCTTCTATGAACATGGCGATGGCTGCTGCTGC 529
QY 481 CCCACGAGCACCCCTGGGGAGCTGTCCAGAGCGCTGTGCGCTGTGCGCTGAGAGCAG 540
|||||
Db 530 CCCACGAGCACCCCTGGGGAGCTGTCCAGAGCGCTGTGCGCTGTGCGCTGAGAGCAG 589
QY 541 ATGTTCTGG 549
|
Db 590 AGTAAGTGG 598

RESULT 5
A1140043 562 bp mRNA linear EST 13-APR-1999
LOCUS A1140043
DEFINITION qa87a04.x1 Soares_fetal_heart_NDHL19W Homo sapiens cDNA clone
IMAGE:1693710 3' similar to SW:WSL1_HUMAN Q93038 WSL-1 PROTEIN
PRECURSOR ; mRNA sequence.
ACCESSION A1140043
VERSION A1140043.1 GI:3647500
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 562)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
This clone is available royalty-free through LNL ; contact the

IMAGE Consortium (info@image.jnl.gov) for further information.
Insert Length: 1640 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 494.
location/Qualifiers

FEATURES
source

1. 562
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1693710"
/clone_lib="Soares_fetal_heart_NbHL19W"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: heart; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTACCAATCTGAAGTGGAGCGGCGCATCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by
M.Fatima Bonaldo. This library was constructed from the
same fetus as the fetal lung library, Soares fetal lung
NbHL19W."

BASE COUNT 88 a 182 c 180 g 111 t 1 others
ORIGIN

Query Match 92.3%; Score 512; DB 9; Length 562;
Best Local Similarity 99.8%; Pred. No. 6.2e-126;
Matches 512; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGGGGCCCCGGCCAGGCGGCACTGTCAGCCAGGTGTGACTGTGCCGGTACTTC 60
|||||
Db 50 CTGGGGCCCCGGGGGGGGGGGGCGGCGGCACTGTCAGCCAGGTGTGACTGTGCCGGTACTTC 109
QY 61 CACAAGAGATTGCTGTCTTTTGTGAGAGGCTGCCAGCGGGGCACTACTCTGAAGGCC 120
|||||
Db 110 CACAAGAGATTGCTGTCTTTTGTGAGAGGCTGCCAGCGGGGCACTACTCTGAAGGCC 169
QY 121 CCTTGACGAGCCCTGCGGCACTCCACCTGCTGTGTGTGCCCAAGACACCTTCTTG 180
|||||
Db 170 CCTTGACGAGCCCTGCGGCACTCCACCTGCTGTGTGTGCCCAAGACACCTTCTTG 229
QY 181 GCCTGGAGAACCACTAATTTCTGAATGTGCCCCGCTGCCAGGCTGTGATGAGCAGGCC 240
|||||
Db 230 GCCTGGAGAACCACTAATTTCTGAATGTGCCCCGCTGCCAGGCTGTGATGAGCAGGCC 289
QY 241 TCCAGGTGCGCTGGAGAACTGTTTCAGAGTGGCCGACACCCGCTGTGCTGTAAAGCCA 300
|||||
Db 290 TCCAGGTGCGCTGGAGAACTGTTTCAGAGTGGCCGACACCCGCTGTGCTGTAAAGCCA 349
QY 301 GGCTGTTTGTGAGTGCAGGTCAGCCAAATGTGTACAGCAGTTCAACCTTCTACTGCCAA 360
|||||
Db 350 GGCTGTTTGTGAGTGCAGGTCAGCCAAATGTGTACAGCAGTTCAACCTTCTACTGCCAA 409
QY 361 CCATGCTAGACTGCGGGCCCTGCACCGCCACACAGGCTACTGTTCGGCAGAGAT 420
|||||
Db 410 CCATGCTAGACTGCGGGCCCTGCACCGCCACACAGGCTACTGTTCGGCAGAGAT 469
QY 421 ACTGACTGTGGAGCTGCTGCTGCTTCTATGAACATGGCGATGGCTGCTGCTGC 480
|||||
Db 470 ACTGACTGTGGAGCTGCTGCTGCTTCTATGAACATGGCGATGGCTGCTGCTGC 529
QY 481 CCCACGAGCACCCCTGGGGAGCTGTCCAGAGGCC 513
|||||
Db 530 CCCACGAGCACCCCTGGGGAGCTGTCCAGAGGCC 562

RESULT 6
BM783972 552 bp mRNA linear EST 05-MAR-2002
LOCUS BM783972
DEFINITION K-EST0062019 S6SNU620 Homo sapiens cDNA clone S6SNU620-31-H06 5',

OY	61	CACAAGAAGATTGGTCTGTGTTTGTTGTCAGAGGCGTGCACGCGGGGCACTACCCTGAAGGCC	120
Db	110	CACAAGAAGATTGGTCTGTGTTTGTTGTCAGAGGCGTGCACGCGGGGCACTACCCTGAAGGCC	169
OY	121	CCTTGACGAGGCCCTGCGGCACTCCACCCTGCTGTGTGTCCCAAGACACCTTCTTG	180
Db	170	CCTTGACGAGGCCCTGCGGCACTCCACCCTGCTGTGTGTCCCAAGACACCTTCTTG	229
OY	181	GCCGTGGAGAACCAACCATTAATCTGAATGTGCCCGCTGCCAGGCCCTGTGATGAGCAGGCC	240
Db	230	GCCTGGAGAAACCAACCATTAATCTGAATGTGCCCGCTGCCAGGCCCTGTGATGAGCAGGCC	289
OY	241	TCCCAGGTGGCGCTGAGAACTGTTCAAGCAGTGGCCGACACCCGCTGTGCTGTAAGCCA	300
Db	290	TCCCAGGTGGCGCTGAGAACTGTTCAAGCAGTGGCCGACACCCGCTGTGCTGTAAGCCA	349
OY	301	GGCTGCTTTGTGGAGTGCAGGTCAGCCATGTGTCAAGCAGTTCAACCTTCTACTGCCAA	360
Db	350	GGCTGCTTTGTGGAGTGCAGGTCAGCCATGTGTCAAGCAGTTCAACCTTCTACTGCCAA	409
OY	361	CCATGCCCTAGACTGCGGGGCCCTGCACCGCCACACACGGCTACTCTGTTCCCGCAGAGAT	420
Db	410	CCATGCCCTAGACTGCGGGGCCCTGCACCGCCACACACGGCTACTCTGTTCCCGCAGAGAT	469
OY	421	ACTGACTGTGGGACCTGCCTGCCTGGCTTCTATGAACATGGCGATGGCTGCGTGTCTGC	480
Db	470	ACTGACTGTGGGACCTGCCTGCCTGGCTTCTATGAACATGGCGATGGCTGCGTGTCTGC	529
OY	481	CCCACGAGCACCCCTGG	496
Db	530	CCCACGTAATTCCTAG	545

```

RESULT 8
BM756372
LOCUS
DEFINITION BM756372 514 bp mRNA linear EST 04-MAR-2002
K-EST0034666 S6SNU620 Homo sapiens CDNA clone S6SNU620-27-G03 5',
mRNA sequence.
ACCESSION BM756372
VERSION
KEYWORDS
SOURCE EST.
ORGANISM human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 514)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@email.kribb.re.kr
Plate: 27 row: G column: 03
High quality sequence stop: 514.
FEATURES
location/Qualifiers
1..514
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="S6SNU620-27-G03"
/clone_1lb="S6SNU620"
/sex="F"
/tissue_type="Ascites"
/cell_type="Scattering floating"
/cell_line="SNU-620"
/lab_host="Top10F'"
/note="Organ: Stomach; Vector: pcNS; Site_1: EcorI;

```

Site_2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

Query Match	87.63;	Score 486;	DB 14;	Length 514;
Best Local Similarity	100.0%;	Pred. No. 5.1e-119;		
Matches 486;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY 1	CTGGGGGGCCCCGGGGCCAGGGGGGCACTCGTAGCCCCAGGTGTGACTGTGCGGGTGAATTC	60		
Db 23	CTGGGGGGCCCCGGGGCCAGGGGGGCACTCGTAGCCCCAGGTGTGACTGTGCGGGTGAATTC	82		
QY 61	CACAAGAAGATTGGTCTGTTTTTGTGACAGAGGCTGCCAGCGGGGCACTACCTGAAGCC	120		
Db 83	CACAAGAAGATTGGTCTGTTTTTGTGACAGAGGCTGCCAGCGGGGCACTACCTGAAGCC	142		
QY 121	CCTTGCACGGAGCCCTGCGGCACTCCACCCTGCTTGTGTGTCCCAAGACACACCTTCTG	180		
Db 143	CCTTGCACGGAGCCCTGCGGCACTCCACCCTGCTTGTGTGTCCCAAGACACACCTTCTG	202		
QY 181	GCTTGGGAGAACCAACCATTAATTCTGAATGTGCCCGCTGCCAGGCGCTGTGATGAGCAGGCC	240		
Db 203	GCTTGGGAGAACCAACCATTAATTCTGAATGTGCCCGCTGCCAGGCGCTGTGATGAGCAGGCC	262		
QY 241	TCCAGGTTGGCGCTGGAGAACTGTTACAGAGTGGCCGACACCCGCTGTGGCTGTAAGCCA	300		
Db 263	TCCAGGTTGGCGCTGGAGAACTGTTACAGAGTGGCCGACACCCGCTGTGGCTGTAAGCCA	322		
QY 301	GGCTGGTTTGTGGAGTGCAGAGTCAGCCAATGTGTACAGAGTTACACCTTCTACTGCCAA	360		
Db 323	GGCTGGTTTGTGGAGTGCAGAGTCAGCCAATGTGTACAGAGTTACACCTTCTACTGCCAA	382		
QY 361	CCATGCTTAGACTGCGGGGCTTGACCGCCACACACAGGCTACTCTGTTCGCCGAGAGAT	420		
Db 383	CCATGCTTAGACTGCGGGGCTTGACCGCCACACACAGGCTACTCTGTTCGCCGAGAGAT	442		
QY 421	ACTGACTGTGGACCTGCCCTGCTGGCTTCTATGAACAATGGCGATGGCTGCGTGTCTGC	480		
Db 443	ACTGACTGTGGACCTGCCCTGCTGGCTTCTATGAACAATGGCGATGGCTGCGTGTCTGC	502		
QY 481	CCGACG 486			
Db 503	CCGACG 508			

RESULT	9
BM783979	
LOCUS	514 bp
DEFINITION	mRNA
K-EST0062030 S6SNU620 Homo sapiens CDNA clone S6SNU620-32-A05 5',	linear EST 05-MAR-2002
BM783979	
ACCESSION	
VERSION	
KEYWORDS	
SOURCE	human.
ORGANISM	Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	
AUTHORS	Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
1 (bases 1 to 514)	

TITLE Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
JOURNAL 21C Frontler Korean EST Project 2001
COMMENT Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 32 row: A column: 05
High quality sequence stop: 514.
Location/Qualifiers

FEATURES
source 1. 514
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="S6SNU620-32-A05"
/clone_lib="S6SNU620"
/sex="F"
/tissue_type="Asclites"
/cell_type="Scattering floating"
/cell_line="SNU-620"
/lab_host="Top10F,"
/note="Organ: Stomach; Vector: pcNS; Site_1: EcoRI; Site_2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

BASE COUNT 86 a 166 c 153 g 109 t
ORIGIN

Query Match 87.6%; Score 486; DB 14; Length 514;
Best Local Similarity 100.0%; Pred. No. 5.1e-119;
Matches 486; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTGGGGGGCCCCGGCCGACACTCGTAGCCCCCAGGTGTGACTGTGCCGGTACTTC 60
Db 23 CTGGGGGGCCCCGGCCGACACTCGTAGCCCCCAGGTGTGACTGTGCCGGTACTTC 82
OY 61 CACAAGAGATTGGTCTGTTTGTTCAGAGGGCTGCCAGCGGGGCACTACCTGAAGGCC 120
Db 83 CACAAGAGATTGGTCTGTTTGTTCAGAGGGCTGCCAGCGGGGCACTACCTGAAGGCC 142
OY 121 CCTTGCACGAGCCCTCGCGCACTCCACCTGCTGTGTGTCCCAAGACACCTCTTG 180
Db 143 CCTTGCACGAGCCCTCGCGCACTCCACCTGCTGTGTGTCCCAAGACACCTCTTG 202
OY 181 GCCTGGGAGAACCACTAATCTGATGTGCCCGTCCAGGCTGTGATGAGCAGGCC 240
Db 203 GCCTGGGAGAACCACTAATCTGATGTGCCCGTCCAGGCTGTGATGAGCAGGCC 262
OY 241 TCCCAAGTGGCGCTGAGACTGTTCAGCAGTGGCCGACACCCGCTGTGGCTGAAGCCA 300
Db 263 TCCCAAGTGGCGCTGAGACTGTTCAGCAGTGGCCGACACCCGCTGTGGCTGAAGCCA 322
OY 301 GGCTGGTTTGTGAGTCCAGAGTCAGCCAATGTGTCAAGCAGTTACCCCTTCTACTGCCAA 360
Db 323 GGCTGGTTTGTGAGTCCAGAGTCAGCCAATGTGTCAAGCAGTTACCCCTTCTACTGCCAA 382
OY 361 CCATGCTAGACTGGGGGGCTGCACCGCCACACAGCGCTACTCTGTTCCCGCAGAGAT 420
|||||

Db 383 CCATGCTAGACTGGGGGGCTGCACCGCCACACAGCGCTACTCTGTCCCGCAGAGAT 442
OY 421 ACTGACTGTGGACCTGCGCTGCTGCTTATGACATGGCGATGGCTGCTGCTGC 480
Db 443 ACTGACTGTGGACCTGCGCTGCTGCTTATGACATGGCGATGGCTGCTGCTGC 502
OY 481 CCCACG 486
Db 503 CCCACG 508
|||||

RESULT 10
LOCUS BM744307 565 bp mRNA linear EST 01-MAR-2002
DEFINITION K-EST0017828 S6SNU620 Homo sapiens cDNA clone S6SNU620-17-C06 5', mRNA sequence.
ACCESSION BM744307
VERSION BM744307.1 GI:19065636
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 565)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
TITLE 21C Frontler Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 17 row: C column: 06
High quality sequence stop: 565.
Location/Qualifiers

FEATURES
source 1. 565
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="S6SNU620-17-C06"
/clone_lib="S6SNU620"
/sex="F"
/tissue_type="Asclites"
/cell_type="Scattering floating"
/cell_line="SNU-620"
/lab_host="Top10F,"
/note="Organ: Stomach; Vector: pcNS; Site_1: EcoRI; Site_2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

BASE COUNT 95 a 175 c 178 g 117 t
ORIGIN

Query Match 87.4%; Score 484.8; DB 14; Length 565;
Best Local Similarity 98.6%; Pred. No. 1.1e-118;
Matches 489; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CTGGGGGGGGGGCCGACACTCGTAGCCCCAGGTGTGACTGTGCCGGTACTTC 60
|||||


```

|||||
Db 23 CTGGGGCCCGGGCCAGTGGCGACTGTAGCCCCAGGTGTGACTGTGCCGGTACTTC 82
QY 61 CACAAGAGATTGGTCTGTTTGTTCAGAGGCTGCCAGCGGGCACTACTGAAGGCC 120
Db 83 CACAAGAGATTGGTCTGTTTGTTCAGAGGCTGCCAGCGGGCACTACTGAAGGCC 142
QY 121 CCTTGCAGGAGCCCTGCGCAACTGCCCTGTGTGTGCCCAAGACACCTTCCTG 180
Db 143 CCTTGCAGGAGCCCTGCGCAACTGCCCTGTGTGTGCCCAAGACACCTTCCTG 202
QY 181 GCCTGGAGAACCAACCATATATTCGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCC 240
Db 203 GCCTGGAGAACCAACCATATATTCGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCC 262
QY 241 TCCAGAGTGGCGCTGGAGAACTGTTCAGAGTGGCCGACACCCGCTGTGGCTGTAAGCCA 300
Db 263 TCCAGAGTGGCGCTGGAGAACTGTTCAGAGTGGCCGACACCCGCTGTGGCTGTAAGCCA 322
QY 301 GGCTGTTTGTGAGAGTCCAGAGTCCAGCAATGTGTACAGAGTTCACCCCTTCTACTGCCAA 360
Db 323 GGCTGTTTGTGAGAGTCCAGAGTCCAGCAATGTGTACAGAGTTCACCCCTTCTACTGCCAA 382
QY 361 CCATGCTAGACTGGCGGGCCCTGCACCCGACACACAGGCTACTCTGTTCGCCGAGAGAT 420
Db 383 CCATGCTAGACTGGCGGGCCCTGCACCCGACACACAGGCTACTCTGTTCGCCGAGAGAT 442
QY 421 ACTGACTGTGGAGCTGCCCTGCTTCTATGAACATGGCGATGGCTGCTGCTGC 480
Db 443 ACTGACTGTGGAGCTGCCCTGCTTCTATGAACATGGCGATGGCTGCTGCTGC 502
QY 481 CCCACGAGCACCTGG 496
Db 503 CCCACGTAATCTTAG 518

RESULT 11
LOCUS 508 bp mRNA linear EST 29-OCT-1998
AI203624
DEFINITION ge75f02.x1 Soares_fetal_lung_NbHL19w Homo sapiens cDNA clone
IMAGE:1744827 3' similar to SW:WSL1_HUMAN Q93038 WSL-1 PROTEIN
PRECUSOR ; mRNA sequence.
ACCESSION AI203624 GI:3756230
VERSION AI203624
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
REFERENCE 1 (bases 1 to 508)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TUMOR National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Insert Length: 1699 Std Error: 0.00
Seq primer: -40UP from GIBCO
High quality sequence stop: 442.
location/Qualifiers
1. 508
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1744827"
/clone_lib="Soares_fetal_lung_NbHL19w"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: lung; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer
[5'-TGTTACCAATCTGAAGTGGAGCGCGCCCAATTTTCTTTT-3'],

```

```

double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M.Fatima Bonaldo. This library was constructed
from the same fetus as the fetal heart library, Soares
fetal heart NbHL19w."
BASE COUNT 82 a 161 c 159 g 106 t
ORIGIN
Query Match 85.9%; Score 477; DB 9; Length 508;
Best Local Similarity 100.0%; Pred. No. 1.3e-116;
Matches 477; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGGGGCCCGGGCCAGGCGGCACTGTAGCCCCAGGTGTGACTGTGCCGGTACTTC 60
Db 32 CTGGGGCCCGGGCCAGGCGGCACTGTAGCCCCAGGTGTGACTGTGCCGGTACTTC 91
QY 61 CACAAGAGATTGGTCTGTTTGTTCAGAGGCTGCCAGCGGGCACTACTGAAGGCC 120
Db 92 CACAAGAGATTGGTCTGTTTGTTCAGAGGCTGCCAGCGGGCACTACTGAAGGCC 151
QY 121 CCTTGCAGGAGCCCTGCGCAACTCCACCTGCTGTGTGCCCAAGACACCTTCCTG 180
Db 152 CCTTGCAGGAGCCCTGCGCAACTCCACCTGCTGTGTGCCCAAGACACCTTCCTG 211
QY 181 GCCTGGAGAACCAACCATATATTCGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCC 240
Db 212 GCCTGGAGAACCAACCATATATTCGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCC 271
QY 241 TCCAGAGTGGCGCTGGAGAACTGTTCAGAGTGGCCGACACCCGCTGTGGCTGTAAGCCA 300
Db 272 TCCAGAGTGGCGCTGGAGAACTGTTCAGAGTGGCCGACACCCGCTGTGGCTGTAAGCCA 331
QY 301 GGCTGTTTGTGAGAGTCCAGAGTCCAGCAATGTGTACAGAGTTCACCCCTTCTACTGCCAA 360
Db 332 GGCTGTTTGTGAGAGTCCAGAGTCCAGCAATGTGTACAGAGTTCACCCCTTCTACTGCCAA 391
QY 361 CCATGCTAGACTGGCGGGCCCTGCACCCGACACACAGGCTACTCTGTTCGCCGAGAGAT 420
Db 392 CCATGCTAGACTGGCGGGCCCTGCACCCGACACACAGGCTACTCTGTTCGCCGAGAGAT 451
QY 421 ACTGACTGTGGAGCTGCCCTGCTTCTATGAACATGGCGATGGCTGCTGCTGC 477
Db 452 ACTGACTGTGGAGCTGCCCTGCTTCTATGAACATGGCGATGGCTGCTGCTGC 508

RESULT 12
LOCUS 492 bp mRNA linear EST 01-MAR-2002
BM741016
DEFINITION K-EST0013376 S6SNU620 Homo sapiens cDNA clone S6SNU620-2-C03 5',
mRNA sequence.
ACCESSION BM741016 GI:19062345
VERSION BM741016
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
REFERENCE 1 (bases 1 to 492)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: Yongsung@email.kribb.re.kr

```


OY	1	CTGGGGGCCCCCGCCAGGGGCGGCACACTCGTAGCCCCAGGTGTGACTGTGCCGGTGACTTC	60
Db	23	CTGGGGGCCCCCGCCAGGGGCGGCACACTCGTAGCCCCAGGTGTGACTGTGCCGGTGACTTC	82
OY	61	CACAAGAAGATTGGTCTGTTTTTTGTTCAGAGGCTGCCAGCGGGGCACTACCTGAAGGCC	120
Db	83	CACAAGAAGATTGGTCTGTTTTTTGTTCAGAGGCTGCCAGCGGGGCACTACCTGAAGGCC	142
OY	121	CCTTGACGAGGCCCTGGCGCAACTCCACCCTGCTGTGTGTCCCAAGACACCTTCTTG	180
Db	143	CCTTGACGAGGCCCTGGCGCAACTCCACCCTGCTGTGTGTCCCAAGACACCTTCTTG	202
OY	181	GCGTGGGAGAACCACCAATAATCTGAAATGTGCCCGCTGCCAGGCGCTGTGATGAGCAGGCC	240
Db	203	GCGTGGGAGAACCACCAATAATCTGAAATGTGCCCGCTGCCAGGCGCTGTGATGAGCAGGCC	262
OY	241	TCCCAGGTGGCGCTGGAGAAGCTGTTTCAGCAGTGGCCGACACCCGCTGTGGCTGTAAAGCA	300
Db	263	TCCCAGGTGGCGCTGGAGAAGCTGTTTCAGCAGTGGCCGACACCCGCTGTGGCTGTAAAGCA	322
OY	301	GGCTGGTTTGTGAGTGCACAGGTTCAGCCAATGTGTACAGCAGTTACCCCTTCTACTGCCAA	360
Db	323	GGCTGGTTTGTGAGTGCACAGGTTCAGCCAATGTGTACAGCAGTTACCCCTTCTACTGCCAA	382
OY	361	CCATGCCCTAGACTGCGGGGCCCTGCACCGCCACACACAGGCTACTCTGTTCGCCGACAGAT	420
Db	383	CCATGCCCTAGACTGCGGGGCCCTGCACCGCCACACACAGGCTACTCTGTTCGCCGACAGAT	442
OY	421	ACTGACTGTGGGACCTGCGCTGCGCTGCTTCTATGAACATGGCGATG	466
Db	443	ACTGACTGTGGGACCTGCGCTGCGCTTCTATGAACATGGCGATG	488
RESULT	14		
LOCUS	BQ068309	1010 bp	mRNA linear EST 02-APR-2002
DEFINITION	AGENCOURT_6794093 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5770562		
ACCESSION	BQ068309		
VERSION	BQ068309.1	GI:19897355	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
TITLE	1 (bases 1 to 1010)		
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/.		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)		
	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgabbs-remail.nih.gov		
	Tissue Procurement: Life Technologies, Inc.		
	cDNA Library Preparation: Life Technologies, Inc.		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)		
	DNA Sequencing by: Agencourt Bioscience Corporation		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LLNL at:		
	http://image.llnl.gov		
	Plate: LRAM12833 row: n column: 03		
	High quality sequence stop: 689.		
FEATURES	location/Qualifiers		
Source	1..1010		

cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH-MGC Library."

Query Match	79.28;	Score 439.4;	DB 14;	Length 1010;
Best Local Similarity	99.88;	Pred. No. 2e-106;		
Matches 440;	Conservative	0;	Mismatches 1;	Indels 0;
				Gaps 0;

QY	101	CGGGGCACTACCTGAAAGGCCCTTGCACGGAGGCCCTGCGGCAACTCCACTGCCTTGCT	160
Db	48	CAGGGCACTACCTGAAAGGCCCTTGCACGGAGGCCCTGCGGCAACTCCACTGCCTTGCT	107
QY	161	GTCCCCAAGACACCTTCTTGCCCTGGGAGAACCAACCATTAATTCGAAATGTGCCGCTGCC	220
Db	108	GTCCCCAAGACACCTTCTTGCCCTGGGAGAACCAACCATTAATTCGAAATGTGCCGCTGCC	167
QY	221	AGGCGTGTATGAGCAGGCGCTCCAGGTGGCGCTGGAGAACTGTTACAGAGTGGCCGACA	280
Db	168	AGGCGTGTATGAGCAGGCGCTCCAGGTGGCGCTGGAGAACTGTTACAGAGTGGCCGACA	227
QY	281	CCGCGTGTGGCTGTAAGCCAGGCGTGTGTGTGAGTGCAGGTACGCCAATGTGTACGA	340
Db	228	CCGCGTGTGGCTGTAAGCCAGGCGTGTGTGTGAGTGCAGGTACGCCAATGTGTACGA	287
QY	341	GTTCAACCTTCTACTGCCAACCATGCTAGACTGCGGGGCCCTGCACCGCCACACACGGC	400
Db	288	GTTCAACCTTCTACTGCCAACCATGCTAGACTGCGGGGCCCTGCACCGCCACACACGGC	347
QY	401	TACTCTGTCCCCGACAGATACTGACTGTGGGACCTGCCTGCCTGGCTTCTATGAACATG	460
Db	348	TACTCTGTCCCCGACAGATACTGACTGTGGGACCTGCCTGCCTGGCTTCTATGAACATG	407
QY	461	GCGATGGCTGCGTGTCTCTGCCCCACGACACACCTTGGGGAGCTGTCCAGAGCGCTGTGCCG	520
Db	408	GCGATGGCTGCGTGTCTCTGCCCCACGACACACCTTGGGGAGCTGTCCAGAGCGCTGTGCCG	467
QY	521	CTGTCTGTGGCTGGAAGGCAGA 541	
Db	468	CTGTCTGTGGCTGGAAGGCAGA 488	

RESULT 15
AW002222
LOCUS
DEFINITION
478 bp mRNA linear EST 09-MAR-2000
wt85c09.x1 Soares_thymus.NHFTb Homo sapiens cDNA clone
IMAGE:2514256 3' similar to TR:O14866 O14866 SOLUBLE DEATH RECEPTOR
3 BETA., ;, mRNA sequence.
ACCESSION
AW002222
VERSION
AW002222.1 GI:5849138
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 478)
NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
JOURNAL
Contact: Robert Strausberg, Ph.D.
COMMENT
Email: cgaps-r@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1648 Std Error: 0.00
Seq primer: -40UP from G1bco
High quality sequence stop: 410.
FEATURES
Location/Qualifiers
1..478
source
/organism="Homo sapiens"

THIS PAGE BLANK (USPTO)

GenCore version 5.1.4_p5-4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 6, 2003, 15:03:59 ; Search time 111 Seconds
(without alignments)
4385.839 Million cell updates/sec

Title: US-09-993-234-9_COPY_146_700
Perfect score: 555
Sequence: 1 CTGGGGGGCCGGCCAGG.....GCCAGATGTCTGGGTCAG 555

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 593429 seqs, 438583890 residues

Total number of hits satisfying chosen parameters: 1186858

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	555	100.0	1254	10	US-09-333-966-3 Sequence 3, Appli
2	555	100.0	1634	9	US-10-081-280-9 Sequence 9, Appli
3	555	100.0	1634	9	US-10-112-793-9 Sequence 9, Appli
4	555	100.0	1634	9	US-10-112-793-11 Sequence 11, Appli
5	555	100.0	1634	10	US-09-993-234-9 Sequence 9, Appli
6	555	100.0	1783	10	US-09-333-966-1 Sequence 1, Appli
7	541	97.5	1743	9	US-09-954-531-1389 Sequence 1389, Ap
8	486.4	87.6	816	10	US-09-964-824A-292 Sequence 292, App
9	486.4	87.6	1438	9	US-10-081-280-5 Sequence 5, Appli
10	486.4	87.6	1438	9	US-10-112-793-5 Sequence 5, Appli
11	486.4	87.6	1438	9	US-10-112-793-5 Sequence 5, Appli
12	486.4	87.6	1438	10	US-09-884-733-5 Sequence 5, Appli
13	486.4	87.6	1438	10	US-09-993-234-5 Sequence 2, Appli
14	350.6	63.2	433	9	US-10-081-280-2 Sequence 2, Appli
15	350.6	63.2	433	9	US-10-112-793-2 Sequence 2, Appli
16	350.6	63.2	433	9	US-10-112-793-2 Sequence 2, Appli
17	350.6	63.2	433	10	US-09-884-733-2 Sequence 2, Appli
18	350.6	63.2	433	10	US-09-993-234-2 Sequence 2, Appli
19	171	30.8	10797	9	US-10-092-154-1577 Sequence 1577, Ap

20	171	30.8	10797	10	US-09-764-847-1577	Sequence 1577, Ap
21	55.4	10.0	346	10	US-09-783-590-1252	Sequence 1252, Ap
22	42.2	7.6	543	10	US-09-970-532-3	Sequence 3, Appli
23	42.2	7.6	2440	10	US-09-970-532-1	Sequence 1, Appli
24	40.4	7.3	671	9	US-10-184-644-346	Sequence 346, App
25	38	6.8	2130	10	US-09-917-800A-1601	Sequence 1601, Ap
26	37.4	6.7	5870	10	US-09-838-718A-8	Sequence 8, Appli
27	36.4	6.6	301	9	US-10-070-676-7	Sequence 7, Appli
28	35	6.3	1345	9	US-09-853-450-7	Sequence 7, Appli
29	34.8	6.3	2173	9	US-09-898-429A-14	Sequence 14, Appli
30	34.8	6.3	2173	9	US-09-898-429A-24	Sequence 24, Appli
31	34.8	6.3	2173	9	US-09-792-356-14	Sequence 14, Appli
32	34.8	6.3	2173	10	US-09-899-422-14	Sequence 14, Appli
33	34.8	6.3	4898	10	US-09-919-497-35	Sequence 35, Appli
34	34.8	6.3	4898	10	US-09-919-497-35	Sequence 35, Appli
35	34.8	6.3	5988	12	US-10-044-090-90	Sequence 90, Appli
36	34.6	6.2	20556	10	US-09-880-107-3945	Sequence 3945, Ap
37	34.4	6.2	896	10	US-09-884-441-22	Sequence 22, Appli
38	33.2	6.0	15540	9	US-09-999-121-12	Sequence 12, Appli
39	33.2	6.0	37113	9	US-09-999-121-11	Sequence 11, Appli
40	33.2	6.0	155074	9	US-10-026-188-6	Sequence 6, Appli
41	32	5.8	1780	10	US-09-917-800A-1521	Sequence 1521, Ap
42	31.6	5.7	299	10	US-09-864-761-25435	Sequence 25435, A
43	31.6	5.7	518	10	US-09-864-761-8725	Sequence 8725, Ap
44	31.6	5.7	746	10	US-09-910-943-165	Sequence 165, App
45	31.6	5.7	1801	10	US-09-822-830A-128	Sequence 128, App

ALIGNMENTS

RESULT 1
US-09-333-966-3
Sequence 3, Application US/09333966
Patent No. US20020009773A1
GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang
APPLICANT: Ni, Jian
APPLICANT: Dixit, Vishva
APPLICANT: Gentz, Reiner L.
APPLICANT: Dillon, Patrick J.
TITLE OF INVENTION: Death Domain Containing Receptors
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/333,966
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/815,469
FILING DATE:
APPLICATION NUMBER: NO. US20020009773A1 Yet Assigned
FILING DATE: 06-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,711
FILING DATE: 17-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,285
FILING DATE: 12-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688

REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1254 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1251
US-09-333-966-3

Query Match 100.0%; Score 555; DB 10; Length 1254;
Best Local Similarity 100.0%; Pred. No. 3e-161;
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGGGCCCGCCAGGCGGCGACTGTAAGCCAGGTGTGACTGTGCGGTGACTTC 60
DB 58 CTGGGGCCCGCCAGGCGGCGGCGACTGTAAGCCAGGTGTGACTGTGCGGTGACTTC 117
QY 61 CACAAGAGATGCTGTTTGTGTCAGAGGCTGCCAGCGGGGCGACTGTAAGGCC 120
DB 118 CACAAGAGATGCTGTTTGTGTCAGAGGCTGCCAGCGGGGCGACTGTAAGGCC 177
QY 121 CCTGCACGAGCGCTGCGGCACTCCACTGCTGTGTGTGCCCAAGACACTTCTTG 180
DB 178 CCTGCACGAGCGCTGCGGCACTCCACTGCTGTGTGTGCCCAAGACACTTCTTG 237
QY 181 GCCTGGAGAACCACTATATTTGATGTGCGCGCTGCCAGGCGGTGATGAGCAGGCC 240
DB 238 GCCTGGAGAACCACTATATTTGATGTGCGCGCTGCCAGGCGGTGATGAGCAGGCC 297
QY 241 TCCAGAGTGGCGCTGAGAACTGTTCAGAGTGGCCGACACACCGGCTGTGCTGTAAGCCA 300
DB 298 TCCAGAGTGGCGCTGAGAACTGTTCAGAGTGGCCGACACACCGGCTGTGCTGTAAGCCA 357
QY 301 GGCTGTTTGTGAGTGCAGGTCAGGCAATGTGTGAGCAGTTCACCCCTTCTACTGCCAA 360
DB 358 GGCTGTTTGTGAGTGCAGGTCAGGCAATGTGTGAGCAGTTCACCCCTTCTACTGCCAA 417
QY 361 CCATGCTAGACTGCGGGGCGCTGCACCGCCACACACGCGTACTTCTTCCCGCAGAGAT 420
DB 418 CCATGCTAGACTGCGGGGCGCTGCACCGCCACACACGCGTACTTCTTCCCGCAGAGAT 477
QY 421 ACTGACTGTGGGACCTGCGCTGCTTCTATGACATGGCGATGGCTGCGTGTCTGC 480
DB 478 ACTGACTGTGGGACCTGCGCTGCTTCTATGACATGGCGATGGCTGCGTGTCTGC 537
QY 481 CCCACGAGACCCCTGGGAGCTGTTCAGAGCGGCTGTGCGGCTGTGCTGAGGAGCAG 540
DB 538 CCCACGAGACCCCTGGGAGCTGTTCAGAGCGGCTGTGCGGCTGTGCTGAGGAGCAG 597
QY 541 ATGTTCTGGGTCAG 555
DB 598 ATGTTCTGGGTCAG 612

RESULT 2
US-10-081-280-9
Sequence 9, Application US/10081280
Patent No. US20020165157A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco

STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/081,280
FILING DATE: 21-Feb-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/829,270
FILING DATE: 31-Mar-1997
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007R1
TELEPHONE: 415/225-5416
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1634 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-081-280-9

Query Match 100.0%; Score 555; DB 9; Length 1634;
Best Local Similarity 100.0%; Pred. No. 3.2e-161;
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGGGCCCGCCAGGCGGCGACTGTAAGCCAGGTGTGACTGTGCGGTGACTTC 60
DB 146 CTGGGGCCCGCCAGGCGGCGGCGACTGTAAGCCAGGTGTGACTGTGCGGTGACTTC 205
QY 61 CACAAGAGATGCTGTTTGTGTCAGAGGCTGCCAGCGGGGCACTGTAAGGCC 120
DB 206 CACAAGAGATGCTGTTTGTGTCAGAGGCTGCCAGCGGGGCACTGTAAGGCC 265
QY 121 CCTGCACGAGCGCTGCGGCACTCCACTGCTGTGTGTGCCCAAGACACTTCTTG 180
DB 266 CCTGCACGAGCGCTGCGGCACTCCACTGCTGTGTGTGCCCAAGACACTTCTTG 325
QY 181 GCCTGGAGAACCACTATATTTGATGTGCGCGCTGCCAGGCGGTGATGAGCAGGCC 240
DB 326 GCCTGGAGAACCACTATATTTGATGTGCGCGCTGCCAGGCGGTGATGAGCAGGCC 385
QY 241 TCCAGAGTGGCGCTGAGAACTGTTCAGAGTGGCCGACACCGGCTGTGCTGTAAGCCA 300
DB 386 TCCAGAGTGGCGCTGAGAACTGTTCAGAGTGGCCGACACCGGCTGTGCTGTAAGCCA 445
QY 301 GGCTGTTTGTGAGTGCAGGTCAGGCAATGTGTGAGCAGTTCACCCCTTCTACTGCCAA 360
DB 446 GGCTGTTTGTGAGTGCAGGTCAGGCAATGTGTGAGCAGTTCACCCCTTCTACTGCCAA 505
QY 361 CCATGCTAGACTGCGGGGCGCTGCACCGCCACACACGCGTACTTCTTCCCGCAGAGAT 420
DB 506 CCATGCTAGACTGCGGGGCGCTGCACCGCCACACACGCGTACTTCTTCCCGCAGAGAT 565
QY 421 ACTGACTGTGGGACCTGCGCTGCTTCTATGACATGGCGATGGCTGCGTGTCTGC 480
DB 566 ACTGACTGTGGGACCTGCGCTGCTTCTATGACATGGCGATGGCTGCGTGTCTGC 625
QY 481 CCCACGAGACCCCTGGGAGCTGTCCAGAGCGGCTGTGCGGCTGTGCTGAGGAGCAG 540
DB 626 CCCACGAGACCCCTGGGAGCTGTCCAGAGCGGCTGTGCGGCTGTGCTGAGGAGCAG 685
QY 541 ATGTTCTGGGTCAG 555

Db	146	CTGGGGCCCCGGGCCAGGGCGGCACTCGTAGCCCCAGGTGTGACTGTGCCGGTGACTTC	205
QY	61	CACAAGAAGATTGCTCTGTTTTGTTCAGAGGCTGCCAGCGGGGCACTACTGAAGCC	120
Db	206	CACAAGAAGATTGCTCTGTTTTGTTCAGAGGCTGCCAGCGGGGCACTACTGAAGCC	265
QY	121	CCTTGCACGGAGCCCCCTGCGGCACTCCACCTGCGCTTGTGTCCCCAAGACACCTTCTTG	180
Db	266	CCTTGCACGGAGCCCCCTGCGGCACTCCACCTGCGCTTGTGTCCCCAAGACACCTTCTTG	325
QY	181	GCCTTGGAGAACCAACCATTAATTCTGAATGTGCCCGCTGCCAGGCGCTGTATGACAGGCC	240
Db	326	GCCTTGGAGAACCAACCATTAATTCTGAATGTGCCCGCTGCCAGGCGCTGTATGACAGGCC	385
QY	241	TCCCAAGTGGCGCTGGAGAACTGTTACAGTGGCCGACACCCGCTGTGGCTGTAAGCCA	300
Db	386	TCCCAAGTGGCGCTGGAGAACTGTTACAGTGGCCGACACCCGCTGTGGCTGTAAGCCA	445
QY	301	GGCTGCTTTGTGGAGTGCACAGTCAAGCCAATGTGTCAAGAGTTCACCCCTTCTACTGCCAA	360
Db	446	GGCTGCTTTGTGGAGTGCACAGTCAAGCCAATGTGTCAAGAGTTCACCCCTTCTACTGCCAA	505
QY	361	CCATGCTTAGACTGCGGGGCCCTGCACCGCCACACACGGCTACTCTGTCCCGCAGAGAT	420
Db	506	CCATGCTTAGACTGCGGGGCCCTGCACCGCCACACACGGCTACTCTGTCCCGCAGAGAT	565
QY	421	ACTGACTGTGGGACCTGCGCTGCTGCTTCTATGAACATGGGATGGCTGCGTCTCTGC	480
Db	566	ACTGACTGTGGGACCTGCGCTGCTGCTTCTATGAACATGGGATGGCTGCGTCTCTGC	625
QY	481	CCCAAGAGCACCCCTGGGGAGCTGTCCAGAGCGGCTGTGCCGCTGTCTGTGGCTGGAGGCAG	540
Db	626	CCCAAGAGCACCCCTGGGGAGCTGTCCAGAGCGGCTGTGCCGCTGTCTGTGGCTGGAGGCAG	685
QY	541	ATGTTCTGGGTCCAG 555	
Db	686	ATGTTCTGGGTCCAG 700	

RESULT 5
US-09-993-234-9
Sequence 9, Application US/09993234
Patent No. US20020146768A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 Li AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/993,234
FILING DATE: 19-NO. US20020146768A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,683
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5416

```

; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 1634 base pairs
;   TYPE: Nucleic Acid
;   STRANDEDNESS: Single
;   TOPOLOGY: Linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-993-234-9

```

Query Match	100.0%;	Score 555;	DB 10;	Length 1634;
Best Local Similarity	100.0%;	Pred. No. 3.2e-161;		
Matches 555; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	CTGGGGCCCCGGGCCCAAGGGCGGACACTGTAAGCCCCAGGTGTGACTGTGCCGGTGACTTC	60
Db	146	CTGGGGCCCCGGGCCCAAGGGCGGACACTGTAAGCCCCAGGTGTGACTGTGCCGGTGACTTC	205
QY	61	CACAAGAAGATGTGTTCTGTTTTGTTCAGAGGCTGCCAGCGGGCAGTACCTGAAGGCC	120
Db	206	CACAAGAAGATGTGTTCTGTTTTGTTCAGAGGCTGCCAGCGGGCAGTACCTGAAGGCC	265
QY	121	CCTTGCACGAGACCCCTGCGGCACTCCACCTGCTTGTGTGTCCCAAGACACCTTCTTG	180
Db	266	CCTTGCACGAGACCCCTGCGGCACTCCACCTGCTTGTGTGTCCCAAGACACCTTCTTG	325
QY	181	GCCTGGGAGAACCAACCATTAATTCGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCC	240
Db	326	GCCTGGGAGAACCAACCATTAATTCGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCC	385
QY	241	TCCCAGGTGGCGCTGGAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGGCTGTAAAGCCA	300
Db	386	TCCCAGGTGGCGCTGGAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGGCTGTAAAGCCA	445
QY	301	GGCTGTTTGTGGAGTGCACAGGTCAAGCCAAATGTGTACAGCAGTTCAACCCTTACTGCCAA	360
Db	446	GGCTGTTTGTGGAGTGCACAGGTCAAGCCAAATGTGTACAGCAGTTCAACCCTTACTGCCAA	505
QY	361	CCATGCTTAAGACTGCGGGGCCCTGCACCGCCACACACAGGCTACTCTGTTCCCGCAGAGAT	420
Db	506	CCATGCTTAAGACTGCGGGGCCCTGCACCGCCACACACAGGCTACTCTGTTCCCGCAGAGAT	565
QY	421	ACTGACTGTGGGACCTGCCTGCTTGCGCTTCTATGAACAATGGCGATGGCTGCGTTCCTGC	480
Db	566	ACTGACTGTGGGACCTGCCTGCTTGCGCTTCTATGAACAATGGCGATGGCTGCGTTCCTGC	625
QY	481	CCCACGAGCACCCCTGGGAGAGCTTCACAGAGCGCTGTGCCGCTGTCTGTGGCTGGAGGCAG	540
Db	626	CCCACGAGCACCCCTGGGAGAGCTTCACAGAGCGCTGTGCCGCTGTCTGTGGCTGGAGGCAG	685
QY	541	ATGTTCTGGGTTCCAG 555	
Db	686	ATGTTCTGGGTTCCAG 700	

RESULT 6
 US-09-333-966-1
 ; Sequence 1, Application US/09333966
 ; Patent No. US20020009773A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Yu, Guo-Liang
 ; APPLICANT: Ni, Jian
 ; APPLICANT: Dixit, Vishva
 ; APPLICANT: Gentz, Reiner L.
 ; APPLICANT: Dillon, Patrick J.
 ; TITLE OF INVENTION: Death Domain Containing Receptors
 ; NUMBER OF SEQUENCES: 17
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C
 ; STREET: 1100 New York Ave., NW, Suite 600
 ; CITY: Washington
 ; STATE: DC


```
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/333,966
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/815,469
FILING DATE:
APPLICATION NUMBER: No. US20020009773A1 Yet Assigned
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,711
FILING DATE: 06-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,711
FILING DATE: 17-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,285
FILING DATE: 12-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1783 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 198..1481
US-09-333-966-1
```

```
Query Match 100.0%; Score 555; DB 10; Length 1783;
Best Local Similarity 100.0%; Pred. No. 3.2e-161;
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGGGCCCCGGCCAGGGGGGCGACTCGTAGCCCCAGGTGTGACTGTGCCGTGACTTC 60
Db 288 CTGGGGCCCCGGCCAGGGGGGCGACTCGTAGCCCCAGGTGTGACTGTGCCGTGACTTC 347
QY 61 CACAAGAAGATGTGCTGTTTGTGTCAGAGGCTGCCAGCGGGGCGACTTGAAGGCC 120
Db 348 CACAAGAAGATGTGCTGTTTGTGTCAGAGGCTGCCAGCGGGGCGACTTGAAGGCC 407
QY 121 CCTTGCACGGAGCCCTGCGGCACTCCACCTGCTGTGTGTCGCCCAAGACACTTCTTG 180
Db 408 CCTTGCACGGAGCCCTGCGGCACTCCACCTGCTGTGTGTCGCCCAAGACACTTCTTG 467
QY 181 GCCTGGAGAACCACTAATTTGATGTGCCCGCTGCCAGGCTGTGATGACAGGCC 240
Db 468 GCCTGGAGAACCACTAATTTGATGTGCCCGCTGCCAGGCTGTGATGACAGGCC 527
QY 241 TCCAGAGTGGCGTGGAGAACTGTTACAGAGTGGCCGACACCCGCTGTGCTGTAAGCA 300
Db 528 TCCAGAGTGGCGTGGAGAACTGTTACAGAGTGGCCGACACCCGCTGTGCTGTAAGCA 587
QY 301 GGCTGTTTGTGAGTGCAGGTACAGCCAAATGTGTACAGAGTTCACCCCTTCTACTGCCAA 360
Db 588 GGCTGTTTGTGAGTGCAGGTACAGCCAAATGTGTACAGAGTTCACCCCTTCTACTGCCAA 647
QY 361 CCATGCTAGACTGGGGGGCCCTGACCGGCCACACAGGGCTACTCTGTTCGGCAGAGAT 420
Db 648 CCATGCTAGACTGGGGGGCCCTGACCGGCCACACAGGGCTACTCTGTTCGGCAGAGAT 707
```

```
QY 421 ACTGACTGTGGACCTGCTGCTGCTGCTTCTATGACATGGCGATGGCTGCGTGTCTGC 480
Db 708 ACTGACTGTGGACCTGCTGCTGCTGCTTCTATGACATGGCGATGGCTGCGTGTCTGC 767
QY 481 CCCACGAGCACCTGGGAGCTGTCCAGAGCGCTGTGCCGTGTGTGGCTGAGGCGAG 540
Db 768 CCCACGAGCACCTGGGAGCTGTCCAGAGCGCTGTGCCGTGTGTGGCTGAGGCGAG 827
QY 541 ATGTTCTGGGTCCAG 555
Db 828 ATGTTCTGGGTCCAG 842
```

```
RESULT 7
US-09-954-531-1389
; Sequence 1389, Application US/09954531
; Patent No. US20020165180A1
; GENERAL INFORMATION:
; APPLICANT: Weaver, Zoe
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C
; FILE REFERENCE: 689290-77
; CURRENT APPLICATION NUMBER: US/09/954,531
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: US/60/233,133
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,009
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,034
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,509
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US/60/234,567
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 1392
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1389
; LENGTH: 1743
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-531-1389
```

```
Query Match 97.5%; Score 541; DB 9; Length 1743;
Best Local Similarity 99.1%; Pred. No. 6.5e-157;
Matches 544; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CTGGGGCCCCGGCCAGGGGGGCGACTCGTAGCCCCAGGTGTGACTGTGCCGTGACTTC 60
Db 126 CTGGGGCCCCGGCCAGGGGGGCGACTCGTAGCCCCAGGTGTGACTGTGCCGTGACTTC 185
QY 61 CACAAGAAGATGTGCTGTTTGTGTCAGAGGCTGCCAGCGGGGCGACTTGAAGGCC 120
Db 186 CACAAGAAGATGTGCTGTTTGTGTCAGAGGCTGCCAGCGGGGCGACTTGAAGGCC 245
QY 121 CCTTGCACGGAGCCCTGCGGCACTCCACCTGCTGTGTGTCGCCCAAGACACTTCTTG 180
Db 246 CCTTGCACGGAGCCCTGCGGCACTCCACCTGCTGTGTGTCGCCCAAGACACTTCTTG 305
QY 181 GCCTGGAGAACCACTAATTTGATGTGCCCGCTGCCAGGCTGTGATGACAGGCC 240
Db 306 GCCTGGAGAACCACTAATTTGATGTGCCCGCTGCCAGGCTGTGATGACAGGCC 365
QY 241 TCCAGAGTGGCGTGGAGAACTGTTACAGAGTGGCCGACACCCGCTGTGCTGTAAGCA 300
Db 366 TCCAGAGTGGCGTGGAGAACTGTTACAGAGTGGCCGACACCCGCTGTGCTGTAAGCA 425
QY 301 GGCTGTTTGTGAGTGCAGGTACAGCCAAATGTGTACAGAGTTCACCCCTTCTACTGCCAA 360
Db 426 GGCTGTTTGTGAGTGCAGGTACAGCCAAATGTGTACAGAGTTCACCCCTTCTACTGCCAA 485
QY 361 CCATGCTAGACTGGGGGGCCCTGACCGGCCACACAGGGCTACTCTGTTCGGCAGAGAT 420
Db 486 CCATGCTAGACTGGGGGGCCCTGACCGGCCACACAGGGCTACTCTGTTCGGCAGAGAT 545
```

QY 421 ACTGACTGTGGGACCTGCTGCTGCTTCTATGAACATGGCGATGGCTGCTGCTGC 480
|||||
Db 546 ACTGACTGTGGGACCTGCTGCTGCTTCTATGAACATGGCGATGGCTGCTGCTGC 605
QY 481 CCCACGAGACCTGGGGAGCTGTCCAGAGCGCTGTGCTGTGCTGGAGGCAG 540
|||||
Db 606 CCCACGAGACCTGGGGAGCTGTCCAGAGCGCTGTGCTGTGCTGGAGGCAG 665
QY 541 ATGTTCTGG 549
|
Db 666 AGTAGGTGG 674

RESULT 8

US-09-964-824A-292
; Sequence 292, Application US/09964824A
; Patent No. US20020102531A1
; GENERAL INFORMATION:
; APPLICANT: Horrigan, Stephen
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-73
; CURRENT APPLICATION NUMBER: US/09/964,824A
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/60/236,033
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,032
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,028
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 583
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 292
; LENGTH: 816
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-824A-292

Query Match 87.6%; Score 486.4; DB 10; Length 816;
Best Local Similarity 98.8%; Pred. No. 3.6e-140;
Matches 490; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CTGGGGGGCCCCGGCCAGGGGCGCACTGCTAGCCCCAGGTGTGACTGTGCCGGTGAATTC 60
|||||
Db 42 CTGGGGGGCCCCGGCCAGGGGCGCACTGCTAGCCCCAGGTGTGACTGTGCCGGTGAATTC 101
QY 61 CACAAGAAGATTGTTCTGTTTGTGACAGAGGCTGCCACGGGGCAGCTACTGGAAGGCC 120
|||||
Db 102 CACAAGAAGATTGTTCTGTTTGTGACAGAGGCTGCCACGGGGCAGCTACTGGAAGGCC 161
QY 121 CCTTGACGAGGAGCCCTGGCGCACTCCACTGCTGTGTGTGTCCCAAGACACCTTCTTG 180
|||||
Db 162 CCTTGACGAGGAGCCCTGGCGCACTCCACTGCTGTGTGTGTCCCAAGACACCTTCTTG 221
QY 181 GCCTGGGAGAACCAACATAATTCTGAATGTGCCCGTCCAGGGCTGTGATGAGCAGGCC 240
|||||
Db 222 GCCTGGGAGAACCAACATAATTCTGAATGTGCCCGTCCAGGGCTGTGATGAGCAGGCC 281
QY 241 TCCCAAGGTGGCGCTGAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGGCTGTAAAGCCA 300
|||||
Db 282 TCCCAAGGTGGCGCTGAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGGCTGTAAAGCCA 341
QY 301 GGCTGGTTTGTGAGTGCAGGTCAGCCAAATGTGTGACAGTTCACCCCTTCTACTGCCAA 360
|||||
Db 342 GGCTGGTTTGTGAGTGCAGGTCAGCCAAATGTGTGACAGTTCACCCCTTCTACTGCCAA 401
QY 361 CCATGCCCTAGACTGCGGGGCCCTGCACCGCCACACAGGGCTACTCTGTCCCGAGAGAT 420
|||||
Db 402 CCATGCCCTAGACTGCGGGGCCCTGCACCGCCACACAGGGCTACTCTGTCCCGAGAGAT 461
QY 421 ACTGACTGTGGGACCTGCTGCTGCTTCTATGAACATGGCGATGGCTGCTGCTGC 480
|||||

Db 462 ACTGACTGTGGGACCTGCTGCTGCTTCTATGAACATGGCGATGGCTGCTGCTGC 521
QY 481 CCCACGAGACCTGG 496
|||||
Db 522 CCCACGTAATTCCTAG 537

RESULT 9

US-10-081-280-5
; Sequence 5, Application US/10081280
; Patent No. US20020165157A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinpatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/081,280
; FILING DATE: 21-Feb-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/829,270
; FILING DATE: 31-Mar-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1007R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5416
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1438 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-081-280-5

Query Match 87.6%; Score 486.4; DB 9; Length 1438;
Best Local Similarity 98.8%; Pred. No. 3.9e-140;
Matches 490; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CTGGGGGGCCCCGGCCAGGGGCGCACTGCTAGCCCCAGGTGTGACTGTGCCGGTGAATTC 60
|||||
Db 434 CTGGGGGGCCCCGGCCAGGGGCGCACTGCTAGCCCCAGGTGTGACTGTGCCGGTGAATTC 493
QY 61 CACAAGAAGATTGTTCTGTTTGTGACAGAGGCTGCCACGGGGCAGCTACTGGAAGGCC 120
|||||
Db 494 CACAAGAAGATTGTTCTGTTTGTGACAGAGGCTGCCACGGGGCAGCTACTGGAAGGCC 553
QY 121 CCTTGACGAGGAGCCCTGGCGCACTCCACTGCTGTGTGTGTCCCAAGACACCTTCTTG 180
|||||
Db 554 CCTTGACGAGGAGCCCTGGCGCACTCCACTGCTGTGTGTGTCCCAAGACACCTTCTTG 613
QY 181 GCCTGGGAGAACCAACATAATTCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCC 240
|||||
Db 614 GCCTGGGAGAACCAACATAATTCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCC 673
QY 241 TCCCAAGGTGGCGCTGAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGCTGTAAAGCCA 300
|||||

Db 674 TCCAGGTGGCGCTGAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGGCTGTAGCCA 733

QY 301 GGCTGGTTTGTGAGTGGCCAGTTCAGCCAATGTGTTCAGACATTCACCTTCTACTGCCAA 360
|||||

Db 734 GGCTGGTTTGTGAGTGGCCAGTTCAGCCAATGTGTTCAGACATTCACCTTCTACTGCCAA 793

QY 361 CCATGCTAGACTGGGGGGCTGCACCGCCACACAGGCTACTCTGTTCGGCAGAGAT 420
|||||

Db 794 CCATGCTAGACTGGGGGGCTGCACCGCCACACAGGCTACTCTGTTCGGCAGAGAT 853

QY 421 ACTGACTGTGGACCTGCTGCTGCTGTCTATGAACATGGCGATGGCTGCTGCTGC 480
|||||

Db 854 ACTGACTGTGGACCTGCTGCTGCTGTCTATGAACATGGCGATGGCTGCTGCTGC 913

QY 481 CCCACGAGCACCCTGG 496
|||||

Db 914 CCCACGTAATTCCTAG 929

RESULT 10
US-10-112-793-5
; Sequence 5, Application US/10112793
; Publication No. US20020192729A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/112,793
; FILING DATE: 28-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,683A
; FILING DATE: 31-Mar-1997
; APPLICATION NUMBER: 08/625328
; FILING DATE: 1-Apr-1996
; APPLICATION NUMBER: 08/710802
; FILING DATE: 23-Sep-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1007P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1438 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-112-793-5

Query Match 87.6%; Score 486.4; DB 9; Length 1438;
Best Local Similarity 98.8%; Pred. No. 3.9e-140;
Matches 490; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CTGGGGGCGCGGCCAGGGGGCACTGTAGCCCGAGTGTGACTGTGCCGTGACTTC 60
|||||

Db 434 CTGGGGGCGCGGCCAGGGGGCACTGTAGCCCGAGTGTGACTGTGCCGTGACTTC 493

QY 61 CACAAGAGATTGCTGTGTTTGTTCAGAGGCTGCCAGCGGGGCACTACCTGAAGGCC 120
|||||

Db 494 CACAAGAGATTGCTGTGTTTGTTCAGAGGCTGCCAGCGGGGCACTACCTGAAGGCC 553

QY 121 CCTGGACGAGACCCCTGCGGCACTCCACCTGCTGTGTGTGTCCCAAGACACCTTCTTG 180
|||||

Db 554 CCTGGACGAGACCCCTGCGGCACTCCACCTGCTGTGTGTGTCCCAAGACACCTTCTTG 613

QY 181 GCCTGGAGAACCAACCATTAATTCGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCC 240
|||||

Db 614 GCCTGGAGAACCAACCATTAATTCGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCC 673

QY 241 TCCAGGTGGCGCTGGAGAACTGTTCAGCAGTGGCCGACACCGCTGTGGCTGAAGCCA 300
|||||

Db 674 TCCAGGTGGCGCTGGAGAACTGTTCAGCAGTGGCCGACACCGCTGTGGCTGAAGCCA 733

QY 301 GGCTGGTTTGTGAGTGGCCAGGTGACCCAAATGTGTTCAGCAGTTCACCTTCTACTGCCAA 360
|||||

Db 734 GGCTGGTTTGTGAGTGGCCAGGTGACCCAAATGTGTTCAGCAGTTCACCTTCTACTGCCAA 793

QY 794 CCATGCTAGACTGCGGGGCTGCACCGCCACACAGGCTACTGTTCGCCGAGAGAT 853

QY 421 ACTGACTGTGGACCTGCTGCTGCTGTCTATGAACATGGCGATGGCTGCTGCTGC 480
|||||

Db 854 ACTGACTGTGGACCTGCTGCTGCTGTCTATGAACATGGCGATGGCTGCTGCTGC 913

QY 481 CCCACGAGCACCCTGG 496
|||||

Db 914 CCCACGTAATTCCTAG 929

RESULT 11
US-10-112-193-5
; Sequence 5, Application US/10112193
; Publication No. US20030004313A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-3 POLYPEPTIDE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/112,193
; FILING DATE: 28-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/928,069
; FILING DATE: 11-Sep-1997
; APPLICATION NUMBER: 60/026943
; FILING DATE: 23-Sep-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1052R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1438 base pairs

```

; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-112-193-5

```

Query Match	87.6%;	Score 486.4;	DB 9;	Length 1438;
Best Local Similarity	98.8%;	Pred. No. 3.9e-140;		
Matches 490; Conservative	0;	Mismatches 6;	Indels 0;	Gaps 0;

QY	1	CTGGGGCCCCGGGCCCCAGGGCGGCACTGTAAGCCAGGTGTGACTGTGCCGTTGACTTC	60
Db	434	CTGGGGGGCCCCGGGCCCCAGGGCGGCACTGTAAGCCAGGTGTGACTGTGCCGTTGACTTC	4933
QY	61	CACAAGAAGATTGCTCTGTTTTTTGTGCAGAGGCTGCCAGCGGGGCACTACTGAAGGCC	120
Db	494	CACAAGAAGATTGCTCTGTTTTTTGTGCAGAGGCTGCCAGCGGGGCACTACTGAAGGCC	5533
QY	121	CCTTGCACGAGCCCTGCGGCAACTCCACCTGCCTGTGTGTGCCCAAGACACCTCTTG	180
Db	554	CCTTGCACGAGCCCTGCGGCAACTCCACCTGCCTGTGTGTGCCCAAGACACCTTCTTG	6133
QY	181	GCCTTGGGAGAACCAACCATATTCTGAATGTGCCCGCTGCCAGGCCCTGTATGACGAGCC	240
Db	614	GCCTTGGGAGAACCAACCATATTCTGAATGTGCCCGCTGCCAGGCCCTGTATGACGAGCC	6733
QY	241	TCCCAAGTGGCGCTGGAGAACTGTTACAGCAATGGCCGACACCCGCTGTGGCTGTAAGCCA	300
Db	674	TCCCAAGTGGCGCTGGAGAACTGTTACAGCAATGGCCGACACCCGCTGTGGCTGTAAGCCA	7333
QY	301	GGCTGTGTTGTGGAGTGCACAGTCAAGCCAAATGTGTACAGCAATTCAACCTTTCTACTGCCAA	360
Db	734	GGCTGTGTTGTGGAGTGCACAGTCAAGCCAAATGTGTACAGCAATTCAACCTTTCTACTGCCAA	7933
QY	361	CCATGCTTAGACTGCGGGGCCCTGCACCCGCCACACACGGCTACTCTGTTCCCGAGAGAT	420
Db	794	CCATGCTTAGACTGCGGGGCCCTGCACCCGCCACACACGGCTACTCTGTTCCCGAGAGAT	8533
QY	421	ACTGACTGTGGGACCTGCCTGCCTGGCTTCTATGAACATGGGATGGCTGCCTGCCTGC	480
Db	854	ACTGACTGTGGGACCTGCCTGCCTGGCTTCTATGAACATGGGATGGCTGCCTGCCTGC	9133
QY	481	CCCACGAGCACCCCTGG 496	
Db	914	CCCACGTAATTCCTAG 929	

RESULT 12
 US-09-884-733-5
 ; Sequence 5, Application US/09884733
 ; Patent No. US20020123116A1
 ;
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: Ashkenazi, Avi J.
 ; TITLE OF INVENTION: Apo-2 Ligand Inhibitor
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESSES:
 ;
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 460 Point San Bruno Blvd
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ;
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WinPatIn (Genentech)
 ;
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/884,733
 ; FILING DATE: 19-Jun-2001
 ; CLASSIFICATION: <Unknown>
 ;
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/304,003
 ;

? FILING DATE: 14-JUNE-2000
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: Marschang, Diane L.
 ? REGISTRATION NUMBER: 35,600
 ? REFERENCE/DOCKET NUMBER: PI007
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: 415/225-5416
 ? TELEFAX: 415/952-9881
 ? TELEX: 910/371-7168
 ? INFORMATION FOR SEQ ID NO: 5:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 1438 base pairs
 ? TYPE: Nucleic Acid
 ? STRANDEDNESS: Single
 ? TOPOLOGY: Linear
 ? SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Query Match	87.68;	Score 486.4;	DB 10;	Length 1438;
Best Local Similarity	98.88;	Pred. No. 3.9e-140;		
Matches 490; Conservative	0;	Mismatches 6;	Indels 0;	Gaps 0;

QY	1	CTGGGGGGCCCCAGGGCCAGGGCGGACCTCGTAGCCCCAGGTGTGACTGTGCCGTGACTTC	60
Db	434	CTGGGGGGCCCCAGGGCCAGGGCGGACCTCGTAGCCCCAGGTGTGACTGTGCCGTGACTTC	493
QY	61	CACAAGAAGATTGGTCTGTTTTGTGTGCAGAGGCTGCCAGCGGGGCACTACCTGAAGGCC	120
Db	494	CACAAGAAGATTGGTCTGTTTTGTGTGCAGAGGCTGCCAGCGGGGCACTACCTGAAGGCC	553
QY	121	CCTTGACCGAGCGCCCTGCGGCAACTCCACTGCGCTTGTGTGTGCCAAGACACCTTCCTTG	180
Db	554	CCTTGACCGAGCGCCCTGCGGCAACTCCACTGCGCTTGTGTGTGCCAAGACACCTTCCTTG	613
QY	181	GCCTGGGAGAACCAACCATTAATTCGAAATGCCCCGCTGCCAGGCTGTGATGAGAGGCC	240
Db	614	GCCTGGGAGAACCAACCATTAATTCGAAATGCCCCGCTGCCAGGCTGTGATGAGAGGCC	673
QY	241	TCCCAGGTGGCGCTGGAGAACTGTTCAAGAGTGGCCGACACCCCGTGTGGCTGTAAAGCCA	300
Db	674	TCCCAGGTGGCGCTGGAGAACTGTTCAAGAGTGGCCGACACCCCGTGTGGCTGTAAAGCCA	733
QY	301	GGCTGTTTTGTGGAGTGGCCAGGTCAGCCCAATGTGTACAGCAGTTCAACCTTCTACTGCCAA	360
Db	734	GGCTGTTTTGTGGAGTGGCCAGGTCAGCCCAATGTGTACAGCAGTTCAACCTTCTACTGCCAA	793
QY	361	CCATGCCCTAAGACTGCGGGGGCCCTGCACCGCCACACACGCGTACTCTGTTCCCGCAGAGAT	420
Db	794	CCATGCCCTAAGACTGCGGGGGCCCTGCACCGCCACACACGCGTACTCTGTTCCCGCAGAGAT	853
QY	421	ACTGACTGTGGGAACCTGCGCTGCGCTGCTTCTATGAACATGCGGATGGCTGCGTGTCTGC	480
Db	854	ACTGACTGTGGGAACCTGCGCTGCGCTGCTTCTATGAACATGCGGATGGCTGCGTGTCTGC	913
QY	481	CCCACGACGACCCCTGG 496	
Db	914	CCCACGTAATTCCTAG 929	

RESULT 13
 US-09-993-234-5
 ; Sequence 5, Application US/09993234
 ; Patent No. US20020146768A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 460 Point San Bruno Blvd
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ;

ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/993,234
FILING DATE: 19-No. US20020146768A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,683
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5416
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1438 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-993-234-5

Query Match 87.6%; Score 486.4; DB 10; Length 1438;
Best Local Similarity 98.8%; Pred. No. 3.9e-140;
Matches 490; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 CTGGGGGCCCCGGCCAGGGGGGCACTCGTAGCCCCAGGTGTGACTGTGCGGTGACTTC 60
Db 434 CTGGGGGCCCCGGCCAGGGGGGCACTCGTAGCCCCAGGTGTGACTGTGCGGTGACTTC 493
OY 61 CACAAGAAGATTGCTGTTTGTTCAGAGAGGCTGCCAGCGGGGCACTACCTGAAGGCC 120
Db 494 CACAAGAAGATTGCTGTTTGTTCAGAGAGGCTGCCAGCGGGGCACTACCTGAAGGCC 553
OY 121 CCTTGCACGGAGCCCTGCGGCACTCCACCTGCTGTGTGTCCTCCCAAGACACCTTCTTG 180
Db 554 CCTTGCACGGAGCCCTGCGGCACTCCACCTGCTGTGTGTCCTCCCAAGACACCTTCTTG 613
OY 181 GCCTGGGAGAACCACCATTAATCTGAATGTGCCCGCTGCGAGCCCTGTGATGAGAGGCC 240
Db 614 GCCTGGGAGAACCACCATTAATCTGAATGTGCCCGCTGCGAGCCCTGTGATGAGAGGCC 673
OY 241 TCCCAAGGTGGCGCTGGAGACTGTTCAGCAGTGGCCGACACCCGCTGTGGCTGTAAGCCA 300
Db 674 TCCCAAGGTGGCGCTGGAGACTGTTCAGCAGTGGCCGACACCCGCTGTGGCTGTAAGCCA 733
OY 301 GCGTGGTTTGTGAGTGGCCAGGTTCAGCCAATGTGTCAAGCAGTTCAACCTTCTACTGCCAA 360
Db 734 GCGTGGTTTGTGAGTGGCCAGGTTCAGCCAATGTGTCAAGCAGTTCAACCTTCTACTGCCAA 793
OY 361 CCATGCTAGACTGCGGGGCTGCACCGCCACACAGCGGCTACTCTGTCCGCGAGAGAT 420
Db 794 CCATGCTAGACTGCGGGGCTGCACCGCCACACAGCGGCTACTCTGTCCGCGAGAGAT 853
OY 421 ACTGACTGTGGACCTGCTGCTGCTTCTATGAACATGGCGATGGCTGCTGCTGC 480
Db 854 ACTGACTGTGGACCTGCTGCTGCTTCTATGAACATGGCGATGGCTGCTGCTGC 913
OY 481 CCCACGAGCACCTGG 496
Db 914 CCCACGTAATTCTTAG 929

RESULT 14
US-10-081-280-2

Sequence 2, Application US/10081280
Patent No. US20020165157A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/081,280
FILING DATE: 21-Feb-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/829,270
FILING DATE: 31-Mar-1997
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5416
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 433 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-081-280-2

Query Match 63.2%; Score 350.6; DB 9; Length 433;
Best Local Similarity 96.4%; Pred. No. 1.9e-98;
Matches 400; Conservative 0; Mismatches 11; Indels 4; Gaps 4;

OY 1 CTGGGGGCCCCGGCCAGGGGGGCACTCGTAGCCCCAGGTGTGACTGTGCGGTGACTTC 60
Db 4 CTGGGGGCCCCGGCCAGNGCGGCACTGTAGCCCCAGGTGTGACTGTGCGGTGACTTC 63
OY 61 CACAAGAAGATTGCTGTTTGTTCAGAGAGGCTGCCAGCGGGGCACTACCTGAAGGC 119
Db 64 CACAAGAAGATTGCTGTTTGTTCAGAGAGGCTGCCAGCGGGGCACTACCTGAAGGC 123
OY 120 CCTTGCACGGAGCCCTGCGGCACTCCACCTGCTGTGTGTCCTCCCAAGACACCTTCTT 179
Db 124 CCTTGCACGGAGCCCTGC-GCAACTGCACCTGCTGTGTGTCCTCCCAAGACACCTTCTT 182
OY 180 GGCTGGGAGAACCACCATTAATCTGAATGTGCCCGCTGCGAGCCCTGTGATGAGCAGGC 239
Db 183 GGCTGGGAGAACCACCATTAATCTGAATGTGCCCGCTGCGAGCCCTGTGATGAGCAGGC 242
OY 240 CTCCAGGTGGCGCTGGAGACTGTTCAGCAGTGGCCGACACCCGCTGTGGCTGTAAGCC 299
Db 243 CTCCAGGTGGCGCTGGAGACTGTTCAGCAGTGGCCGACACCCGCTGTGGCTGTAAGCC 302
OY 300 AGCTGTTTGTGAGTGCCA-GGTCAAGCCAATGTGTACAGAG-TTCACCTTCTACTGC 357
Db 303 AGCTGTTTGTGAGTGCCAGAGGTTCAGCCAATGTGTACAGAGTTTCAACCTTCTAATGC 362
OY 358 CAACCATGCTAGACTGCGGGGCTGCACCGCCACACACAGCGGCTACTGTGCTCC 412
Db 363 CAACCATGCTAGACTGCGGGGCTGCACCGCCACACACAGCGGCTAATGTGTTCC 417

RESULT 15
US-10-112-793-2

; Sequence 2, Application US/10112793
; Publication No. US20020192729A1
; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 Inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/112,793
; FILING DATE: 28-Mar-2002
; CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/828,683A
; FILING DATE: 31-Mar-1997
; APPLICATION NUMBER: 08/625328
; FILING DATE: 1-Apr-1996
; APPLICATION NUMBER: 08/710802
; FILING DATE: 23-Sep-1996

ATTORNEY/AGENT INFORMATION:

; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1007P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 433 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-112-793-2

Query Match 63.2%; Score 350.6; DB 9; Length 433;

Best Local Similarity 96.4%; Pred. No. 1.9e-98;

Matches 400; Conservative 0; Mismatches 11; Indels 4; Gaps 4;

QY 1 CTGGGGCCCCGAGGCGGCGACTCGTACCCAGGTGTGACTGTGCGGCTGACTTC 60
DB 4 CTGGGGCCCCGAGGCGGCGACTCGTACCCAGGTGTGACTGTGCGGCTGACTTC 63
QY 61 CACAAGAAGATTGCTGTTTGTTCAGAGGCTGCCAGCGGGGC-CTACCTGAAGGC 119
DB 64 CACAAGAAGATTGCTGTTTGTTCAGAGGCTGCCAGCGGGGC-CTACCTGAAGGC 123
QY 120 CCCTTGACGAGCCCTGCGCACTCCACTGCTGTGTGCTCCCAAGACACTTCTT 179
DB 124 CCCTTGACGAGCCCTGCGCACTCCACTGCTGTGTGCTCCCAAGACACTTCTT 182
QY 180 GGCTGGGAGAACCATATATCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGC 239
DB 183 GGCTGGGAGAACCATATATCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGC 242
QY 240 CTCCAGGTGGCGCTGAGAACTGTTCAGCAGTGGCCGACACCCCGCTGTGCTGTAAGCC 299
DB 243 CTCCAGGTGGCGCTGAGAACTGTTCAGCAGTGGCCGACACCCCGCTGTGCTGTAAGCA 302

QY 300 AGGCTGTTTGTGAGTGCCA-GGTACGCCAATGTGTACAGAG-TTCACCCCTTCTACTGC 357
DB 303 GGGCTGTTTGTGAGTGCCAGGGTCAGCCCAATGTGTACAGAGTTTCACCCCTTCTAATGC 362
QY 358 CAACCATGCTAGACTGCGGGGGCCCTGCACCCGCCACACACAGGCTACTCTGTTC 412
DB 363 CAACCATGCTAGACTGCGGGGGCCCTGCACCCGCCACACACAGGCTAATNTGTTCC 417

Search completed: April 6, 2003, 16:30:18
Job time : 128 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 6, 2003, 14:24:03 ; Search time 54 Seconds
(without alignments)
3151.956 Million cell updates/sec

Title: US-09-993-234-9_COPY_146_700

Perfect score: 555
Sequence: 1 CTGGGGGGCCCCGGCCAGGG.....GGCAGATGTTCTGGGTCAG 555

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*

- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/PCRTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	555	100.0	1254	3	US-08-815-469-3	Sequence 3, Appli
2	555	100.0	1634	4	US-08-928-069-11	Sequence 11, Appli
3	555	100.0	1634	4	US-08-828-683A-9	Sequence 9, Appli
4	555	100.0	1783	3	US-08-815-469-1	Sequence 1, Appli
5	486.4	87.6	1438	4	US-08-928-069-5	Sequence 5, Appli
6	486.4	87.6	1438	4	US-08-828-683A-5	Sequence 2, Appli
7	350.6	63.2	433	4	US-08-928-069-2	Sequence 2, Appli
8	350.6	63.2	433	4	US-08-828-683A-2	Sequence 2, Appli
9	42.2	7.6	543	4	US-09-513-007-3	Sequence 3, Appli
10	42.2	7.6	2440	4	US-09-513-007-1	Sequence 1, Appli
11	37.6	6.8	28804	2	US-08-592-874-1	Sequence 1, Appli
12	37.6	6.8	28804	3	US-09-096-942-2	Sequence 2, Appli
13	37.6	6.8	28804	3	US-09-096-867-2	Sequence 2, Appli
14	37.4	6.7	1956	2	US-08-762-308-10	Sequence 10, Appli
15	35	6.3	1345	1	US-08-592-214A-7	Sequence 7, Appli
16	35	6.3	1345	3	US-08-659-188-7	Sequence 7, Appli
17	35	6.3	1345	3	US-08-655-227-7	Sequence 7, Appli
18	35	6.3	1345	3	US-08-655-241-7	Sequence 7, Appli
19	35	6.3	1345	3	US-09-149-976-7	Sequence 7, Appli
20	35	6.3	1345	4	US-09-398-326-7	Sequence 7, Appli
21	34.4	6.2	896	4	US-09-404-879A-22	Sequence 22, Appli
22	34.2	6.2	15664	1	US-08-402-282-3	Sequence 3, Appli
23	34.2	6.2	15664	1	US-08-508-004-3	Sequence 3, Appli
24	34.2	6.2	15664	1	US-08-402-066-3	Sequence 3, Appli
25	34.2	6.2	15664	1	US-08-402-068-3	Sequence 3, Appli
26	33.2	6.0	718	4	US-08-918-288-10	Sequence 10, Appli
27	33.2	6.0	718	4	US-09-282-357-10	Sequence 10, Appli

28	33.2	6.0	744	4	US-08-918-288-8	Sequence 8, Appli
29	33.2	6.0	744	4	US-09-282-357-8	Sequence 8, Appli
30	33	5.9	2240	4	US-09-221-017B-687	Sequence 687, App
31	31	5.6	1691	2	US-08-993-118-8	Sequence 8, Appli
32	31	5.6	1691	3	US-08-845-528C-8	Sequence 8, Appli
33	31	5.6	2419	1	US-07-807-043B-7	Sequence 7, Appli
34	31	5.6	2419	1	US-08-299-849B-7	Sequence 7, Appli
35	31	5.6	2419	2	US-08-142-368A-7	Sequence 7, Appli
36	31	5.6	2419	3	US-08-967-727-7	Sequence 7, Appli
37	31	5.6	2419	4	US-08-037-230D-7	Sequence 7, Appli
38	31	5.6	2420	1	US-08-465-167A-23	Sequence 23, Appli
39	31	5.6	2420	4	US-09-056-105-4	Sequence 4, Appli
40	31	5.6	2420	4	US-08-627-820-23	Sequence 23, Appli
41	31	5.6	5674	1	US-07-807-043B-8	Sequence 8, Appli
42	31	5.6	5674	1	US-08-190-411A-1	Sequence 1, Appli
43	31	5.6	5674	1	US-08-299-849B-8	Sequence 8, Appli
44	31	5.6	5674	2	US-08-560-024-1	Sequence 1, Appli
45	31	5.6	5674	2	US-08-142-368A-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-08-815-469-3
Sequence 3, Application US/08815469
Patent No. 6153402
GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang
APPLICANT: Ni, Jian
APPLICANT: Dixit, Vishva
APPLICANT: Gentz, Reiner L.
APPLICANT: Dillon, Patrick J.
TITLE OF INVENTION: Death Domain Containing Receptors
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/815,469
FILING DATE: HERewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: NO. 6153402 yet Assigned
FILING DATE: 06-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,711
FILING DATE: 17-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,285
FILING DATE: 12-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1254 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: both

MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1251
US-08-815-469-3

Query Match 100.0%; Score 555; DB 3; Length 1254;
Best Local Similarity 100.0%; Pred. No. 8.5e-148;
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGGGGCCCCGGCCAGGGGGGGGCGGCGACTGTAGCCCCAGGTGTGACTGTGCGCGTGAATTG 60
DB 58 CTGGGGGCCCCGGCCAGGGGGGGGCGGCGACTGTAGCCCCAGGTGTGACTGTGCGCGTGAATTG 117
QY 61 CACAGAAGATTGCTGTTTGTGTGAGAGGCTGCCAGCGGGGCGACTACCTGAAGGCC 120
DB 118 CACAGAAGATTGCTGTTTGTGTGAGAGGCTGCCAGCGGGGCGACTACCTGAAGGCC 177
QY 121 CCTGCACGAGCGCCCTGCGGCACTCCACCTGCTGTGTGCCCAAGACACTTCTTG 180
DB 178 CCTGCACGAGCGCCCTGCGGCACTCCACCTGCTGTGTGCCCAAGACACTTCTTG 237
QY 181 GCCTGGAGAACCACTAATTTCTGAATGTGCGCGCTGCCAGGCGCTGTGATGAGCAGGCC 240
DB 238 GCCTGGAGAACCACTAATTTCTGAATGTGCGCGCTGCCAGGCGCTGTGATGAGCAGGCC 297
QY 241 TCCAGAGTGGCGCTGGAGAACTGTTCAGACAGTGGCGGACACCGCGCTGTGCTGAAGCCA 300
DB 298 TCCAGAGTGGCGCTGGAGAACTGTTCAGACAGTGGCGGACACCGCGCTGTGCTGAAGCCA 357
QY 301 GGCTGTTTGTGAGTGCAGGTTCAGCCAAATGTGTGAGCAGTTTACCCCTTACTGCCAA 360
DB 358 GGCTGTTTGTGAGTGCAGGTTCAGCCAAATGTGTGAGCAGTTTACCCCTTACTGCCAA 417
QY 361 CCATGCTAGACTGCGGGGCGCTGCACCGCCACACAGCGCTACTCTGTGCCGAGAGAT 420
DB 418 CCATGCTAGACTGCGGGGCGCTGCACCGCCACACAGCGCTACTCTGTGCCGAGAGAT 477
QY 421 ACTGACTGTGGGACCTGCGCTGCTTCTATGAACATGGCGATGGCTGTCTCTGC 480
DB 478 ACTGACTGTGGGACCTGCGCTGCTTCTATGAACATGGCGATGGCTGTCTCTGC 537
QY 481 CCCACGAGCACTGGGGAGCTGTCCAGAGCGCTGTGCGGCTGTGTGGCTGGAGGCGAG 540
DB 538 CCCACGAGCACTGGGGAGCTGTCCAGAGCGCTGTGCGGCTGTGTGGCTGGAGGCGAG 597
QY 541 ATGTTCTGGGTCCAG 555
DB 598 ATGTTCTGGGTCCAG 612

RESULT 2

US-08-928-069-11
Sequence 11, Application US/08928069
Patent No. 6462176
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-3 POLYPEPTIDE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,069

FILING DATE: 11-Sep-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/026943
FILING DATE: 09/23/1996
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1052R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/952-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1634 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-928-069-11

Query Match 100.0%; Score 555; DB 4; Length 1634;
Best Local Similarity 100.0%; Pred. No. 9.3e-148;
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGGGGCCCCAGGGGGGGGCGGCGACTGTAGCCCCAGGTGTGACTGTGCGCGTGAATTG 60
DB 146 CTGGGGGCCCCAGGGGGGGGCGGCGACTGTAGCCCCAGGTGTGACTGTGCGCGTGAATTG 205
QY 61 CACAGAAGATTGCTGTTTGTGTGAGAGGCTGCCAGCGGGGCGACTACCTGAAGGCC 120
DB 206 CACAGAAGATTGCTGTTTGTGTGAGAGGCTGCCAGCGGGGCGACTACCTGAAGGCC 265
QY 121 CCTGCACGAGCGCCCTGCGGCACTCCACCTGCTGTGTGCCCAAGACACTTCTTG 180
DB 266 CCTGCACGAGCGCCCTGCGGCACTCCACCTGCTGTGTGCCCAAGACACTTCTTG 325
QY 181 GCCTGGAGAACCACTAATTTCTGAATGTGCGCGCTGCCAGGCGCTGTGATGAGCAGGCC 240
DB 326 GCCTGGAGAACCACTAATTTCTGAATGTGCGCGCTGCCAGGCGCTGTGATGAGCAGGCC 385
QY 241 TCCAGAGTGGCGCTGGAGAACTGTTCAGACAGTGGCGGACACCGCGCTGTGCTGAAGCCA 300
DB 386 TCCAGAGTGGCGCTGGAGAACTGTTCAGACAGTGGCGGACACCGCGCTGTGCTGAAGCCA 445
QY 301 GGCTGTTTGTGAGTGCAGGTTCAGCCAAATGTGTGAGCAGTTTACCCCTTACTGCCAA 360
DB 446 GGCTGTTTGTGAGTGCAGGTTCAGCCAAATGTGTGAGCAGTTTACCCCTTACTGCCAA 505
QY 361 CCATGCTAGACTGCGGGGCGCTGCACCGCCACACAGCGCTACTCTGTGCCGAGAGAT 420
DB 506 CCATGCTAGACTGCGGGGCGCTGCACCGCCACACAGCGCTACTCTGTGCCGAGAGAT 565
QY 421 ACTGACTGTGGGACCTGCGCTGCTTCTATGAACATGGCGATGGCTGTCTCTGC 480
DB 566 ACTGACTGTGGGACCTGCGCTGCTTCTATGAACATGGCGATGGCTGTCTCTGC 625
QY 481 CCCACGAGCACTGGGGAGCTGTCCAGAGCGCTGTGCGGCTGTGTGGCTGGAGGCGAG 540
DB 626 CCCACGAGCACTGGGGAGCTGTCCAGAGCGCTGTGCGGCTGTGTGGCTGGAGGCGAG 685
QY 541 ATGTTCTGGGTCCAG 555
DB 686 ATGTTCTGGGTCCAG 700

RESULT 3

US-08-828-683A-9
Sequence 9, Application US/08828683A
Patent No. 6469144
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,683A
FILING DATE: 31-Mar-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/625328
FILING DATE: 1-Apr-1996
APPLICATION NUMBER: 08/710802
FILING DATE: 23-Sep-1996
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1634 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-08-828-683A-9
Query Match 100.0%; Score 555; DB 4; Length 1634;
Best Local Similarity 100.0%; Pred. No. 9.3e-148;
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGGGGCCCCGGCCAGGGCGGCGACTGTCAGCCCGAGGTGTGACTGTGCGGTGACTTC 60
DB 146 CTGGGGCCCCGGCCAGGGCGGCGACTGTCAGCCCGAGGTGTGACTGTGCGGTGACTTC 205
QY 61 CACAAGAGATGTGCTGTTTGTGTGACAGAGGCTGCCAGCGGGGCGACTACCTGAAGGCC 120
DB 206 CACAAGAGATGTGCTGTTTGTGTGACAGAGGCTGCCAGCGGGGCGACTACCTGAAGGCC 265
QY 121 CCTTGACGAGCCCTGCGGCACTCCACCCTGTGTGTGTCCCAAGACACCTTCTTG 180
DB 266 CCTTGACGAGCCCTGCGGCACTCCACCCTGTGTGTGTCCCAAGACACCTTCTTG 325
QY 181 GCCTGGAGAACCATATATTTGATGTGCGCGCTGCCAGGCGCTGTGATGACGAGGCC 240
DB 326 GCCTGGAGAACCATATATTTGATGTGCGCGCTGCCAGGCGCTGTGATGACGAGGCC 385
QY 241 TCCAGAGTGGCGTGGAGAACTGTTACAGAGTGGCGGACACCCGCTGTGGCTGAAGCCA 300
DB 386 TCCAGAGTGGCGTGGAGAACTGTTACAGAGTGGCGGACACCCGCTGTGGCTGAAGCCA 445
QY 301 GGCTGTTGTGAGTGCAGGTACAGCCATGTCTACAGAGTTCACCCCTTCTACTGCCAA 360
DB 446 GGCTGTTGTGAGTGCAGGTACAGCCATGTCTACAGAGTTCACCCCTTCTACTGCCAA 505
QY 361 CCATGCTAGACTGCGGGGGCGCTGCACCGCCACACACGCGCTACTCTGTCCCGACAGAGAT 420
DB 506 CCATGCTAGACTGCGGGGGCGCTGCACCGCCACACACGCGCTACTCTGTCCCGACAGAGAT 565
QY 421 ACTGACTGTGGGACTGCTGCTGCTGCTTCTATGAACATGGCGATGGCTGCTCCTGC 480
DB 566 ACTGACTGTGGGACTGCTGCTGCTGCTTCTATGAACATGGCGATGGCTGCTCCTGC 625

QY 481 CCCACGAGACCCCTGGGAGACTGTCCAGAGCGCCTGTGCCCTGTCTGTGGCTGAGAGCAG 540
DB 626 CCCACGAGACCCCTGGGAGACTGTCCAGAGCGCCTGTGCCCTGTCTGTGGCTGAGAGCAG 685
QY 541 ATGTTCTGGGTCCAG 555
DB 686 ATGTTCTGGGTCCAG 700
RESULT 4
US-08-815-469-1
Sequence 1, Application US/08815469
Patent No. 6153402
GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang
APPLICANT: Ni, Jian
APPLICANT: Dixit, Vishva
APPLICANT: Gentz, Reiner L.
APPLICANT: Dillon, Patrick J.
TITLE OF INVENTION: Death Domain Containing Receptors
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/815,469
FILING DATE: HEREWITH
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: No. 6153402 yet Assigned
FILING DATE: 06-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,711
FILING DATE: 17-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,285
FILING DATE: 12-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1783 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 198..1481
US-08-815-469-1
Query Match 100.0%; Score 555; DB 3; Length 1783;
Best Local Similarity 100.0%; Pred. No. 9.6e-148;
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGGGGCCCCGGCCAGGGCGGCGACTGTCAGCCCGAGGTGTGACTGTGCGGTGACTTC 60
DB 288 CTGGGGCCCCGGCCAGGGCGGCGACTGTCAGCCCGAGGTGTGACTGTGCGGTGACTTC 347

QY	61	CACAGAGA	ATTTGGTCTGTTTGTGTCAGAGGCTGCCACGCGGGGCAC	TACTGAA	GCC	120
Db	348	CACAGAGA	ATTGGTCTGTTTGTGTCAGAGGCTGCCACGCGGGGCAC	TACTGAA	GCC	407
QY	121	CCTTGCAC	GGAGCCCTGCGGCAACTCCACCTGCCTTGTGTGTC	CCCCAAGACACTTCTTG		180
Db	408	CCTTGCAC	GGAGCCCTGCGGCAACTCCACCTGCCTTGTGTGTC	CCCCAAGACACTTCTTG		467
QY	181	GCCTGGGA	GAACCAACCATTAATTTGAAATGTGCCCCGCTG	CCAGGCTGTGATGACAGCC		240
Db	468	GCCTGGGA	GAACCAACCATTAATTTGAAATGTGCCCCGCTG	CCAGGCTGTGATGACAGCC		527
QY	241	TCCACGGT	GGCGCTGGAGAACTGTTACAGCAGTGGCCGACAC	CCCGCTGTGGCTGTAGCCA		300
Db	528	TCCACGGT	GGCGCTGGAGAACTGTTACAGCAGTGGCCGACAC	CCCGCTGTGGCTGTAGCCA		587
QY	301	GGCTGGTT	TGTGAGTGCACAGTTCAGCCAAATGTGTACAG	ATTACACCTTCTACTGCCAA		360
Db	588	GGCTGGTT	TGTGAGTGCACAGTTCAGCCAAATGTGTACAG	ATTACACCTTCTACTGCCAA		647
QY	361	CCATGCTT	AGACTGCGGGCCCTGCACCGCCACACACAGGCT	ACTCTGTGTCCCGCAGAGAT		420
Db	648	CCATGCTT	AGACTGCGGGCCCTGCACCGCCACACACAGGCT	ACTCTGTGTCCCGCAGAGAT		707
QY	421	ACTGACTG	TGGGACCTGCCCTGCCCTTCTATGAACATGG	CGATGGCTGCGTGCCTGC		480
Db	708	ACTGACTG	TGGGACCTGCCCTGCCCTTCTATGAACATGG	CGATGGCTGCGTGCCTGC		767
QY	481	CCCACGAG	CACCCCTGGGGAGCTGTCCAGAGCGCTGTGCC	GTCTGTGGCTGGAGGCAG		540
Db	768	CCCACGAG	CACCCCTGGGGAGCTGTCCAGAGCGCTGTGCC	GTCTGTGGCTGGAGGCAG		827
QY	541	ATGTTCT	GGGTCCAG	555		
Db	828	ATGTTCT	GGGTCCAG	842		

RESULT 5
 US-08-928-069-5
 Sequence 5, Application US/08928069
 Patent No. 6462176
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi J.
 TITLE OF INVENTION: Apo-3 POLYPEPTIDE
 NUMBER OF SEQUENCES: 15
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatIn (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/928, 069
 FILING DATE: 11-Sep-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/026943
 FILING DATE: 09/23/1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Mairschang, Diane L.
 REGISTRATION NUMBER: 35,600
 REFERENCE/DOCKET NUMBER: P1052R1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/225-5416
 TELEFAX: 650/952-9881
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:

```

; LENGTH: 1438 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
US-08-928-069-5

```

Query Match	87.68;	Score 486.4;	DB 4;	Length 1438;
Best Local Similarity	98.8%;	Pred. No. 2.2e-128;		
Matches 490;	Conservative 0;	Mismatches 6;	Indels 0;	Gaps 0;

QY	1	CTGGGGGGCCCCCAGGGCGGCACCTCGTAGCCCCAGGTGTGACTGTGCCGGTGACTTC	60
Db	434	CTGGGGGGCCCCCAGGGCGGCACCTCGTAGCCCCAGGTGTGACTGTGCCGGTGACTTC	4933
QY	61	CACAGAAGATTGGTCTGTTTGTGTGAGAGGCTGCCAGCGGGCACTACCTGAAGGCC	120
Db	494	CACAGAAGATTGGTCTGTTTGTGTGAGAGGCTGCCAGCGGGCACTACCTGAAGGCC	5533
QY	121	CCTTGCACGGAGCCCTGCGGCAACTCCACCTGCCTTGTGTGCCCAAGACACCTTCCTG	180
Db	554	CCTTGCACGGAGCCCTGCGGCAACTCCACCTGCCTTGTGTGCCCAAGACACCTTCCTG	6133
QY	181	GCCTGGGAGAACCAACCATTAATTCTGAATGTGCCCGCTGCCAGCCCTGTGATGAGAGGCC	240
Db	614	GCCTGGGAGAACCAACCATTAATTCTGAATGTGCCCGCTGCCAGCCCTGTGATGAGAGGCC	6733
QY	241	TCCCAGGTGGCGCTGGAGAACTGTTCAGCAGTGGCCGACACCCCGCTGTGCTGTAAGCCA	300
Db	674	TCCCAGGTGGCGCTGGAGAACTGTTCAGCAGTGGCCGACACCCCGCTGTGCTGTAAGCCA	7333
QY	301	GGCTGTTTGTGAGTGCACAGTTCAGCCATGTGTACAGCAGTTCACCCCTTCTACTGCCAA	360
Db	734	GGCTGTTTGTGAGTGCACAGTTCAGCCATGTGTACAGCAGTTCACCCCTTCTACTGCCAA	7933
QY	361	CCATGCTTAGACTGCGGGGCCCTGCACCCGCCACACACCGGCTACTCTGTTCCCGCAAGAT	420
Db	794	CCATGCTTAGACTGCGGGGCCCTGCACCCGCCACACACCGGCTACTCTGTTCCCGCAAGAT	8533
QY	421	ACTGACTGTGGGACCTGCCTGCCTGCCTTCTATGAACATGGCGATGGCTGCCTGTCTGC	480
Db	854	ACTGACTGTGGGACCTGCCTGCCTGCCTTCTATGAACATGGCGATGGCTGCCTGTCTGC	9133
QY	481	CCCACGAGCACCCCTGG 496	
Db	914	CCCACGTAATTCCTAG 929	

RESULT 6
 US-08-828-683A-5
 ; Sequence 5, Application US/08828683A
 ; Patent No. 6469144
 ;
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: Ashkenazi, Avi J.
 ; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
 ; NUMBER OF SEQUENCES: 28
 ;
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 1 DNA way
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ;
 ; ZIP: 94080
 ;
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Winpatin (Genentech)
 ;
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/828,683A
 ; FILING DATE: 31-Mar-1997
 ; CLASSIFICATION: <Unknown>
 ;
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/625328

FILING DATE: 1-Apr-1996
APPLICATION NUMBER: 08/710802
FILING DATE: 23-Sep-1996
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1438 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-08-828-683A-5

Query Match 87.6%; Score 486.4; DB 4; Length 1438;
Best Local Similarity 98.8%; Pred. No. 2.2e-128;
Matches 490; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CTGGGGCCCCGGCCAGGGGGGCGACCTGTAAGCCAGGTGTGACTGTGCCGGTGAATTC 60
DB 434 CTGGGGCCCCGGCCAGGGGGGCGACCTGTAAGCCAGGTGTGACTGTGCCGGTGAATTC 493
QY 61 CACAAGAGATGTGCTGTTTGTGTGACAGAGGCTGCCAGCGGGGCGACTACCTGAAGGCC 120
DB 494 CACAAGAGATGTGCTGTTTGTGTGACAGAGGCTGCCAGCGGGGCGACTACCTGAAGGCC 553
QY 121 CCTTGACGAGCCCTGCGGCACTCCACCCTGCTGTGTGTCCCAAGACACTTCTTG 180
DB 554 CCTTGACGAGCCCTGCGGCACTCCACCCTGCTGTGTGTCCCAAGACACTTCTTG 613
QY 181 GCCTGGAGAACCATTAATTTGAAATGTCGCCCTGCCAGCGCTGTGATGAGCAGGCC 240
DB 614 GCCTGGAGAACCATTAATTTGAAATGTCGCCCTGCCAGCGCTGTGATGAGCAGGCC 673
QY 241 TCCAGAGTGGCGGTGAGAACTGTTTCAAGAGTGGCCGACACCCGCTGTGGCTTAAGCCA 300
DB 674 TCCAGAGTGGCGGTGAGAACTGTTTCAAGAGTGGCCGACACCCGCTGTGGCTTAAGCCA 733
QY 301 GGCTGTTTGTGAGTGCAGGTCAAGCAATGTGTACAGAGTTCACCCCTTCTACTGCCAA 360
DB 734 GGCTGTTTGTGAGTGCAGGTCAAGCAATGTGTACAGAGTTCACCCCTTCTACTGCCAA 793
QY 361 CCATGCTAGACTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 420
DB 794 CCATGCTAGACTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 853
QY 421 ACTGACTGTGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
DB 854 ACTGACTGTGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 913
QY 481 CCCACGAGCACCCTGG 496
DB 914 CCCACGTAATTCCTAG 929

RESULT 7
US-08-928-069-2
Sequence 2, Application US/08928069
Patent No. 6462176
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-3 POLYPEPTIDE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California

COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,069
FILING DATE: 11-Sep-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/026943
FILING DATE: 09/23/1996
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1052R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 433 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-928-069-2

Query Match 63.2%; Score 350.6; DB 4; Length 433;
Best Local Similarity 96.4%; Pred. No. 3.6e-90;
Matches 400; Conservative 0; Mismatches 11; Indels 4; Gaps 4;

QY 1 CTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 60
DB 4 CTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 63
QY 61 CACAAGAGATGTGCTGTTTGTGTGACAGAGGCTGCCAGCGGGGCGACTACCTGAAGGC 119
DB 64 CACAAGAGATGTGCTGTTTGTGTGACAGAGGCTGCCAGCGGGGCGACTACCTGAAGGC 123
QY 120 CCCTTGACGAGCCCTGCGGCACTCCACCCTGCTGTGTGTCCCAAGACACTTCTT 179
DB 124 CCCTTGACGAGCCCTGCGGCACTCCACCCTGCTGTGTGTCCCAAGACACTTCTT 182
QY 180 GGCTGGAGAACCATTAATTTGAAATGTCGCCCTGCCAGCGCTGTGATGAGCAGGC 239
DB 183 GGCTGGAGAACCATTAATTTGAAATGTCGCCCTGCCAGCGCTGTGATGAGCAGGC 242
QY 240 CTCCAGGTGGCGGTGAGAACTGTTTCAAGAGTGGCCGACACCCGCTGTGGCTTAAGCC 299
DB 243 CTCCAGGTGGCGGTGAGAACTGTTTCAAGAGTGGCCGACACCCGCTGTGGCTTAAGCC 302
QY 300 AGCTGTTTGTGAGTGCAGGCA-GGTACAGCAATGTGTACAGAGTTCACCCCTTCTACTGC 357
DB 303 GGGCTGTTTGTGAGTGCAGGCAAGGTCAAGCAATGTGTACAGAGTTCACCCCTTCTACTGC 362
QY 358 CAACCATGCTAGACTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 412
DB 363 CAACCATGCTAGACTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 417

RESULT 8
US-08-828-683A-2
Sequence 2, Application US/08828683A
Patent No. 6469144
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way

```

: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Winpatin (Genentech)
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/828,683A
: FILING DATE: 31-Mar-1997
: CLASSIFICATION: <Unknown>
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/625328
: FILING DATE: 1-Apr-1996
: APPLICATION NUMBER: 08/710802
: FILING DATE: 23-Sep-1996
:
: ATTORNEY/AGENT INFORMATION:
: NAME: Marschang, Diane L.
: REGISTRATION NUMBER: 35,600
: REFERENCE/DOCKET NUMBER: P1007P1
:
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650/225-5416
: TELEFAX: 650/952-9881
:
: INFORMATION FOR SEQ ID NO: 2:
:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 433 base pairs
: TYPE: Nucleic Acid
: STRANDEDNESS: Single
: TOPOLOGY: Linear
:
: SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-08-828-683A-2

```

Query Match	63.2%;	Score 350.6;	DB 4;	Length 433;
Best Local Similarity	96.4%;	Pred. No. 3.6e-90;		
Matches 400;	Conservative 0;	Mismatches 11;	Indels 4;	Gaps 4;
QY 1	CTGGGGCCCCGGGGCCCCAGGGCGGCGCTGCTAGCCCCAGGTGTGACTGTGCCGGTGACTTC	60		
Db 4	CTGGGGCCCCGGGGCCAGNGCGCGCTGTAGCCCCAGGTGTGACTGTGCCGGTGACTTC	63		
QY 61	CACAGAAGATTGCTGTTTGTGTTCAGAGGCTGCCAGCGGGG-ACTACCTGAAGGC	119		
Db 64	CACAGAAGATTGCTGTTTGTGTTCAGAGGCTGCCAGCGGGGCACTACCTGAAGGC	123		
QY 120	CCCTTGCACGGAGCCCTGCGGCACTCCACCTGCCCTTGTGTGCCCAAGACACCTTCTT	179		
Db 124	CCCTTGCACGGAGCCCTGCG- GCAACTCCACCTGCCCTTGTGTGCCCAAGACACCTTCTT	182		
QY 180	GCGCTGGGAGAACCACCATATTTCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGC	239		
Db 183	GCGCTGGGAGAACCACCATATTTCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGC	242		
QY 240	CTCCAGGTGGCGCTGGAGAACTGTTACAGAGTGGCCGACACCCGCTGTGGCTGTAAAGCC	299		
Db 243	CTCCAGGTGGCGCTGGAGAACTGTTACAGAGTGGCCGACACCCGCTGTGGCTGTAAAGCA	302		
QY 300	AGGCTGCTTGTGAGTGCCTA-GTTCAGCCCAATGTGTACAGCA-TTCACCCCTTCTACTGC	357		
Db 303	GGGCTGCTTGTGAGTGCCTAAGGCTGTACAGCCCAATGTGTACAGCACTTTCACCCCTTCTAATGC	362		
QY 358	CAACCATGCCTAGACTGCGGGGGCCCTGCACCGCCACACACGGCTACTCTGTTCCC	412		
Db 363	CAACCATGCCTAGACTGCGGGGGCCCTGCACCGCCACACACGGCTAATNTGTTCCC	417		

RESULT 9
US-09-513-007-3
; Sequence 3, Application US/09513007
; Patent No. 6406907
; GENERAL INFORMATION:
; APPLICANT: Taylor, J. Michael

```

1  APPLICANT: Kehrlt, Jr., Marcus
2  APPLICANT: Lee, Eun-Kyung
3  APPLICANT: Mwangi, Simon
4  TITLE OF INVENTION: BOVINE TUMOR NECROSIS FACTOR RECEPTOR-1
5  TITLE OF INVENTION: AND METHODS OF USE
6  FILE REFERENCE: 08411-018001
7  CURRENT APPLICATION NUMBER: US/09/513,007
8  CURRENT FILING DATE: 2000-02-25
9  PRIOR APPLICATION NUMBER: 60/122,156
10 PRIOR FILING DATE: 1999-02-26
11 NUMBER OF SEQ ID NOS: 8
12 SOFTWARE: FastSeq for Windows Version 4.0
13 SEQ ID NO 3
14 LENGTH: 543
15 TYPE: DNA
16 ORGANISM: Bos taurus
17 FEATURE:
18 NAME/KEY: CDS
19 LOCATION: (1)...(543)
20 US-09-513-007-3

```

	Query Match	7.68;	Score 42.2;	DB 4;	Length 543;
	Best Local Similarity	50.28;	Pred. No. 0.0058;		
	Matches 132;	Conservative	0;	Mismatches 128;	Indels 3;
				Gaps	1;
QY	60 CCACAGAAGATTGCTCTGTTTGTTCAGAGGCTGCCAGCGGGCACTACCTGAAGGC	119			
Dp	63 CCACCCGCAAAATAGCACCATTTGCTGCACCAAGTGCCACAAAGTACTTATCTGTACAA	122			
QY	120 CCTTGCACGGAGCCCTGCGCAACTCCACCCTGCCTTGTGTGTCCCAAGACACCTTCTT	179			
Dp	123 TGACTGTCCGGGTCCAGGGCGAGACACGGACTGCAGGGGTGTGTGCCCTTGCCACCTACAC	182			
QY	180 GGCCTTGGAGAACCAACCATTAATTGCAATGTGCCCGCTGCCAGCGCTGTGATGAGCAGGC	239			
Dp	183 TGCCTTGGAGAACCATCTCAGACGATGCTCTGAGCTGCTCCAGGTGCCGGGACGAAATG--	240			
QY	240 CTCACAGGTGGCGCTGGAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGGCTGTAAGCC	299			
Dp	241 -TTCCAGGTGAGATTTCGCCCTGTGTAGTGAGACCGGAGACACTGTGTGCGGCTGCAGGAA	299			
QY	300 AGGCTGGTTTGTGAGTGCCAGG	322			
Dp	300 GAACCAAGTACCGGGAATACTGGG	322			

```

RESULT 10
US-09-513-007-1
; Sequence 1, Application us/09513007
; Patent No. 6406907
; GENERAL INFORMATION:
; APPLICANT: Taylor, J. Michael
; APPLICANT: Kehrl, Jr., Marcus
; APPLICANT: Lee, Eun-Kyung
; APPLICANT: Mwangi, Simon
; TITLE OF INVENTION: BOVINE TUMOR NECROSIS FACTOR RECEPTOR-1
; TITLE OF INVENTION: AND METHODS OF USE
; FILE REFERENCE: 08411-018001
; CURRENT APPLICATION NUMBER: US/09/513,007
; CURRENT FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 60/122,156
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2440
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (294)...(1706)
US-09-513-007-1

```


Query Match 7.6%; Score 42.2; DB 4; Length 2440;
Best Local Similarity 50.2%; Pred. No. 0.0095;
Matches 132; Conservative 0; Mismatches 128; Indels 3; Gaps 1;

```
OY 60 CCACAGAAGATTGCTGTTTGTGTCAGAGGCTGCCACAGCGGGGACACTACCTGAGGC 119
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 443 CCACCCGCAAAATAGCACCATTTGCTGCACCAAGTGCACAAAGGTACTATCTGTACAA 502
OY 120 CCCTTGACAGGAGCCCTGCGGCACTCCACCTGCTGTGTGTCCCAAGACACTTCTT 179
    || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 503 TGACTGTCCGGTCCAGGCGAGACACGAGCTGAGGTTGTGCCCTGACACTACAC 562
OY 180 GGCTTGAGAACACCAATATTTCTGATGTGCCCGCTGCCAGGCTGTGATGAGCAGC 239
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 563 TGCTTGAGAACCATCTCAGACGATGCTGAGCTGCTCCAGGTGCCGGAGCAATG-- 620
OY 240 CTCCAGGTGGCGCTGAGAACTGTACAGAGTGGCCGACACCCGCTGTGCTGTAGCC 299
    || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 621 -TTCCAGGTGAGATTTCCTTGTGTAGTGAGCCGGGACACTGTGTGCGGCTGCAGAA 679
OY 300 AGCTGTGTTGTGAGTGCACG 322
    || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 680 GAACCACTACCGGAAATCTGGG 702
```

RESULT 11

US-08-592-874-1/c
; Sequence 1, Application US/08592874
; Patent No. 5854034

GENERAL INFORMATION:

APPLICANT: POLLOCK, THOMAS J.
APPLICANT: YAMAZAKI, MOTOHIDE
APPLICANT: THORNE, LINDA
APPLICANT: MIKOLAJCZAK, MARCIA
APPLICANT: ARMENTROUT, RICHARD W.
TITLE OF INVENTION: DNA SEGMENTS AND METHODS FOR INCREASING
TITLE OF INVENTION: POLYSACCHARIDE PRODUCTION
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESSES:
ADDRESSEE: JULES E. GOLDBERG
STREET: 261 MADISON AVENUE
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10016-2391

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,874
FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/377,440

FILING DATE: 24-JAN-1995

ATTORNEY/AGENT INFORMATION:

NAME: GOLDBERG, JULES E.

REGISTRATION NUMBER: 24,408

TELEPHONE: 212-986-4090

TELEFAX: 212-818-9479

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 28804 base pairs

TYPE: nucleic acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: DNA (genomic)

FRAGMENT TYPE: N-terminal

US-08-592-874-1

Query Match 6.8%; Score 37.6; DB 2; Length 28804;
Best Local Similarity 57.8%; Pred. No. 0.42;
Matches 67; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

```
OY 209 GTGCCCGCTGCCAGGCTGTGATGACGAGCCCTCCAGGTGGCGCTGAGAACTGTTACG 268
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 7480 GTGCCGCTGGAGGCTTCATGAGAAATTTGTAACCTGTGTAACGGCGGTGCGGCCG 7421
OY 269 CAGTGGCCGACACCCGCTGTGCTGTAAAGCCAGGCTGTTGTGAGTGCAGTGC 324
    || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 7420 CGCTGGCCGCTCCGGATGTGGCAGCAAGCAAGCAAGCTGATTAAGGGCAGGTC 7365
```

RESULT 12

US-09-096-942-2/c
; Sequence 2, Application US/09096942
; Patent No. 6027925

GENERAL INFORMATION:

APPLICANT: Pollock, Thomas J
APPLICANT: Mikolajczak, Marcia
APPLICANT: Yamazaki, Motohide
APPLICANT: Thorne, Linda
APPLICANT: Armentrout, Richard W
TITLE OF INVENTION: Production of Xanthan Gum by *Sphingomonas Bacteria*
TITLE OF INVENTION: Carrying Genes from *Xanthomonas Campestris*
FILE REFERENCE: seq list for appl filed from pro. appl
CURRENT APPLICATION NUMBER: US/09/096,942
EARLIER FILING DATE: 1998-06-12
EARLIER APPLICATION NUMBER: 60/049,428
EARLIER FILING DATE: 1997-06-12
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 28804
TYPE: DNA
ORGANISM: *Sphingomonas sp.* S88

US-09-096-942-2

Query Match 6.8%; Score 37.6; DB 3; Length 28804;
Best Local Similarity 57.8%; Pred. No. 0.42;
Matches 67; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

```
OY 209 GTGCCCGCTGCCAGGCTGTGATGACGAGCCCTCCAGGTGGCGCTGAGAACTGTTACG 268
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 7480 GTGCCGCTGGAGGCTTCATGAGAAATTTGTAACCTGTGTAACGGCGGTGCGGCCG 7421
OY 269 CAGTGGCCGACACCCGCTGTGCTGTAAAGCCAGGCTGTTGTGAGTGCAGTGC 324
    || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 7420 CGCTGGCCGCTCCGGATGTGGCAGCAAGCAAGCAAGCTGATTAAGGGCAGGTC 7365
```

RESULT 13

US-09-096-867-2/c
; Sequence 2, Application US/09096867
; Patent No. 6030817

GENERAL INFORMATION:

APPLICANT: Pollock, Thomas J
APPLICANT: Mikolajczak, Marcia
APPLICANT: Yamazaki, Motohide
APPLICANT: Thorne, Linda
APPLICANT: Armentrout, Richard W
TITLE OF INVENTION: Production of Xanthan Gum by *Sphingomonas Bacteria*
TITLE OF INVENTION: Carrying Genes from *Xanthomonas Campestris*
FILE REFERENCE: seq list for appl filed from pro. appl
CURRENT APPLICATION NUMBER: US/09/096,867
EARLIER FILING DATE: 1998-06-11
EARLIER APPLICATION NUMBER: 60/049,428
EARLIER FILING DATE: 1997-06-12
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 28804
TYPE: DNA

US-09-096-867-2

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 6, 2003, 13:28:53 ; Search time 236 Seconds
(without alignments)
5296.013 Million cell updates/sec

Title: US-09-993-234-9_COPY_146_700

Perfect score: 555
Sequence: 1 CTGGGGGGCCCCGGCCAGGG.....GGCAGATGTCTGGTCCAG 555

Scoring table: IDENTITY_NTC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 segs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_101002:*

1: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
8: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
9: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
11: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	555	100.0	1254	18	AAT89427	Death domain conta
2	555	100.0	1254	20	AAK00925	Death domain conta
3	555	100.0	1254	21	AAC68777	Human death domain
4	555	100.0	1634	18	AAT91180	Human apoptosis pr
5	555	100.0	1634	22	AAH27782	Human genomic DNA
6	555	100.0	1634	24	AAI47186	Human rheumatoid a
7	555	100.0	1662	22	AAC91477	Human PRO779 cDNA.
8	555	100.0	1662	24	ABK40265	cDNA encoding huma
9	555	100.0	1783	18	AAT89426	Death domain conta

10	555	100.0	1783	20	AAK00924	Death domain conta
11	555	100.0	1783	21	AAK68776	Human death domain
12	555	100.0	1847	19	AAV28700	Human apoptosis in
13	541	97.5	1743	24	ABL64119	Breast cancer rela
14	531	95.7	1250	22	AAF83770	Nucleotide sequenc
15	486.4	87.6	787	24	AAI47187	Human rheumatoid a
16	486.4	87.6	816	24	ABL67258	Thyroid cancer rel
17	486.4	87.6	1438	18	AAT91179	Human apoptosis pr
18	244.2	44.0	1251	19	AAV28701	Mouse apoptosis in
19	171	30.8	4825	24	AAI47185	Human DR3 gene ass
20	171	30.8	10797	23	ABK42690	Genomic sequence #
21	60	10.8	60	24	ABN40521	Human spliced tran
22	49.4	8.9	51	22	AAI26809	Human SNP oligonuc
23	38	6.8	2130	24	ABK63694	Human SNP oligonuc
24	37.6	6.8	1036	21	AAA98136	Rat sequence diffe
25	37.6	6.8	28804	17	AAT37329	Human differentiat
26	37.6	6.8	28804	18	AAT92474	Sphingnan biosynthe
27	37.6	6.8	28804	20	AAV99812	Sphingomonas genus
28	37.6	6.8	28804	20	AAV81474	Sphingomonas 588 s
29	37.4	6.7	5870	21	AAA15044	Chromosomal fragme
30	36.4	6.6	301	22	AAF79973	Nucleotide sequenc
31	35.6	6.4	1542	22	AAK85141	Nucleotide sequenc
32	35	6.3	1342	18	AAT99437	Human immune/haema
33	35	6.3	1345	19	AAV58307	Maize floral meris
34	35	6.3	1345	19	AAT86631	Maize floral meris
35	35	6.3	1345	19	AAV02763	Zea mays A1 gene.
36	35	6.3	1345	19	AAV06021	APETALA1 gene from
37	35	6.3	1345	21	AAC61410	Maize floral meris
38	35	6.3	1345	21	AAZ57057	CDNA encoding a AP
39	35	6.3	1345	21	AAZ92144	Gene #2323 used to
40	34.8	6.3	1158	22	AAH22959	Human Tumor Endot
41	34.8	6.3	2173	11	AAQ06284	Corn APETALA1 (Apl
42	34.8	6.3	2568	17	AAT14891	Human phosphatase
43	34.8	6.3	4898	22	AAH81824	Rat Tumour Necrosi
44	34.8	6.3	4898	24	ABN95825	DNA encoding phosph
45	34.8	6.3	4898	24	ABL92096	Human differential

ALIGNMENTS

RESULT 1	
AAT89427	
ID AAT89427 standard; cDNA; 1254 BP.	
XX	
AC AAT89427;	
XX	
DT 02-MAR-1998 (first entry)	
XX	
DE Death domain containing receptor DR3 cDNA.	
XX	
KW Death domain containing receptor; DR3; human; apoptosis;	
KW Inflammation; NF-kappaB; ds.	
XX	
OS Homo sapiens.	
XX	
FH Key	Location/Qualifiers
FT sig_peptide	1..72
FT	/*tag= a
FT mat_peptide	73..1251
FT	/*tag= b
XX	
PN WO9733904-A1.	
XX	
PD 18-SEP-1997.	
XX	
PF 17-OCT-1996; 96WO-US16849.	
XX	
PR 12-MAR-1996; 96US-0013285.	
XX	
PA (HUMA-) HUMAN GENOME SCI INC.	
PA (UNMI) UNIV MICHIGAN.	
XX	

PI. Dillon PJ, Dixit VM, Gentz RL, Ni J, Yu G;
XX
DR WPI; 1997-470812/43.
DR P-PSDB; AAW31517.

XX Death domain containing receptor polypeptide(s) DR3 and DR3-V1 -
PT for activation of apoptosis and NF-kappaB, antagonists can be used
PT to treat inflammatory diseases

XX Claim 6; Page 75-77; 108pp; English.

CC This cDNA clone codes for human death domain containing receptor
CC DR3 (see AAW31517), a novel member of the tumour necrosis factor
CC receptor family. It was isolated from a HUVEC cDNA library.
CC Related death domain containing receptor DR3-V1 cDNA (see AAT89426)
CC was isolated from a human testis tumour cDNA library. The genes
CC have also been identified in cDNA libraries of foetal liver,
CC foetal brain, tonsil and leukocyte. Nucleic acids encoding full-
CC length or mature DR3, or the extracellular, transmembrane,
CC intracellular or especially the death domain of DR3, can be used to
CC produce recombinant polypeptides in transformed host cells. These
CC polypeptides can be used to treat diseases and disorders associated
CC with the inhibition of apoptosis. Antagonists can be used to treat
CC diseases and disorders associated with increased apoptosis and for
CC treating inflammatory diseases and disorders.

XX Sequence 1254 BP; 201 A; 420 C; 407 G; 226 T; 0 other;

Query Match 100.0%; Score 555; DB 18; Length 1254;
Best Local Similarity 100.0%; Pred. No. 2.7e-144;
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGGGCCCCGGCCAGGGCGGCACTGTCAGCCCCAGGTGACTGTGCCGGTGACTTC 60
Db 58 CTGGGGCCCCGGCCAGGGCGGCACTGTCAGCCCCAGGTGACTGTGCCGGTGACTTC 117
QY 61 CACAAGAGATTGGTCTGTTTGTGACAGAGGCTGCCAGCGGGGCACTACCTGAAGGCC 120
Db 118 CACAAGAGATTGGTCTGTTTGTGACAGAGGCTGCCAGCGGGGCACTACCTGAAGGCC 177
QY 121 CCTGCACGGAGCCCTCGGCACTCCACTGCTGTGTGTCTCCCAAGACACCTTCTTG 180
Db 178 CCTGCACGGAGCCCTCGGCACTCCACTGCTGTGTGTCTCCCAAGACACCTTCTTG 237
QY 181 GCCTGGGGAACCAACCATTAATTTGAAATGTGCCCCGCTGCCAGGCTGTGATGAGCAGGCC 240
Db 238 GCCTGGGGAACCAACCATTAATTTGAAATGTGCCCCGCTGCCAGGCTGTGATGAGCAGGCC 297
QY 241 TCCCAAGTGGCGCTGGAGAACTGTTCAAGCAGTGGCGGACACCCGCTGTGGCTGAAGCCA 300
Db 298 TCCCAAGTGGCGCTGGAGAACTGTTCAAGCAGTGGCGGACACCCGCTGTGGCTGAAGCCA 357
QY 301 GGCTGGTTGTGAGTGCCAGGTGACCCAAATGTGTACAGAGTTCAACCCTTCTACTGCCAA 360
Db 358 GGCTGGTTGTGAGTGCCAGGTGACCCAAATGTGTACAGAGTTCAACCCTTCTACTGCCAA 417
QY 361 CCATGCTAGACTGCGGGGCCCTGACCGCCACACACGCGTACTGTGTCCCGCAGAGAT 420
Db 418 CCATGCTAGACTGCGGGGCCCTGACCGCCACACACGCGTACTGTGTCCCGCAGAGAT 477
QY 421 ACTGACTGTGGGACCTGCTGCTGCTTCTATGAACATGGCGATGGCTGCGTCTCTGC 480
Db 478 ACTGACTGTGGGACCTGCTGCTGCTTCTATGAACATGGCGATGGCTGCGTCTCTGC 537
QY 481 CCCACGAGACCCCTGGGAGCTGTCCAGAGCGCTGTGCCGCTGTGGCTGAGGAGCAG 540
Db 538 CCCACGAGACCCCTGGGAGCTGTCCAGAGCGCTGTGCCGCTGTGGCTGAGGAGCAG 597
QY 541 ATGTTCTGGGCTCCAG 555
Db 598 ATGTTCTGGGCTCCAG 612

RESULT 2
AAAX00925
ID AAX00925 standard; cDNA; 1254 BP.

XX
AC AAX00925;
XX

DT 25-MAR-1999 (first entry)

XX Death domain containing receptor polypeptide (DR3) encoding cDNA.

XX Death domain; receptor; DR3-V1; DR3; recombinant; ds.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..1254

FT sig_peptide /product= "Death domain containing receptor DR3"

FT mat_peptide /tag= b

FT /tag= c

PN JP11000170-A.

XX 06-JAN-1999.

XX 12-MAR-1997; 97JP-0057503.

XX 06-FEB-1997; 97US-0037341.

XX 12-MAR-1996; 96US-0013285.

XX 17-OCT-1996; 96US-0028711.

XX (HUMA-) HUMAN GENOME SCI INC.

XX (UNMI) UNIV MICHIGAN.

XX WPI; 1999-124390/11.

XX P-PSDB; AAW95538.

XX New death domain containing receptor and recombinant vector -
optionally comprising leader sequence

XX Claim 6; Fig 3; 50pp; Japanese.

CC The invention provides nucleotide sequences encoding death domain
CC containing receptor polypeptides DR3-V1 and DR3. The DR3-V1 cDNA clone
CC is contained in ATCC deposition No. 97456 and the DR3 cDNA clone is
CC contained in ATCC deposition No. 97757. Recombinant vectors comprising
CC the nucleic acid sequences and optionally the leader sequences are
CC used for the recombinant production of the proteins. The present
CC sequence represents a cDNA encoding the death domain containing
CC receptor polypeptide (DR3).

XX Sequence 1254 BP; 201 A; 420 C; 407 G; 226 T; 0 other;

Query Match 100.0%; Score 555; DB 20; Length 1254;
Best Local Similarity 100.0%; Pred. No. 2.7e-144;
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGGGCCCCGGCCAGGGCGGCACTGTCAGCCCCAGGTGACTGTGCCGGTGACTTC 60
Db 58 CTGGGGCCCCGGCCAGGGCGGCACTGTCAGCCCCAGGTGACTGTGCCGGTGACTTC 117
QY 61 CACAAGAGATTGGTCTGTTTGTGACAGAGGCTGCCAGCGGGGCACTACCTGAAGGCC 120
Db 118 CACAAGAGATTGGTCTGTTTGTGACAGAGGCTGCCAGCGGGGCACTACCTGAAGGCC 177
QY 121 CCTGCACGGAGCCCTCGGCACTCCACTGCTGTGTGTCTCCCAAGACACCTTCTTG 180
Db 178 CCTGCACGGAGCCCTCGGCACTCCACTGCTGTGTGTCTCCCAAGACACCTTCTTG 237
QY 181 GCCTGGGGAACCAACCATTAATTTGAAATGTGCCCCGCTGCCAGGCTGTGATGAGCAGGCC 240

FT		/tag= b
FT	/note= "determined by hydrophathy analysis"	
FT	161..1339	
FT	/tag= c	
XX		
PN	W09737020-A1.	
PD		
XX	09-OCT-1997.	
XX		
PF	31-MAR-1997; 97WO-US05230.	
XX		
PR	23-SEP-1996; 96US-0710802.	
XX	01-APR-1996; 96US-0625328.	
PA	(GETH) GENENTECH INC.	
XX		
PI	Ashkenazi AJ;	
XX		
DR	WPI; 1997-503105/46.	
PT	Polypeptide(s) Apo-3 and Apo-2LI - useful for regulating apoptosis	
PT	in mammalian cells	
XX		
PS	Example 1; Page 45-46; 70pp; English.	
XX		
CC	CDNA clone FH20.57 (ATCC 55820) codes for a novel polypeptide (see	
CC	W26709), designated Apo-3, that stimulates or induces apoptotic	
CC	activity in mammalian cells. It was isolated from a human foetal	
CC	heart cDNA library by screening with probes (see T91183-84) based	
CC	on an EST sequence (GenBank locus W71984) that showed homology to	
CC	the intracellular domain of human TNFR1 and CD95. Amino acid	
CC	residues 1-181 of Apo-3 are identical to another novel apoptosis	
CC	polypeptide, Apo-2LI (see W26708). Nucleic acids encoding Apo-3	
CC	can be used diagnostically for tissue-specific typing and to	
CC	produce recombinant Apo-3 polypeptides, especially the	
CC	extracellular domain (amino acids 1-198) or death domain (amino	
CC	acids 338-417). Apo-3 can be used to induce apoptosis or	
CC	NF-kappa-N- or JNK-mediated gene expression for therapeutic	
CC	purposes. Non-human transgenic animals containing cells that	
CC	express Apo-3 nucleic acid, and knockout animals containing	
CC	cells that have an altered Apo-3 gene, can be used in drug	
CC	screening and development.	
XX		
SQ	Sequence 1634 BP; 300 A; 528 C; 519 G; 287 T; 0 other;	
	Query Match 100.0%; Score 555; DB 18; Length 1634;	
	Best Local Similarity 100.0%; Pred. No. 2.9e-144;	
	Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	1 CTGGGGGCCCCCGGCCAGGGCGGCACACTGTAGCCCCCAGGTGTGACTGTGCCGGTGACTTC	60
DB		
	146 CTGGGGGGCCCCCGGCCAGGGCGGCACACTGTAGCCCCCAGGTGTGACTGTGCCGGTGACTTC	205
OY	61 CACAAGAAGATTGCTGTCTTTTGTGTGAGAGGCTGCCAGCGGGGCACTACCTGAAGGCC	120
DB		
	206 CACAAGAAGATTGCTGTCTTTTGTGTGAGAGGCTGCCAGCGGGGCACTACCTGAAGGCC	265
OY	121 CCTTGACGAGAGCCCTGCGGGCAACTCCACCCTGCTGTGTGTCTCCCAAGACACACCTTCTTG	180
DB		
	266 CCTTGACGAGAGCCCTGCGGGCAACTCCACCCTGCTGTGTGTCTCCCAAGACACACCTTCTTG	325
OY	181 GCCTGGAGAACCAACCATTAATTTCTGAATGTGCCCGCTGCCAGGCTGTGATGACAGGCC	240
DB		
	326 GCCTGGAGAACCAACCATTAATTTCTGAATGTGCCCGCTGCCAGGCTGTGATGACAGGCC	385
OY	241 TCCCAGGTGGCGCTGAGAACTGTTACAGAGTGGCCGACACCCGCTGTGGCTGTAAGCCA	300
DB		
	386 TCCCAGGTGGCGCTGAGAACTGTTACAGAGTGGCCGACACCCGCTGTGGCTGTAAGCCA	445
OY	301 GGCTGTTTGTGGAGTGCACAGGTCAGCCAATGTGTACAGAGTTCACCCCTTCTACTGCCAA	360
DB		
	446 GGCTGTTTGTGGAGTGCACAGGTCAGCCAATGTGTACAGAGTTCACCCCTTCTACTGCCAA	505

QY	361 CCATGCGCTAGACTGGCGGGGCCCTGCACCGCCACACAGGCTACTGTGTTCCCGCAGAGAT	420
Db	506 CCAATGCGCTAGACTGGCGGGGCCCTGCACCGCCACACAGGCTACTGTGTTCCCGCAGAGAT	565
QY	421 ACTGACTGTGGGACCTGCCTGCCTGGCTTCTAATGAACATGGCGATGGCTGCCGTGTCCTGC	480
Db	566 ACTGACTGTGGGACCTGCCTGCCTGGCTTCTAATGAACATGGCGATGGCTGCCGTGTCCTGC	625
QY	481 CCCACGAGCACCCCTGGGGAGCTGTCCAGAGCGCTGTGCCGCTGTCTGTGGCTGGAGGCGAG	540
Db	626 CCCACGAGCACCCCTGGGGAGCTGTCCAGAGCGCTGTGCCGCTGTCTGTGGCTGGAGGCGAG	685
QY	541 ATGTCTGGGTCCAG	555
Db	686 ATGTCTGGGTCCAG	700

RESULT	5
AAH27782	
ID	AAH27782 standard; DNA; 1634 BP
XX	
AC	AAH27782;
XX	
DT	15-AUG-2001 (first entry)

DE Human genomic DNA encoding a rheumatoid arthritis associated protein.
XX
KW Rheumatoid arthritis; transmembrane protein; human; ds.
XX
OS Homo sapiens.

	Key	Location/Qualifiers
FH	CDS	89..1342
FT		/*tag= a
FT		/product= "Rheumatoid arthritis associated protein"
XX		
PN	WO200132921-A2.	

PD 10-MAY-2001.
XX
PF 01-NOV-2000; 2000WO-JP07690
XX
PR 01-NOV-1999; 99JP-0310805.
XX
PA (SHIO/) SHIOZAWA S.
XX
PI Shiozawa S, Konishi Y;
XX
DR WPI; 2001-308750/32.
P-PSDB; AAB97370.

PT Diagnosing rheumatoid arthritis by probing digested human genomic DNA
PT or comparing expression of mRNA or polypeptide of a region of
PT transmembrane protein -
XX
PS Claim 1; Page 14-18; 21pp; Japanese.

CC This invention relates to a method of diagnosing chronic rheumatoid
CC arthritis by digesting human genomic DNA with EcoRI and hybridising it
CC with a probe containing a fragment of the present sequence which
CC represents DNA encoding a transmembrane protein. The method is used for
CC the diagnosis of chronic rheumatoid arthritis, and for developing new
CC treatments.

```

SQ      Sequence 1634 BP; 300 A; 528 C; 519 G; 287 T; 0 other;
Query Match          100.0%; Score 555; DB 22; Length 1634;
Best Local Similarity 100.0%; Pred. No. 2.9e-144;
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 CTGGGGGCCCCCGGCCAGGGGGCCGACCTGTAGCCCCCAGGTGTGACTGTGCCGGTGACTTC 60
        |||||||
Db      146 CTGGGGGCCCCCGGCCAGGGGGCCGACCTGTAGCCCCCAGGTGTGACTGTGCCGGTGACTTC 205

```

OY 61 CACAAGAGATTGCTGTTTGTGTCAGAGGCTGCCAGCGGGGCACTACTGAGGCC 120
|||||
Db 206 CACAAGAGATTGCTGTTTGTGTCAGAGGCTGCCAGCGGGGCACTACTGAGGCC 265
OY 121 CCTTGACGAGAGCCCTGCGGCACTCCACCTGCTGTGTGCCCAAGACACTTCTTG 180
|||||
Db 266 CCTTGACGAGAGCCCTGCGGCACTCCACCTGCTGTGTGCCCAAGACACTTCTTG 325
OY 181 GCCTGGAGAACCATTAATTCGATGTGCCCGCTGCCAGGCTGTGATGAGAGGCC 240
|||||
Db 326 GCCTGGAGAACCATTAATTCGATGTGCCCGCTGCCAGGCTGTGATGAGAGGCC 385
OY 241 TCCCAGGTGGCGCTGAGAACTGTTCAAGCAGTGGCGGACACCCGCTGTGGCTGAAGCCA 300
|||||
Db 386 TCCCAGGTGGCGCTGAGAACTGTTCAAGCAGTGGCGGACACCCGCTGTGGCTGAAGCCA 445
OY 301 GGCTGTTTGTGAGTGCAGGTCCAGCAATGTGTCAGAGTTCAACCTTCTACTGCCAA 360
|||||
Db 446 GGCTGTTTGTGAGTGCAGGTCCAGCAATGTGTCAGAGTTCAACCTTCTACTGCCAA 505
OY 361 CCATGCTAGACTGCGGGCCCTGCACCGGCACACGCGCTACTCTGTGCCGAGAGAT 420
|||||
Db 506 CCATGCTAGACTGCGGGCCCTGCACCGGCACACGCGCTACTCTGTGCCGAGAGAT 565
OY 421 ACTGACTGTGGAGCTGCTGCTGCTTATGAACATGGCGATGGCTGCTGCTGC 480
|||||
Db 566 ACTGACTGTGGAGCTGCTGCTGCTTATGAACATGGCGATGGCTGCTGCTGC 625
OY 481 CCCACGAGACCCCTGGGAGCTGTCCAGAGCGCTGTGCCGCTGTGTGGCTGAGGCCAG 540
|||||
Db 626 CCCACGAGACCCCTGGGAGCTGTCCAGAGCGCTGTGCCGCTGTGTGGCTGAGGCCAG 685
OY 541 ATGTTCTGGGTCCAG 555
|||||
Db 686 ATGTTCTGGGTCCAG 700

RESULT 6
AAL47186
ID AAL47186 standard; cDNA: 1634 BP.
XX
AC AAL47186;
XX
DT 22-AUG-2002 (first entry)
XX
DE Human rheumatoid arthritis associated DR3 gene related cDNA #1.
XX
KW Human; DR3; rheumatoid arthritis; antirheumatic; antiarthritic;
KW gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 89..1342
FT /*tag= a
FT /product= "AA017879"

PN W0200234912-A1.
XX
PD 02-MAY-2002.
XX
PF 24-OCT-2001; 2001WO-JP09313.
XX
PR 24-OCT-2000; 2000JP-0324296.
PR 27-MAR-2001; 2001JP-0090546.
PR 30-MAR-2001; 2001JP-0099990.
XX
PA (NEWI-) NEW IND RES ORG.
PA (SHIO/) SHIOZAWA S.
XX
PI Shiozawa S, Konishi Y;
XX

DR WPI; 2002-417132/44.
DR P-PSDB; AA017879.
XX
PT Genomes, particularly DR3 genomic DNA, participating in rheumatoid
PT arthritis via mutation, useful in evaluating disease onset and its
PT possibility and providing therapy and remedies -
XX
PS Example 1; Page 66-69; 84pp; Japanese.
XX
CC The present invention relates to the human DR3 gene, which is associated
CC with rheumatoid arthritis. Certain mutations in the gene can be linked to
CC the disease. The sequences can be used to evaluate disease onset and its
CC possibility and to provide therapy and remedies. The present sequence is
CC a coding sequence described in the exemplification of the invention.
XX
SQ Sequence 1634 BP; 300 A; 528 C; 519 G; 287 T; 0 other;

Query Match 100.0%; Score 555; DB 24; Length 1634;
Best Local Similarity 100.0%; Pred. No. 2.9e-144;
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTGGGGGCCCCGGCCAGGGGGCACTCGTAGCCCCAGGTGTGACTGTGCCGTGACTTC 60
|||||
Db 146 CTGGGGGCCCCGGCCAGGGGGCACTCGTAGCCCCAGGTGTGACTGTGCCGTGACTTC 205
OY 61 CACAAGAGATTGCTGTTTGTGTCAGAGGCTGCCACCGGGGCACCTACTGAGGCC 120
|||||
Db 206 CACAAGAGATTGCTGTTTGTGTCAGAGGCTGCCACCGGGGCACCTACTGAGGCC 265
OY 121 CCTTGACGAGAGCCCTGCGGCACTCCACCTGCTGTGTGTGCCCAAGACACCTTCTTG 180
|||||
Db 266 CCTTGACGAGAGCCCTGCGGCACTCCACCTGCTGTGTGTGCCCAAGACACCTTCTTG 325
OY 181 GCCTGGAGAACCATTAATTCGATGTGCCCGCTGCCAGGCTGTGATGAGAGGCC 240
|||||
Db 326 GCCTGGAGAACCATTAATTCGATGTGCCCGCTGCCAGGCTGTGATGAGAGGCC 385
OY 241 TCCCAGGTGGCGCTGAGAACTGTTCAAGCAGTGGCGGACACCCGCTGTGCTGAAGCCA 300
|||||
Db 386 TCCCAGGTGGCGCTGAGAACTGTTCAAGCAGTGGCGGACACCCGCTGTGCTGAAGCCA 445
OY 301 GCCTGCTTGTGAGTGCAGGTCCAGCAATGTGTCAGAGTTCAACCTTCTACTGCCAA 360
|||||
Db 446 GCCTGCTTGTGAGTGCAGGTCCAGCAATGTGTCAGAGTTCAACCTTCTACTGCCAA 505
OY 361 CCATGCTAGACTGCGGGCCCTGCACCGGCACACAGGCTACTCTGTGCCGAGAGAT 420
|||||
Db 506 CCATGCTAGACTGCGGGCCCTGCACCGGCACACAGGCTACTCTGTGCCGAGAGAT 565
OY 421 ACTGACTGTGGAGCTGCTGCTGCTTATGAACATGGCGATGGCTGCTGCTGCC 480
|||||
Db 566 ACTGACTGTGGAGCTGCTGCTGCTTATGAACATGGCGATGGCTGCTGCTGCC 625
OY 481 CCCACGAGACCCCTGGGAGCTGTCCAGAGCGCTGTGCCGCTGTGTGGCTGAGGCCAG 540
|||||
Db 626 CCCACGAGACCCCTGGGAGCTGTCCAGAGCGCTGTGCCGCTGTGTGGCTGAGGCCAG 685
OY 541 ATGTTCTGGGTCCAG 555
|||||
Db 686 ATGTTCTGGGTCCAG 700

RESULT 7
AAC91477
ID AAC91477 standard; cDNA: 1662 BP.
XX
AC AAC91477;
XX
DT 21-MAR-2001 (first entry)
XX
DE Human PRO779 CDNA.
XX
KW Human; PRO; antinflammatory; dermatological; antiarthritic;

PF 11-FEB-2000; 2000WO-US03565.
XX 08-MAR-1999; 99WO-US05028.
PR 11-MAR-1999; 99US-123972P.
PR 11-MAY-1999; 99US-133459P.
PR 02-JUN-1999; 99WO-US12252.
PR 22-JUN-1999; 99US-140650P.
PR 22-JUN-1999; 99US-140653P.
PR 20-JUL-1999; 99US-144758P.
PR 26-JUL-1999; 99US-145698P.
PR 28-JUL-1999; 99US-146222P.
PR 17-AUG-1999; 99US-149395P.
PR 31-AUG-1999; 99US-151689P.
PR 01-SEP-1999; 99WO-US20111.
PR 15-SEP-1999; 99WO-US21090.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.
PR 05-JAN-2000; 2000WO-US00219.

XX (GETH) GENENTECH INC.

PI Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL, Hillan KJ;
PI Marsters SA, Pan J, Pittl RM, Roy MA, Smith V, Stone DM;
PI Watanabe CK, Wood WI;

DR WPI; 2002-205567/26.
DR P-PSDB; AAU86139.

XX Thirty five nucleic acids encoding PRO polypeptides, useful for
PT treating benign or malignant tumours, leukaemias and lymphoid
PT malignancies, inflammatory, angiogenic and immunologic disorders -

XX Claim 50; Fig 23; 302pp; English.

XX The present invention relates to the isolation of novel human PRO
CC polypeptides and the polynucleotide sequences encoding them. The
CC PRO polypeptides, agonists, antagonists or anti-PRO antibodies are
CC useful for treating benign or malignant tumours (e.g. renal, kidney,
CC bladder, breast, etc), leukaemias and lymphoid malignancies, other
CC disorders such as neuronal, glial, astrocytal, hypothalamic, glandular,
CC macrophagal, stromal and blastocoelec disorders, inflammatory, immune
CC and angiogenic disorders. The polynucleotide sequences are also
CC useful in gene therapy. ABK40254-ABK40288 encode for the human PRO
CC polypeptides of the invention.

SO Sequence 1662 BP; 302 A; 540 C; 531 G; 289 T; 0 other;

Query Match 100.0%; Score 555; DB 24; Length 1662;
Best Local Similarity 100.0%; Pred. NO. 2.9e-144;
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTGGGGGCGGGCCAGCGGCGCACTGAGCCCGAGGTGACTGTGCCGGTACTTC 60
Db 160 CTGGGGGCGGGCCAGCGGCGCACTGAGCCCGAGGTGACTGTGCCGGTACTTC 219
OY 61 CACAAGAAGATTGCTGTTTGTGAGAGGCTGCCAGCGGGGCACTACTGAAGCC 120
Db 220 CACAAGAAGATTGCTGTTTGTGAGAGGCTGCCAGCGGGGCACTACTGAAGCC 279
OY 121 CCTTGCACGAGCCCTGCGCACTCCACCTGCTTGTGTGTCCTCCCAAGACACCTTCTTG 180
Db 280 CCTTGCACGAGCCCTGCGCACTCCACCTGCTTGTGTGTCCTCCCAAGACACCTTCTTG 339
OY 181 GCCTGGGAGAACCATTAATTCGATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCC 240
Db 340 GCCTGGGAGAACCATTAATTCGATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCC 399
OY 241 TCCAGGTGGCGCTGGAGAACTGTTCAGCAGTGGCGGACACCGCTGTGGCTGAAGCCA 300
Db 400 TCCAGGTGGCGCTGGAGAACTGTTCAGCAGTGGCGGACACCGCTGTGGCTGAAGCCA 459
OY 301 GCCTGTTTGTGAGTGCACGAGGTCAAGCAATGTGTACAGCACTTACCCCTTACTGCCAA 360

Db 460 GGCCTGTTTGTGAGTGCACGAGGTCAAGCAATGTGTACAGCACTTACCCCTTACTGCCAA 519
OY 361 CCATGCCCTAGACTGCGGGGCGCTGCACCGCCACACACAGGCTACTCTGTCCCGCAGAGAT 420
Db 520 CCATGCCCTAGACTGCGGGGCGCTGCACCGCCACACACAGGCTACTCTGTCCCGCAGAGAT 579
OY 421 ACTGACTGTGGGACCTGCCCTGCCCTGCTTATGAACATGGCGATGGCTGCTCTGC 480
Db 580 ACTGACTGTGGGACCTGCCCTGCCCTGCTTATGAACATGGCGATGGCTGCTCTGC 639
OY 481 CCCACGACACCCCTGGGGAGCTGTCCAGAGCGGCTGTGCCGCTGTGTGGCTGAGGCAG 540
Db 640 CCCACGACACCCCTGGGGAGCTGTCCAGAGCGGCTGTGCCGCTGTGTGGCTGAGGCAG 699
OY 541 ATGTTCTGGGTCAG 555
Db 700 ATGTTCTGGGTCAG 714

RESULT 9

AAU89426

ID AAT89426 standard; cDNA; 1783 BP.

XX AAT89426;

DT 02-MAR-1998 (first entry)

DE Death domain containing receptor DR3-V1 cDNA.

KW Death domain containing receptor; DR3-V1; human; apoptosis;
KW inflammation; NF-kappaB; ds.

XX Homo sapiens.

XX Key location/Qualifiers

FT CDS 198..1484

FT sig_peptide /*tag= a

FT /*tag= b

FT mat_peptide 304..1481

FT /*tag= c

XX W09733904-A1.

PD 18-SEP-1997.

PF 17-OCT-1996; 96WO-US16849.

PR 12-MAR-1996; 96US-0013285.

PA (HUMA-) HUMAN GENOME SCI INC.

XX (UNMI) UNIV MICHIGAN.

PI Dillon PJ, Dixit VM, Gentz RL, Ni J, Yu G;

DR WPI; 1997-470812/43.

XX P-PSDB; AAW31516.

Death domain containing receptor polypeptide(s) DR3 and DR3-V1
PT for activation of apoptosis and NF-kappaB, antagonists can be used
PT to treat inflammatory diseases

PS Claim 2; Page 71-73; 108pp; English.

XX This cDNA clone, deposited as ATCC 97456, codes for human death
CC domain containing receptor DR3-V1 (see AAW31516), a novel member of
CC the tumour necrosis factor receptor family. It was isolated from a
CC cDNA library derived from cells of a human testis tumour. Related
CC death domain containing receptor DR3 cDNA (see AAT89427) was isolated
CC from a HUVBC cDNA library. The genes have also been identified in
CC cDNA libraries of foetal liver, foetal brain, tonsil and leukocyte.
CC Nucleic acids encoding full-length or mature DR3-V1 can be used to

CC produce recombinant polypeptides in transformed host cells. These
CC polypeptides can be used to treat diseases and disorders associated
CC with the inhibition of apoptosis. Antagonists, such as antibodies
CC raised against DR3-VI, can be used to treat diseases and disorders
CC associated with increased apoptosis and for treating inflammatory
CC diseases and disorders.

XX
SQ Sequence 1783 BP; 330 A; 562 C; 564 G; 327 T; 0 other;

Query Match 100.0%; Score 555; DB 18; Length 1783;
Best Local Similarity 100.0%; Pred. No. 3e-144;
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGGGGCCCCCGCCAGGGGGCGGCACTCGTAGCCCCAGGTGTGACTGTGCCGGTGAATTC 60
DB 288 CTGGGGGCCCCCGCCAGGGGGCGGCACTCGTAGCCCCAGGTGTGACTGTGCCGGTGAATTC 347
QY 61 CACAAGAGATTGCTGTTTGTGTGAGAGGCTGCCAGCGGGGCACTACTGAAGGCC 120
DB 348 CACAAGAGATTGCTGTTTGTGTGAGAGGCTGCCAGCGGGGCACTACTGAAGGCC 407
QY 121 CCTTGACGAGCGCTGCGGCACTCCACTCCTTGTGTGTCCCAAGACCTTCTTG 180
DB 408 CCTTGACGAGCGCTGCGGCACTCCACTCCTTGTGTGTCCCAAGACCTTCTTG 467
QY 181 GCCTGGAGAACCACTAATTTGAATGTGCCCGCTGCCAGGCTGTGATGAGAGGCC 240
DB 468 GCCTGGAGAACCACTAATTTGAATGTGCCCGCTGCCAGGCTGTGATGAGAGGCC 527
QY 241 TCCAGAGTGGCGGTGAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGGCTGTAAAGCCA 300
DB 528 TCCAGAGTGGCGGTGAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGGCTGTAAAGCCA 587
QY 301 GGCTGTTGTGAGAGTGCCAGGTGACCAATGTGTACAGAGTTACCCCTTCTACTGCCAA 360
DB 588 GGCTGTTGTGAGAGTGCCAGGTGACCAATGTGTACAGAGTTACCCCTTCTACTGCCAA 647
QY 361 CCATGCTTAGACTGCGGGGCGCTGCACCCGACACACAGGCTACTGTGTCCCGCAGAGAT 420
DB 648 CCATGCTTAGACTGCGGGGCGCTGCACCCGACACACAGGCTACTGTGTCCCGCAGAGAT 707
QY 421 ACTGACTGTGGGAACTGCTGCTGCTTCTATGAACATGGCGATGGCTGCTGCTGC 480
DB 708 ACTGACTGTGGGAACTGCTGCTGCTTCTATGAACATGGCGATGGCTGCTGCTGC 767
QY 481 CCCACGAGACCCCTGGGAGCTGTCCAGAGCGCTGTGCCGCTGTGTGGCTGAGGCGAG 540
DB 768 CCCACGAGACCCCTGGGAGCTGTCCAGAGCGCTGTGCCGCTGTGTGGCTGAGGCGAG 827
QY 541 ATGTTCTGGGTCAG 555
DB 828 ATGTTCTGGGTCAG 842

RESULT 10
AAAX00924
ID AAAX00924 standard; cDNA; 1783 BP.

XX
AC AAAX00924;
XX
DT 25-MAR-1999 (first entry)
XX
DE Death domain containing receptor polypeptide (DR3-VI) encoding cDNA.
XX
KW Death domain; receptor; DR3-VI; DR3; recombinant; ds.
XX
OS Homo sapiens.

XX
FH Key Location/Qualifiers
FT CDS 198..1484
FT /tag= a
FT /product= "Death domain containing receptor DR3-VI"
FT sig_peptide 198..300

FT /*tag= b
FT mat_peptide 301..1481
FT /*tag= c

PN JP11000170-A.

XX 06-JAN-1999.

XX 12-MAR-1997; 97JP-0057503.

XX 06-FEB-1997; 97US-0037341.

XX 12-MAR-1996; 96US-0013285.

XX 17-OCT-1996; 96US-0028711.

PA (HUMA-) HUMAN GENOME SCI INC.

PA (UNMI) UNIV MICHIGAN.

DR WPI; 1999-124390/11.

DR P-PSDB; AAW95537.

XX New death domain containing receptor and recombinant vector -
PT optionally comprising leader sequence

PS Claim 2; Fig 1, 2; 50pp; Japanese.

XX
CC The invention provides nucleotide sequences encoding death domain
CC containing receptor polypeptides DR3-VI and DR3. The DR3-VI cDNA clone
CC is contained in ATCC deposition No. 97456 and the DR3 cDNA clone is
CC contained in ATCC deposition No. 97757. Recombinant vectors comprising
CC the nucleic acid sequences and optionally the leader sequences are
CC used for the recombinant production of the proteins. The present
CC sequence represents a cDNA encoding the death domain containing
CC receptor polypeptide (DR3-VI).

SQ Sequence 1783 BP; 330 A; 562 C; 564 G; 327 T; 0 other;

Query Match 100.0%; Score 555; DB 20; Length 1783;
Best Local Similarity 100.0%; Pred. No. 3e-144;
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGGGGCCCCCGCCAGGGGGCGGCACTCGTAGCCCCAGGTGTGACTGTGCCGGTGAATTC 60
DB 288 CTGGGGGCCCCCGCCAGGGGGCGGCACTCGTAGCCCCAGGTGTGACTGTGCCGGTGAATTC 347
QY 61 CACAAGAGATTGCTGTTTGTGTGAGAGGCTGCCAGCGGGGCACTACTGAAGGCC 120
DB 348 CACAAGAGATTGCTGTTTGTGTGAGAGGCTGCCAGCGGGGCACTACTGAAGGCC 407
QY 121 CCTTGACGAGCGCTGCGGCACTCCACTGCTGTGTGTCCCAAGACACCTTCTTG 180
DB 408 CCTTGACGAGCGCTGCGGCACTCCACTGCTGTGTGTCCCAAGACACCTTCTTG 467
QY 181 GCCTGGAGAACCACTAATTTGAATGTGCCCGCTGCAGGGCTGTGATGAGCAGGCC 240
DB 468 GCCTGGAGAACCACTAATTTGAATGTGCCCGCTGCAGGGCTGTGATGAGCAGGCC 527
QY 241 TCCAGAGTGGCGGTGAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGGCTGTAAAGCCA 300
DB 528 TCCAGAGTGGCGGTGAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGGCTGTAAAGCCA 587
QY 301 GGCTGTTGTGAGAGTGCCAGGTTCACCAATGTGTACAGCAGTTACCCCTTCTACTGCCAA 360
DB 588 GGCTGTTGTGAGAGTGCCAGGTTCACCAATGTGTACAGCAGTTACCCCTTCTACTGCCAA 647
QY 361 CCATGCTTAGACTGCGGGGCGCTGCACCGGACACACAGGCTACTGTGTCCCGCAGAGAT 420
DB 648 CCATGCTTAGACTGCGGGGCGCTGCACCGGACACACAGGCTACTGTGTCCCGCAGAGAT 707
QY 421 ACTGACTGTGGGAACTGCTGCTGCTTCTATGAACATGGCGATGGCTGCTGTCCCTGC 480
DB 708 ACTGACTGTGGGAACTGCTGCTGCTTCTATGAACATGGCGATGGCTGCTGTCCCTGC 767
QY 481 CCCACGAGACCCCTGGGAGCTGTCCAGAGCGCTGTGCCGCTGTGTGGCTGAGGCGAG 540

|||||
Db 768 CCCACGACACCTGGGAGCTGTCAGAGCGCTGTGCCCTGTCTGTGGCTGAGGCAG 827
QY 541 ATGTTCTGGGTCAG 555
|||||
Db 828 ATGTTCTGGGTCAG 842
RESULT 11
AAC68776
ID AAC68776 standard; cDNA; 1783 BP.
XX AAC68776;
AC
XX 20-FEB-2001 (first entry)
DE Human death domain containing receptor DR3-V1 coding sequence.
XX
KW Human; death domain containing receptor; DR3-V1; cancer;
KW autoimmune disorder; inflammation; cardiovascular disorder; infection;
KW neurodegenerative disease; angiogenesis; ss.
XX
OS Homo sapiens.
XX WO200064465-A1.
PN
XX 02-NOV-2000.
PD
XX 21-APR-2000; 2000WO-US10741.
PF
XX 22-APR-1999; 99US-0130488.
PR 28-MAY-1999; 99US-0136741.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA (UNMI) UNIV MICHIGAN.
PA (YUGG/) YU G.
PA (NIJ/) NI J.
PA (GENT/) GENTZ R L.
PA (DILL/) DILLON P J.
PA (DIXI/) DIXIT V M.
XX
XX YU G, NI J, Gentz RL, Dillon PJ, Dixit VM;
PI
XX WPI: 2000-687263/67.
DR P-PSDB; AAB36264.
DR
XX
PT Treating graft-versus-host disease, cancer, immunodeficiency or an
PT autoimmune disease comprising administering an antibody to Death Domain
PT Containing Receptor proteins and a second therapeutic agent -
XX
XX Example 1; Fig 1; 273pp; English.
PS
XX The present invention provides the protein and coding sequences for two
CC death domain containing receptors, designated DR3 and DR3-V1. These
CC receptors are involved in apoptosis, and the sequences given can be used
CC in the treatment of cancers, infections, cardiovascular disorders such as
CC arrhythmias, ischaemia, aneurysms, arterial occlusive diseases, embolisms
CC and congenital heart defects, neurodegenerative diseases including
CC Alzheimer's and Parkinson's diseases, autoimmune disease such as multiple
CC sclerosis, arthritis, diabetes, Graves' disease, asthma and psoriasis,
CC and to promote angiogenesis and wound healing.
XX
SQ Sequence 1783 BP; 330 A; 562 C; 564 G; 327 T; 0 other;
Query Match 100.0%; Score 555; DB 21; Length 1783;
Best Local Similarity 100.0%; Pred. No. 3e-144;
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

|||||
Db 348 CACAAGAGATTGGTCTGTTTGTTCAGAGAGGCTGCCAGCGGGCACACTGAGAGGCC 407
QY 121 CCTTGCAGGAGCCCTGCGCAACTCCACTGCTTGTGTGTGCCAAGACACTTCTTG 180
|||||
Db 408 CCTTGCAGGAGCCCTGCGCAACTCCACTGCTTGTGTGTGCCAAGACACTTCTTG 467
QY 181 GCCTGGAGAACCAACCATATTTCTGAATGTGCCCGCTGCCAGGCTGTGATGAGAGGCC 240
|||||
Db 468 GCCTGGAGAACCAACCATATTTCTGAATGTGCCCGCTGCCAGGCTGTGATGAGAGGCC 527
QY 241 TCCAGGTGGCGCTGGAGAACTGTTACAGCAGTGGCCGACACCCGCTGTGCTAAGCCA 300
|||||
Db 528 TCCAGGTGGCGCTGGAGAACTGTTACAGCAGTGGCCGACACCCGCTGTGCTAAGCCA 587
QY 301 GGCTGTTTGTGAGTGCAGGTCAGCCAAATGTGTGACAGAGTTCACCTTCTACTGCCAA 360
|||||
Db 588 GGCTGTTTGTGAGTGCAGGTCAGCCAAATGTGTGACAGAGTTCACCTTCTACTGCCAA 647
QY 361 CCATGCTAGACTGCGGGCCCTGCACCCGACACACAGCGCTACTCTGTCCGACAGAGAT 420
|||||
Db 648 CCATGCTAGACTGCGGGCCCTGCACCCGACACACAGCGCTACTCTGTCCGACAGAGAT 707
QY 421 ACTGACTGTGGGACCTGCGCTGCGCTCTATGACATGGCGATGCGCTGCTCTGC 480
|||||
Db 708 ACTGACTGTGGGACCTGCGCTGCGCTCTATGACATGGCGATGCGCTGCTCTGC 767
QY 481 CCCACGACACCCCTGGGAGAGCTGTCCAGAGCGGCTGTGCCGCTGTGTGGCTGAGGCAG 540
|||||
Db 768 CCCACGACACCCCTGGGAGAGCTGTCCAGAGCGGCTGTGCCGCTGTGTGGCTGAGGCAG 827
QY 541 ATGTTCTGGGTCAG 555
|||||
Db 828 ATGTTCTGGGTCAG 842
RESULT 12
AAV28700
ID AAV28700 standard; cDNA; 1847 BP.
XX
AC AAV28700;
XX
DT 20-AUG-1998 (first entry)
DE Human apoptosis inducing receptor coding sequence.
XX
KW Apoptosis inducing receptor; AIR protein; human; cell death regulator;
KW Type I transmembrane protein; tumour cell death; autoimmune disease;
KW therapy; ss.
XX
XX Homo sapiens.
OS
XX
FH Key location/Qualifiers
FT CDS 236..1489
FT /*tag= a
FT /product= AIR
XX
PN WO9814565-A1.
XX
PD 09-APR-1998.
XX
PF 03-OCT-1997; 97WO-US17876.
XX
PR 04-OCT-1996; 96US-0044456.
XX
PA (IMMV) IMMUNEX CORP.
PI Perkins PA;
XX
DR WPI: 1998-240077/21.
DR P-PSDB; AAW57045.
XX
PT DNA encoding apoptosis inducing receptor - which is type I

PT transmembrane protein, useful for regulating cell death
XX
PS Claim 2; Page 28-30; 45pp; English.
XX
CC This sequence encodes the human apoptosis inducing receptor (AIR) of the
CC invention. AIR is a Type I transmembrane protein, soluble forms of which
CC can be used to regulate cell death in a therapeutic setting. Soluble AIR
CC can also be used in vitro to block apoptosis or AIR-expressing cells, or
CC to screen agonists or antagonists of AIR activity. The cytoplasmic domain
CC of AIR can be used to develop assays for inhibitors of AIR-induced cell
CC death, which is useful to regulate cell death in a therapeutic setting as
CC well as in vitro. Agonists of AIR activity can be used to kill tumour
CC cells that express AIR, or T cells expressing AIR in autoimmune diseases.
XX
SQ Sequence 1847 BP; 316 A; 605 C; 579 G; 347 T; 0 other;

Query Match 100.0%; Score 555; DB 19; Length 1847;
Best Local Similarity 100.0%; Pred. No. 3e-144;
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGGGCCCCCGGCGGCGCACTCGTAGCCCCAGGTGTGACTGTGCCGGTGAATTC 60
DB 293 CTGGGGCCCCCGGCGGCGGCACTCGTAGCCCCAGGTGTGACTGTGCCGGTGAATTC 352
QY 61 CACAAGAAGATGCTCTGTTTGTGTCAGAGGCTGCCAGCGGGGCACTACTGAAAGGCC 120
DB 353 CACAAGAAGATGCTCTGTTTGTGTCAGAGGCTGCCAGCGGGGCACTACTGAAAGGCC 412
QY 121 CCTTGACGGAGCCCTGCGGCACTCCACCTGCTGTGTGTCGCCCAAGACACTTCTTG 180
DB 413 CCTTGACGGAGCCCTGCGGCACTCCACCTGCTGTGTGTCGCCCAAGACACTTCTTG 472
QY 181 GCCTGGAGAACCACTAATTTCTGAATGTGCCCGCTGCCAGGGCTGTGATGACGAGGCC 240
DB 473 GCCTGGAGAACCACTAATTTCTGAATGTGCCCGCTGCCAGGGCTGTGATGACGAGGCC 532
QY 241 TCCAGAGTGGCGCTGGAGAACTGTTCAAGCAGTGGCCGACACCCGCTGTGGCTGTAAGCCA 300
DB 533 TCCAGAGTGGCGCTGGAGAACTGTTCAAGCAGTGGCCGACACCCGCTGTGGCTGTAAGCCA 592
QY 301 GGCTGTTTGTGAGTGCCAGGTGACCCAAATGTGTCAAGCAGTTACCCCTTCTACTGCCAA 360
DB 593 GGCTGTTTGTGAGTGCCAGGTGACCCAAATGTGTCAAGCAGTTACCCCTTCTACTGCCAA 652
QY 361 CCATGCCTAGACTGCGGGGCCCTGCACCGCCACACACAGGCTACTCTGTCTCCGCAAGAT 420
DB 653 CCATGCCTAGACTGCGGGGCCCTGCACCGCCACACACAGGCTACTCTGTCTCCGCAAGAT 712
QY 421 ACTGACTGTGGGACCTGCCCTGCTCTATGAACATGGCGATGCGTGTCTCTGC 480
DB 713 ACTGACTGTGGGACCTGCCCTGCTCTATGAACATGGCGATGCGTGTCTCTGC 772
QY 481 CCCACGAGACCCCTGGGAGCTGTCCAGAGCGCTGTGCCGCTGTCTGTGGCTGAGGACAG 540
DB 773 CCCACGAGACCCCTGGGAGCTGTCCAGAGCGCTGTGCCGCTGTCTGTGGCTGAGGACAG 832
QY 541 ATGTTCTGGGTCCAG 555
DB 833 ATGTTCTGGGTCCAG 847

RESULT 13
ABL64119
ID ABL64119 standard; DNA; 1743 BP.
XX
AC ABL64119;
XX
DT 15-MAY-2002 (first entry)
XX
DE Breast cancer related gene sequence SEQ ID NO:2456.
XX
KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;

KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW gene; ds.
XX
OS Homo sapiens.
XX
PN WO200194629-A2.
XX
PD 13-DEC-2001.
XX
PF 30-MAY-2001; 2001WO-US10838.
XX
PR 05-JUN-2000; 2000US-209473P.
PR 05-JUN-2000; 2000US-209531P.
PR 18-SEP-2000; 2000US-233133P.
PR 18-SEP-2000; 2000US-233617P.
PR 20-SEP-2000; 2000US-234009P.
PR 20-SEP-2000; 2000US-234034P.
PR 20-SEP-2000; 2000US-234052P.
PR 22-SEP-2000; 2000US-234509P.
PR 22-SEP-2000; 2000US-234567P.
PR 25-SEP-2000; 2000US-234923P.
PR 25-SEP-2000; 2000US-234924P.
PR 25-SEP-2000; 2000US-235077P.
PR 25-SEP-2000; 2000US-235082P.
PR 25-SEP-2000; 2000US-235134P.
PR 25-SEP-2000; 2000US-235280P.
PR 26-SEP-2000; 2000US-235637P.
PR 26-SEP-2000; 2000US-235638P.
PR 27-SEP-2000; 2000US-235711P.
PR 27-SEP-2000; 2000US-235720P.
PR 27-SEP-2000; 2000US-235840P.
PR 27-SEP-2000; 2000US-235863P.
PR 28-SEP-2000; 2000US-236028P.
PR 28-SEP-2000; 2000US-236032P.
PR 28-SEP-2000; 2000US-236033P.
PR 28-SEP-2000; 2000US-236034P.
PR 28-SEP-2000; 2000US-236109P.
PR 28-SEP-2000; 2000US-236111P.
PR 29-SEP-2000; 2000US-236842P.
PR 29-SEP-2000; 2000US-236891P.
PR 02-OCT-2000; 2000US-237172P.
PR 02-OCT-2000; 2000US-237173P.
PR 02-OCT-2000; 2000US-237178P.
PR 02-OCT-2000; 2000US-237278P.
PR 02-OCT-2000; 2000US-237294P.
PR 02-OCT-2000; 2000US-237295P.
PR 02-OCT-2000; 2000US-237316P.
PR 03-OCT-2000; 2000US-237425P.
PR 03-OCT-2000; 2000US-237598P.
PR 03-OCT-2000; 2000US-237604P.
PR 03-OCT-2000; 2000US-237606P.
PR 03-OCT-2000; 2000US-237608P.
PR 01-NOV-2000; 2000US-244867P.
PR 01-NOV-2000; 2000US-245084P.
XX
PA (AVAL-) AVALON PHARM.
XX
PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horriqan S;
PI Sopet DR, Weaver Z;
XX
DR WPI; 2002-188264/24.
XX
XX Screening for anti-neoplastic agent involves exposing cells to a
PT chemical agent to be tested for anti-neoplastic activity, and
PT determining a change in expression of a gene of a signature gene set
XX
PS Claim 1; SEQ ID 2456; 44pp; English.
XX
CC The present invention describes a method (M1) for screening for an
CC anti-neoplastic agent. The method involves exposing cells to a chemical
CC agent to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in

CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening
CC an anti-neoplastic agent, and can be used for producing a product which
CC is the data collected with respect to the anti-neoplastic agent as a
CC result of M1, and the data is sufficient to convey the chemical
CC structure and/or properties of the agent. M1 can be used in the
CC treatment of cancer such as colon, breast, stomach, lung, thyroid,
CC oesophageal, ovarian, kidney, prostate or pancreatic cancer,
CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
CC carcinoma, papillary carcinoma and Wilms' tumour.

XX Sequence 1743 BP; 347 A; 543 C; 549 G; 304 T; 0 other;

Query Match 97.5%; Score 541; DB 24; Length 1743;
Best Local Similarity 99.18; Pred. No. 2.3e-140;
Matches 544; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 CTGGGGGCCCCGGCCAGGGGGGCGCACTCGTAGCCCCAGGTGTGACTGTGCCGGTGACTTC 60
Db 126 CTGGGGGCCCCGGCCAGGGGGGCGCACTCGTAGCCCCAGGTGTGACTGTGCCGGTGACTTC 185
OY 61 CACAAGAAGATTGGTCTGTTTGTGTCAGAGGCTGCCAGCGGGGCACTACCTGAAGGCC 120
Db 186 CACAAGAAGATTGGTCTGTTTGTGTCAGAGGCTGCCAGCGGGGCACTACCTGAAGGCC 245
OY 121 CCTTGCACGGAGCCCTGCGGCACTCCACCTGCTGTGTGCCCAAGACACCTTCTTG 180
Db 246 CCTTGCACGGAGCCCTGCGGCACTCCACCTGCTGTGTGCCCAAGACACCTTCTTG 305
OY 181 GCCTGGAGAACCACTAATTTCTGAATGTGCCCGCTGCCAGGCTGTGATGAGAGGCC 240
Db 306 GCCTGGAGAACCACTAATTTCTGAATGTGCCCGCTGCCAGGCTGTGATGAGAGGCC 365
OY 241 TCCAGAGTGGCGCTGGAGAAGTGTTCAGCAGTGGCCGACACCCGCTGTGCTGTAGCCA 300
Db 366 TCCAGAGTGGCGCTGGAGAAGTGTTCAGCAGTGGCCGACACCCGCTGTGCTGTAGCCA 425
OY 301 GGCTGTTTGTGAGTCCAGGTCAGGCAATGTGTACAGATTCACCTTCTACTGCCAA 360
Db 426 GGCTGTTTGTGAGTCCAGGTCAGGCAATGTGTACAGATTCACCTTCTACTGCCAA 485
OY 361 CCATGCCCTAGACTCGGGGGCCCTGCACCGCCACACAGGCTACTCTGTGCCGAGAGAT 420
Db 486 CCATGCCCTAGACTCGGGGGCCCTGCACCGCCACACAGGCTACTCTGTGCCGAGAGAT 545
OY 421 ACTGACTGTGGAGCTGCTGCTGCTTCTATGACATGCGATGGCTGCTGCTTCC 480
Db 546 ACTGACTGTGGAGCTGCTGCTGCTTCTATGACATGCGATGGCTGCTGCTTCC 605
OY 481 CCCACGAGCACCCTGGGAGCTGTCCAGAGAGCGGTGCGCTGTCTGTGGTGAAGCCAG 540
Db 606 CCCACGAGCACCCTGGGAGCTGTCCAGAGAGCGGTGCGCTGTCTGTGGTGAAGCCAG 665
OY 541 ATGTTCTGG 549
Db 666 AGTAGGTGG 674

RESULT 14

ID AAF83770 standard; DNA; 1250 BP.

XX AAF83770;

DT 06-AUG-2001 (first entry)

DE Nucleotide sequence of human TR3 gene.

KW TR3: cell proliferation; leukemia; immunosuppressive; cytostatic;
KW dermatological; antiarthritic; antidiabetic; neuroprotective; cardiant;
KW antithyroid; antinflammatory; antiallergic; T-cell-inhibitor; ds.
XX

OS Homo sapiens.

XX Key Location/Qualifiers
FH CDS 1..1250

FT /tag- a
FT /transl_except- "(pos:481..482, aa:Asp)"
FT /note- "this codon has an apparent 1 nucleotide
FT deletion which alters the reading frame"
FT /transl_except- "(pos:558..559, aa:Cys)"
FT /note- "this codon has an apparent 1 nucleotide
FT deletion which alters the reading frame"
FT /transl_except- "(pos:638..639, aa:Leu)"
FT /note- "this codon has an apparent 1 nucleotide
FT deletion which alters the reading frame"
FT /transl_except- "(pos:718..719, aa:Met)"
FT /note- "this codon has an apparent 1 nucleotide
FT deletion which alters the reading frame"
FT sig_peptide 1..72
FT /tag- b
FT mat_peptide 73..1247
FT /tag- c

W0200135995-A2.

25-MAY-2001.

17-NOV-2000; 2000WO-US31692.

19-NOV-1999; 99US-0166583.

(TITV/) TITTLE T V.
(WEGM/) WEGMANN K W.

Tittle TV, Wegmann KW;

WPI: 2001-343711/36.

P-PSDB; AAB84941.

Composition for treatment of T-cell mediated disease e.g. arthritis,
cancer comprises a biologically active TR3-specific binding agent
especially a monoclonal antibody -

Disclosure; Page 72; 77pp; English.

The invention relates to a composition comprising a biologically active
TR3-specific binding agent (I) that binds to TR3 and inhibits the
proliferation of cells expressing TR3. (I) identified by the methods are
useful for treating a subject suspected of having a disease associated
with a proliferation of cells expressing TR3 especially leukemias or
CC lymphomas or a T-cell mediated disease especially autoimmune diseases
CC such as myasthenia gravis, systemic lupus erythematosus, rheumatoid
CC arthritis, diabetes, multiple sclerosis, sarcoidosis, myocarditis,
CC thyroiditis and tumours. (I) is also useful for treating a subject
CC suspected of having graft-versus-host disease, rejection of a
CC transplanted organ such as heart, liver, lung, kidney, pancreas, bowel,
CC skin or an appendage, or inflammatory diseases, allergies and contact
CC dermatitis. The present sequence represents the nucleotide sequence of
CC human TR3 gene.

SO Sequence 1250 BP; 201 A; 419 C; 406 G; 224 T; 0 other;

Query Match 95.78; Score 531; DB 22; Length 1250;
Best Local Similarity 99.6%; Pred. No. 1.2e-137;
Matches 553; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

OY 1 CTGGGGGCCCCGGCCAGGGGGGCGCACTCGTAGCCCCAGGTGTGACTGTGCCGGTGACTTC 60
Db 58 CTGGGGGCCCCGGCCAGGGGGGCGCACTCGTAGCCCCAGGTGTGACTGTGCCGGTGACTTC 117
OY 61 CACAAGAAGATTGGTCTGTTTGTGTCAGAGGCTGCCAGCGGGGCACTACCTGAAGGCC 120
Db 118 CACAAGAAGATTGGTCTGTTTGTGTCAGAGGCTGCCAGCGGGGCACTACCTGAAGGCC 177

QY 121 CCTTGACGAGCCCTGCGGCACTCCACCTGCTGTGTGCCCAAGACACTTCTG 180
DB 178 CCTTGACGAGCCCTGCGGCACTCCACCTGCTGTGTGTGCCCAAGACACTTCTG 237
QY 181 GCCTGGAGAACCATTAATTTGATGTGCCCCGCTGCCAGGCCGTGTATGAGCAGGCC 240
DB 238 GCCTGGAGAACCATTAATTTGATGTGCCCCGCTGCCAGGCCGTGTATGAGCAGGCC 297
QY 241 TCCAGAGTGGCGGTGAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGCTGTAAGCCA 300
DB 298 TCCAGAGTGGCGGTGAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGCTGTAAGCCA 357
QY 301 GGCTGGTTGTGGAGTGCAGGTCAGCCAAATGTGTCAGCAGTTACCCCTTCTACTGCCAA 360
DB 358 GGCTGGTTGTGGAGTGCAGGTCAGCCAAATGTGTCAGCAGTTACCCCTTCTACTGCCAA 417
QY 361 CCATGCTAGACTGCGGGCCCTGCACCGCCACACAGGCTACTCTGTTCGCCAGAGAT 420
DB 418 CCATGCTAGACTGCGGGCCCTGCACCGCCACACAGGCTACTCTGTTCGCCAGAGAT 477
QY 421 ACTGACTGTGGGACCTGCGCTGCTGCTATGAAATGCGATGGCTGCTGCTGCTGC 480
DB 478 AC-GACTGTGGGACCTGCGCTGCTGCTATGAAATGCGATGGCTGCTGCTGCTGC 536
QY 481 CCCACGAGACCCCTGGGGAGCTGTCCAGAGCGCTGTGCGGCTGTGTGCTGAGGCGAG 540
DB 537 CCCACGAGACCCCTGGGGAGC-GTCCAGAGCGCTGTGCGGCTGTGTGCTGAGGCGAG 595
QY 541 ATGTTCTGGGTCAG 555
DB 596 ATGTTCTGGGTCAG 610

RESULT 15
AAL47187
ID AAL47187 standard; cDNA; 787 BP.
XX AAL47187;
AC 22-AUG-2002 (first entry)
DT 22-AUG-2002 (first entry)
XX Human rheumatoid arthritis associated DR3 gene related cDNA #2.
DE Human; DR3; rheumatoid arthritis; antirheumatic; antiarthritic;
KW gene therapy; gene; ss.
XX Homo sapiens.
OS
FH Key Location/Qualifiers
FT CDS 89..655
FT /*tag= a
FT /product= "AAO17880"
XX
PN WO200234912-A1.
XX 02-MAY-2002.
PD 24-OCT-2001; 2001WO-JP09313.
PE 24-OCT-2001; 2000JP-0324296.
XX 24-OCT-2000; 2000JP-0324296.
PR 27-MAR-2001; 2001JP-0090546.
PR 30-MAR-2001; 2001JP-0099990.
XX
PA (NEWI-) NEW IND RES ORG.
PA (SHIO/) SHIOZAWA S.
XX
PI Shiozawa S, Konishi Y;
XX
DR WPI; 2002-417132/44.
DR P-PSDB; AAO17880.
XX
PT Genomes, particularly DR3 genomic DNA, participating in rheumatoid
PT arthritis via mutation, useful in evaluating disease onset and its

PT possibility and providing therapy and remedies -
XX
PS Example 1; Page 71-72; 84bp; Japanese.
XX
CC The present invention relates to the human DR3 gene, which is associated
CC with rheumatoid arthritis. Certain mutations in the gene can be linked to
CC the disease. The sequences can be used to evaluate disease onset and its
CC possibility and to provide therapy and remedies. The present sequence is
CC a coding sequence described in the exemplification of the invention.
XX
SQ Sequence 787 BP; 133 A; 249 C; 250 G; 155 T; 0 other;

Query Match 87.6%; Score 486.4; DB 24; Length 787;
Best Local Similarity 99.8%; Pred. No. 2.6e-125;
Matches 487; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGGGGGCCCCGGCCAGGGCGGCACTGTAAGCCCAAGGTGTGACTGTGCCGCTGCTTC 60
DB 146 CTGGGGGCCCCGGCCAGGGCGGCACTGTAAGCCCAAGGTGTGACTGTGCCGCTGCTTC 205
QY 61 CACAAGAAGATTGCTGTTTGTGTCAGAGGCTGCCAGCGGGCACTACTGAAGGCC 120
DB 206 CACAAGAAGATTGCTGTTTGTGTCAGAGGCTGCCAGCGGGCACTACTGAAGGCC 265
QY 121 CCTTGACGAGCCCTGCGGCAACTCCACTGCTGTGTGTGCCCAAGACACTTCTTG 180
DB 266 CCTTGACGAGCCCTGCGGCAACTCCACTGCTGTGTGTGCCCAAGACACTTCTTG 325
QY 181 GCCTGGAGAACCATTAATTTGATGTGCCCCGCTGCCAGGCCGTGTATGAGCAGGCC 240
DB 326 GCCTGGAGAACCATTAATTTGATGTGCCCCGCTGCCAGGCCGTGTATGAGCAGGCC 385
QY 241 TCCAGAGTGGCGCTGAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGCTGTAAGCCA 300
DB 386 TCCAGAGTGGCGCTGAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGCTGTAAGCCA 445
QY 301 GCCTGGTTGTGAGTGCAGGTCAGCCAAATGTGTGAGCAGTTCACTTCTACTGCCAA 360
DB 446 GCCTGGTTGTGAGTGCAGGTCAGCCAAATGTGTGAGCAGTTCACTTCTACTGCCAA 505
QY 361 CCATGCTAGACTGCGGGCCCTGCACCGCCACACAGGCTACTGTTCGCCAGAGAT 420
DB 506 CCATGCTAGACTGCGGGCCCTGCACCGCCACACAGGCTACTGTTCGCCAGAGAT 565
QY 421 ACTGACTGTGGGACCTGCTGCTGCTTCTATGAACATGGCGATGGCTGCTGCTGCTGC 480
DB 566 ACTGACTGTGGGACCTGCTGCTGCTTCTATGAACATGGCGATGGCTGCTGCTGCTGC 625
QY 481 CCCACGAG 488
DB 626 CCCACTAG 633

Search completed: April 6, 2003, 14:30:04
Job time : 246 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 6, 2003, 16:19:54 ; Search time 444.113 Seconds

(without alignments)
2589.161 Million cell updates/sec

Title: US-09-993-234-6_COPY_339_409

Perfect score: 368

Sequence: 1 MDVAPARRMKFVRLGLRE.....LGAVYALERMGLDGCYEDL 71

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL-frame+_p2n.model -DEV=xlh
-O=/cgn2_1/USPTO_spool/US0993234/runat_27032003_115456_15362/app_query.fasta_1.2346
-DB-EST-QFMT=fastap -SUFFIX=first -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blsum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=90 -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US0993234_@CGN_1_1_4749_@runat_27032003_115456_15362 -NCPU=6 -ICPU=3
-NO_XLPHY -NO_MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	368	100.0	510	14	BM695193	BM695193 UI-E-CQ1-
2	368	100.0	550	13	BM666370	BM666370 UI-E-CQ1-
3	368	100.0	687	10	BE670189	BE670189 7e31c12.x
4	361	98.1	618	10	AW074008	AW074008 xb06c09.x
5	354	96.2	587	9	AI380959	AI380959 tg18c01.x
6	354	96.2	623	9	AI811528	AI811528 tw43h06.x
7	351	95.4	289	12	BF655336	BF655336 279811 MA
8	345	93.8	582	10	AW182875	AW182875 xp99a04.x
9	328	89.1	647	14	BM794760	BM794760 K-EST0076
10	325	88.3	544	9	AI380900	AI380900 tg17f01.x
11	323	87.8	439	14	BM824360	BM824360 K-EST0095
12	323	87.8	633	10	BB212432	BB212432 BB212432
13	316	85.9	274	12	BF552058	BF552058 UI-R-C2p-
14	305	82.9	499	14	BQ027499	BQ027499 UI-H-CO0-
15	304	82.6	507	10	AW964958	AW964958 EST376926
16	291	79.1	539	12	BF726557	BF726557 by08d05.y
17	289	78.5	537	9	AI266746	AI266746 qg11c06.x
18	278	75.5	523	14	W71984	W71984 zd66a06.s1
19	272	73.9	681	10	BE563566	BE563566 601334867
20	246.5	67.0	739	9	AA524052	AA524052 ng33b06.s
21	225	61.1	292	9	AA088350	AA088350 z182d08.r
22	213	57.9	433	10	AW134494	AW134494 UI-H-B11-
23	204.5	55.6	605	9	AI913906	AI913906 wd03f01.x
24	191	51.9	437	10	AW492480	AW492480 UI-M-BH3-
25	187	50.8	651	13	BM009354	BM009354 603629813
26	169	45.9	348	9	AI703436	AI703436 we24c02.x
27	162	44.0	596	9	AA887388	AA887388 o37a02.s
28	161	43.8	530	10	BE014705	BE014705 126529 MA
29	161	43.8	619	10	BE334962	BE334962 us91b07.y
30	161	43.8	789	12	BF138948	BF138948 601783079
31	161	43.8	853	13	BI525375	BI525375 602924303
32	154	41.8	506	12	BF118096	BF118096 uz11910.y
33	152	41.3	582	10	AW355430	AW355430 pnf-b.pk0
34	151	41.0	504	13	BI468367	BI468367 id87f12.y
35	151	41.0	556	14	W99099	W99099 mf92c12.r1
36	151	41.0	591	14	BM694442	BM694442 UI-E-C11-
37	151	41.0	620	14	BM767536	BM767536 K-EST0050
38	151	41.0	636	12	BG035257	BG035257 602324771
39	151	41.0	669	14	BM742388	BM742388 K-EST0015
40	151	41.0	739	13	BI520191	BI520191 603071439
41	151	41.0	889	9	AU117362	AU117362 AU117362
42	151	41.0	894	14	BQ880824	BQ880824 AGENCOURT
43	151	41.0	923	14	BQ228387	BQ228387 AGENCOURT
44	151	41.0	1055	13	BM555065	BM555065 AGENCOURT
45	151	41.0	1076	14	BM923204	BM923204 AGENCOURT

ALIGNMENTS

RESULT 1
BM695193
LOCUS BM695193 510 bp mRNA linear EST 28-FEB-2002
DEFINITION UI-E-CQ1-aev-1-03-0-UI.r1 UI-E-CQ1 Homo sapiens cDNA clone
ACCESSION BM695193
VERSION BM695193.1 GI:19008451
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 510)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene

discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
COMMENT Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 Reverse.

FEATURES
source
1. .510
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="UI-E-CQ1-aev-1-03-0-UI"
/clone_lib="UI-E-CQ1"
/tissue_type="optic nerve"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-E-CQ1 is a normalized CDNA library containing the
following tissue(s): optic nerve. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand CDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded CDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT7T3-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand CDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
CCATTAAAGTG. This library was created for the program, Gene
Discovery in the Visual System, supported by National Eye
Institute (NEI)."

BASE COUNT 100 a 152 c 170 g 88 t
ORIGIN

Alignment Scores:
Pred. No.: 1.62e-38 Length: 510
Score: 368.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-09-993-234-6_COPY_339_409 (1-71) x BM695193 (1-510)

QY 1 MetaspAlaValProAlaArgTrpLysGluPheValArgThrLeuGlyLeuArgGlu 20
|||||
Db 4 ATGGACGGCGTCCACAGCGCGCGCTGGAAGAGATTCTGTCGCCACGCTGGGGCTGCGGAG 63
|||||
QY 21 AlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnIleTyrGluMet 40
|||||
Db 64 GCAGAGATCGAAGCCGCTGGAGGTGAGATCGCGCTTCGAGACCAAGACAGTACGAGATG 123
|||||
QY 41 LeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGlu 60
|||||
Db 124 CTCAGCGCTGGCGCCAGCAGACGCCGCGGCTCGAGCCGCTTACGCCGCCCTGAG 183
|||||
QY 61 ArgMetGlyLeuAspGlyCysValGluAspLeu 71
|||||
Db 184 CGCATGGGGCTGGACGGCTGCGTGAAGACTTG 216
|||||

RESULT 2
BM666370/c

LOCUS BM666370 550 bp mRNA linear EST 27-FEB-2002
DEFINITION UI-E-CQ1-aev-1-03-0-UI.s1 UI-E-CQ1 Homo sapiens CDNA clone
UI-E-CQ1-aev-1-03-0-UI 3', mRNA sequence.
ACCESSION BM666370
VERSION BM666370.1 GI:18974007
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 550)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
The following repetitive elements were found in this CDNA
sequence: 1-37, >POLY_A#Simple_repeat (matched compliment)
Seq primer: M13 Forward
POLYA=Yes.

FEATURES
source
1. .550
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="UI-E-CQ1-aev-1-03-0-UI"
/clone_lib="UI-E-CQ1"
/tissue_type="optic nerve"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-E-CQ1 is a normalized CDNA library containing the
following tissue(s): optic nerve. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand CDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded CDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT7T3-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand CDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
CCATTAAAGTG. This library was created for the program, Gene
Discovery in the Visual System, supported by National Eye
Institute (NEI)."
TAG_LIB=UI-E-CQ1
TAG_TISSUE=human optic nerve
TAG_SEQ=CCATTAAAGTG"

BASE COUNT 90 a 175 c 156 g 129 t
ORIGIN

Alignment Scores:
Pred. No.: 1.81e-38 Length: 550
Score: 368.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-09-993-234-6_COPY_339_409 (1-71) x BM666370 (1-550)

QY 1 MetaspAlaValProAlaArgTrpLysGluPheValArgThrLeuGlyLeuArgGlu 20
|||||
Db 536 ATGACCGCGTCCAGCGCGCGCTTGGAAGAGTTCGTGCGCACGCTGGGGCTCCGAG 477

QY 21 AlaGluIleGluAlaValAlaGluValIleGlyArgPheArgAspGlnGlnTyrGluMet 40
|||||
Db 476 GCAGAGATCGAAGCCGTGGAGGTGAGATCGCGCTTCCGAGACCAGCAGTACGAGATG 417

QY 41 LeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGlu 60
|||||
Db 416 CTCAGCGCTGGCGCCAGCAGACGCCCGGGCTCGAGCCGTTACGGCGCCCTGGAG 357

QY 61 ArgMetGlyLeuAspGlyCysValGluAspLeu 71
|||||
Db 356 CGCATGGGGCTGGACGGCTGCGTGAAGACTTG 324

RESULT 3
BE670189/c 687 bp mRNA linear EST 08-SEP-2000
LOCUS 7e31c12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284086 3'
DEFINITION similar to SW:WSL1_HUMAN Q93038 WSL-1 PROTEIN PRECURSOR ;, mRNA
sequence.
ACCESSION BE670189
VERSION BE670189.1 GI:10030730
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 687)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLES National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 466.
FEATURES
source
1. 687
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3284086"
/clone_lib="NCI_CGAP_Lu24"
/tissue_type="carcinoid"
/lab_host="DH10B"
/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; Plasmid DNA from the normalized
library NCI_CGAP_Lu5 was prepared, and ss circles were
made in vitro. Following HAP purification, this DNA was
used as tracer in a subtractive hybridization reaction.
The driver was PCR-amplified cDNAs from a pool of 5,000
clones made from the same library (clonids
1414920-1417991 and 1520904-1522439). Subtraction by Bento
Soares and M. Fatima Bonaldo."

BASE COUNT 111 a 215 c 225 g 134 t 2 others
ORIGIN

Alignment Scores:
Pred. No.: 2.51e-38 Length: 687
Score: 368.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

DB: 10 Gaps: 0
US-09-993-234-6_COPY_339_409 (1-71) x BE670189 (1-687)

QY 1 MetaspAlaValProAlaArgTrpLysGluPheValArgThrLeuGlyLeuArgGlu 20
|||||
Db 516 ATGACCGCGTCCAGCGCGCGCTGGAAGAGTTCGTGCGCACGCTGGGGCTCCGAG 457

QY 21 AlaGluIleGluAlaValAlaGluValIleGlyArgPheArgAspGlnGlnTyrGluMet 40
|||||
Db 456 GCAGAGATCGAAGCCGTGGAGGTGAGATCGCGCTTCCGAGACCAGCAGTACGAGATG 397

QY 41 LeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGlu 60
|||||
Db 396 CTCAGCGCTGGCGCCAGCAGACGCCCGGGCTCGAGCCGTTACGGCGCCCTGGAG 337

QY 61 ArgMetGlyLeuAspGlyCysValGluAspLeu 71
|||||
Db 336 CGCATGGGGCTGGACGGCTGCGTGAAGACTTG 304

RESULT 4
AW074008/c 618 bp mRNA linear EST 13-OCT-1999
LOCUS xb06c09.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2575504 3'
DEFINITION similar to TR:000278 O00278 LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH
7. [2] TR:000279 ;, mRNA sequence.
ACCESSION AW074008
VERSION AW074008.1 GI:6029006
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 618)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLES National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: Life
Technologies, Inc. CDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/DbRP/Image/Image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 383.
FEATURES
source
1. 618
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2575504"
/clone_lib="NCI_CGAP_GU1"
/tissue_type="2 pooled high-grade transitional cell
tumors"
/lab_host="DH10B"
/note="Organ: genitourinary tract; Vector: pCMV-SPORT6;
Site_1: SalI; Site_2: NotI; Cloned unidirectionally.
Primer: Oligo dt. Library constructed by Life
Technologies."

BASE COUNT 110 a 204 c 182 g 120 t 2 others
ORIGIN

Alignment Scores:
Pred. No.: 1.8e-37 Length: 618
Score: 361.00 Matches: 70
Percent Similarity: 98.59% Conservative: 0
Best Local Similarity: 98.59% Mismatches: 1
Query Match: 98.10% Indels: 0
DB: 10 Gaps: 0

Percent Similarity: 97.18% Conservative: 0
Best Local Similarity: 97.18% Mismatches: 2
Query Match: 96.20% Indels: 0
DB: 9 Gaps: 0

US-09-993-234-6_COPY_339_409 (1-71) x AI811528 (1-623)

OY 1 MetaspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGlu 20
||| |||||
DB 515 ATGNACGGGCTCCAGCGCGCGCTGGAAGAGTTCGTGCGACGCTGNGCGCGGAG 456
OY 21 AlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGluMet 40
|||||
DB 455 GCAGAGATCGAAGCCGTCGAGGTGAGATCGCCGCTTCCGAGACCAGCAGTACGAGATG 396
OY 41 LeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGlu 60
|||||
DB 395 CTCAAGCGCTGGCGCCAGCAGCAGCCCGCGGCTCGAGCCGTTTACGCGCGCTGGAG 336
OY 61 ArgMetGlyLeuAspGlyCysValGluAspLeu 71
|||||
DB 335 CGCATGGGGCTGGACGGCTGCGTGAAGACTTG 303

RESULT 7
LOCUS BF655336 289 bp mRNA linear EST 25-APR-2001
DEFINITION 279811 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BF655336
VERSION BF655336.1 GI:11920468
KEYWORDS EST.
SOURCE COW.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 289)
AUTHORS Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,
G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G.,
Perteau,G., Holt,I., Karameycheva,S., Liang,F., Quackenbush,J. and
Keeler,J.W.
TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle

JOURNAL Genome Res. 11 (4), 626-630 (2001)
MEDLINE 21180013
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -mismatch 12 options.

PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCAGTCACGACG
Plate: 76 row: G column: 4
Seq primer: ATTTAGGTGACACTATAG.

FEATURES
source
1. .289
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 3BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: PCMV SPORT6; Site_1: NotI; Site_2: SalI;
Library made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendonsus muscle, and fetal
longissimus muscle."

BASE COUNT 41 a 90 c 116 g 42 t
ORIGIN

Alignment Scores:
Pred. No.: 1.23e-36 Length: 289
Score: 351.00 Matches: 67
Percent Similarity: 97.18% Conservative: 2
Best Local Similarity: 94.37% Mismatches: 2
Query Match: 95.38% Indels: 0
DB: 12 Gaps: 0

US-09-993-234-6_COPY_339_409 (1-71) x BF655336 (1-289)

OY 1 MetaspAlaValProAlaArgArgTrpLysGluPheValArgThrLeuGlyLeuArgGlu 20
|||||
DB 6 ATGACGCGCTGCCCGCGCGCTTGAAGAGTTCATGCCACGCTAGGGTTGCCGAG 65
OY 21 AlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnTyrGluMet 40
|||||
DB 66 GCGAGATCGAGCGGCTGAGGTGAGGTGCGCCGCTTCCGACACGACGAGTACGAGATG 125
OY 41 LeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGlu 60
|||||
DB 126 CTCAAGCGCTGGCGCCAGCAGCAGCGGGGCTTGGGCGCGCTTACGCGGCGCTGGAG 185
OY 61 ArgMetGlyLeuAspGlyCysValGluAspLeu 71
|||||
DB 186 CGCATGGGGCTGGACGGCTGCCAGAGACACTG 218

RESULT 8
LOCUS AW182875 582 bp mRNA linear EST 18-NOV-1999
DEFINITION XP99a04.x1 Soares_NHCEC_cervical_tumor Homo sapiens cDNA clone
IMAGE:2748462.3' similar to TR:000278 000278 LYMPHOCTYE ASSOCIATED
RECEPTOR OF DEATH 7. [2] TR:000279 ;, mRNA sequence.
ACCESSION AW182875
VERSION AW182875.1 GI:6451335
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 582)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco

High quality sequence stop: 461.
FEATURES
source
1. .582
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2748462"
/clone_lib="Soares_NHCEC_cervical_tumor"
/tissue_type="tumor"
/lab_host="DH10B (phage-resistant)"
/note="Organ: cervix; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGCCGCGAAGTTTCTTTTCTTTTCTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT7T3 vector.
Library is normalized; constructed by Bento Soares and
M.Fatima Bonaldo."

BASE COUNT 99 a 189 c 178 g 115 t 1 others
ORIGIN
Alignment Scores:
Pred. No.: 2.12e-35 Length: 582
Score: 345.00 Matches: 67

BASE COUNT 92 a 174 c 168 g 108 t 2 others
ORIGIN

Alignment Scores:
Pred. No.: 8.32e-33 Length: 544
Score: 325.00 Matches: 65
Percent Similarity: 91.55% Conservative: 0
Best Local Similarity: 91.55% Mismatches: 6
Query Match: 88.32% Indels: 0
DB: 9 Gaps: 0

US-09-993-234-6_COPY_339_409 (1-71) x AI380900 (1-544)

OY 1 MetaspalavalProalaArgTrpLysGluPheValArgThrLeuGlyLeuArgGlu 20
Db 515 ATGNACGGCTCCCGCGCGCGCTGNAAGAGAGTTCGCGCACGCTGGGGCTGGCGAG 456
OY 21 AlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnIntyrglumet 40
Db 455 GCAGAGATCGAGCCCGTGAGAGTGAGATCGCCGCTTCCGAGACACAGACAGTACAGATG 396
OY 41 LeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGlu 60
Db 395 CTCAGCGCGTGGCGCCACAGACAGCCCGCGGCTCGAGCCGTTTACGCGCGCTGGAG 336
OY 61 ArgMetGlyLeuAspGlyCysValGluAspLeu 71
Db 335 CGCATGGGGCTGGACGGCTGCTGGAAGACTTG 303

RESULT 11 439 bp mRNA linear EST 06-MAR-2002
LOCUS BM824360 K-EST0095844 S22SNU16n1 Homo sapiens cDNA clone S22SNU16n1-85-D08
DEFINITION 5', mRNA sequence.
ACCESSION BM824360
VERSION BM824360.1 GI:19180773
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 439)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.

TITLE 21C Frontlier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@email.kribb.re.kr
Plate: 85 row: D column: 08
High quality sequence stop: 439.
Location/Qualifiers
1. 439

FEATURES
source
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="S22SNU16n1-85-D08"
/clone_lib="S22SNU16n1"
/sex="F"
/issue_type="Ascites"
/cell_type="Lymphoblast-like"
/cell_line="SNU-16"
/lab_host="DH10B"
/note="Organ: Stomach; Vector: pT7T3-Pac; Site_1: EcoRI;
Site_2: NotI; The S22SNU16 library was contributed by the
Soares laboratory and it was constructed as described by
Bonaldio, M.F., Lennon, G. and Soares, M.B. (1996), Genome
Research 6(9): 791-806. RNA was prepared from harvested

cells of SNU-16 culture. SNU-16 cell was obtained from
Korean Cell Line Bank (KCLB). SNU-16 was established from
ascitic fluids of Korean patients by Park J.G. et al.
(1990), Cancer Res 50: 2773-2780."

BASE COUNT 76 a 148 c 150 g 65 t
ORIGIN

Alignment Scores:
Pred. No.: 1.11e-32 Length: 439
Score: 323.00 Matches: 62
Percent Similarity: 90.14% Conservative: 2
Best Local Similarity: 87.32% Mismatches: 7
Query Match: 87.77% Indels: 0
DB: 14 Gaps: 0

US-09-993-234-6_COPY_339_409 (1-71) x BM824360 (1-439)

OY 1 MetaspalavalProalaArgTrpLysGluPheValArgThrLeuGlyLeuArgGlu 20
Db 194 ATGCAGCGCGTCCCAACGCGCGCTGCAAGAGATTATTCGCGCACGCTGGGGCTGGCGAG 253
OY 21 AlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnIntyrglumet 40
Db 254 GCATTAATCGAAGCCCGGAGAGATATCGCCGCTTACGAGACACAGACAGTACGAGATG 313
OY 41 LeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGlu 60
Db 314 CTCAGCGCGTGGCGCCACAGACAGATCCCGGGGCTCGAGCCGTTTACGCGCGCTGGAG 373

OY 61 ArgMetGlyLeuAspGlyCysValGluAspLeu 71
Db 374 CGCATGGGGCTGGACGGCTGCTGGAAGACTTG 406

RESULT 12 633 bp mRNA linear EST 31-AUG-2001
LOCUS BB212432 BB212432 RIKEN full-length enriched, 0 day neonate thymus Mus
DEFINITION musculus cDNA clone A430110L22 3', mRNA sequence.
ACCESSION BB212432
VERSION BB212432.2 GI:15410061
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 633)
Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,
' Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda
' M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki
' D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
Muramatsu,M. and Hayashizaki,Y.

RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
On Jun 30, 2000 this sequence version replaced gi:8877385.
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216

Email: genome-resesc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
' M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagI,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
' S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kita,A. and

Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. *Genome Res.* 10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA Encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. *Genome Res.* 11 (2), 281-289 (2001)
Yamanaka, I., Kiyosawa, H., Kondo, S., Saito, T., Shinagawa, A., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K., Arakawa, T., Ishii, Y. and Hayashizaki, Y.
Mapping of 19032 mouse cDNAs on mouse chromosomes. *J. Struct. Funct. Genomics* 2 pre, L72-L86 (2001)
Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

FEATURES

Source

```

/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="A430110L22"
/clone_1tb="RIKEN full-length enriched, 0 day neonate
thymus"
/tissue_type="thymus"
/dev_stage="0 day neonate"
/lab_host="DH10B"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAGAGGATCCAGAGATCCTTTTTTTTTTTTTTTT 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 10.0 and subtraction to Rot = 459.0. Second
strand cDNA was prepared with the primer adapter of
sequence [5' GAGAGAGAGATTCGAGTTAATTAATTAATTC
3']. cDNA was cleaved with XhoI and BamHI. Vector: a
modified pBluescript KS(+) after bulk excision from Lambda
FLC I."

```

Alignment Scores:	
Pred. No.:	1.91e-32
Score:	323.00
Percent Similarity:	95.77%
Best Local Similarity:	92.96%
Query Match:	87.77%
DB:	10
Length:	633
Matches:	66
Conservative:	2
Mismatches:	3
Indels:	1
Gaps:	0

US-09-993-234-6_COPY_339_409 (1-71) x BB212432 (1-633)

QY	1	MELASPALAVALPROALAARGARTRPLYSGLUPHEVALARGTHRLEUGLYLEUARGGLU	20
Dd	135	ATGGATCGGCTCCACGACGAAGGTGAAGAGATTCTGTGCACACTGGGGCTGCGGAA	194
QY	21	ALAGLILEGUALAVAIGLUVALGIURIEGLYARGPHEARGASPLNGLINTRYGLUMET	40
Dd	195	GCGGAATTGAAGCCGTGGAGGTGGAATACTGCCGCTTCGAGACCAGCAGTATGAGATG	254
QY	41	LEULYSARGTRPARGGINGLINGINPROIALAGLYLEUGLYALAVAITRYLAALALEUGLU	60
Dd	255	CTCAAGCGCTGGCTCAGCACGACCTTGCAAGCCCTGGTGCCATTATCG-GCTTTGAG	313

```

QY      61  ArgMetGlyLeuaspGlyCysValGluaspLeu  71
          |||||
Db      314  CGCATGGGCTCGAAGGCTGTGCCGAGACCTG  346

```

RESULT 13	BF552058	274 bp	mRNA	linear	EST 12-DEC-2000
LOCUS	BF552058				
DEFINITION	UI-R-C2p-oh-b-10-0-UI.r1	UI-R-C2p	Rattus norvegicus	CDNA clone	
	UI-R-C2p-oh-b-10-0-UI 5',	mRNA sequence.			
ACCESSION	BF552058				
VERSION	BF552058.1	GI:11661788			
KEYWORDS	EST.				
SOURCE	Norway rat.				

REFERENCE	AUTHORS	TITLE
1 (bases 1 to 274)	Bonaldo, M.F., Lennon, G. and Soares, M.B.	Normalization and subtraction: two approaches to facilitate gene

JOURNAL	Genome Res. 6 (9), 791-806 (1996)
MEDLINE	97044477
COMMENT	Contact: Soares, MB

6
 7
 8
 9
 10
 11
 12

Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
cDNA Library Preparation: M.B. Soares Lab Clone distribution:
clones will be available through Research Genetics (www.resgen.com)
This clone is also available through the I.M.A.G.E. Consortium at
ILNt (info@image.llnl.gov). IMAGE ID= 1787481
Seq primer: M13Forward.

FEATURES

source

/organism="Rattus norvegicus"
 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
 /clone="UI-R-C2p-oh-b-10-0-UI"
 /clone_1ib="UI-R-C2p"
 /dev_stage="adult"
 /lab_host="DH10B (Life Technologies)"
 /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-C2p
 library is a subtracted library derived from the UI-R-C1
 library, which is a subtracted library derived from the
 UI-R-C0 library. The UI-R-C0 library consisted of a
 mixture of individually tagged normalized libraries
 constructed from rat placenta, adult lung, liver,
 kidney, heart, spleen, ovary, muscle, 8, 12 and 18-day
 embryo. The tag is a string of 3-5 nucleotides present
 between the Not I site and the oligo-dT track which allows
 identification of the library of origin of a clone within
 the mixture. The subtracted library (UI-R-C2p) was
 constructed as follows: PCR amplified cDNA inserts from
 UI-R-C1 clones from which 3' ESTs had been derived was
 used as a driver in a hybridization with the UI-R-C1
 library in the form of single-stranded circles. The
 remaining single-stranded circles (subtracted library) was
 purified by hydroxyapatite column chromatography,
 converted to double-stranded circles and electroporated
 into DH10B bacteria (Life Technologies) to generate the
 UI-R-C2p library. This procedure has been previously
 described (Bonaldo, Lennon and Soares, Genome Research 6:
 191-806, 1996)"

BASE COUNT	49 a	80 c	99 g	46 t
ORIGIN				

Alignment Scores:	
Pred. No.:	4.66e-32
Score:	316.00
	Length: 274
	Matches: 61

Percent Similarity: 98.46%
Best Local Similarity: 93.85%
Query Match: 85.87%
DB: 12
Conservative: 3
Mismatches: 1
Indels: 0
Gaps: 0

US-09-993-234-6_COPY_339_409 (1-71) x BF552058 (1-274)

OY 1 MetaspAlaValProAlaArgTrpLysGluPheValArgThrLeuGlyLeuArgGlu 20
|||||
DB 80 ATGATGCGGTCCAGCCAGCAGAAGGTGAAGAGATTGTGCGCAGCAGCTGGGGCTGGCGAG 139
OY 21 AlaGluIleGluAlaValGluValGluIleGlyArgPheArgAspGlnGlnIleTyrGluMet 40
|||||
DB 140 GCAAAATGTAGCGCTGTGAGGTGAGATCTGCCCTTCCGAGACCAGCAGTATGAGATG 199
OY 41 LeuLysArgTrpArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGlu 60
|||||
DB 200 CTCAGCGCTGGCGGCGCAGCAGCCTGACGCTGGTGGCATCTATGCGGCCCTGGAG 259
OY 61 ArgMetGlyLeuAsp 65
|||||
DB 260 CGCATGGGCTGGA 274

RESULT 14
BQ027499/c 499 bp mRNA linear EST 27-MAR-2002
LOCUS UT-H-C00-aqg-a-09-0-UI.s1 NCI_CGAP_Sub9 Homo sapiens cDNA clone
DEFINITION IMAGE:3104895 3', mRNA sequence.
ACCESSION BQ027499
VERSION BQ027499.1 GI:19762778
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 499)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
Seq primer: M13 FORWARD
POLYA-Yes.

FEATURES

source

Location/Qualifiers
1..499
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3104895"
/clone_lib="NCI_CGAP_Sub9"
/tissue_type="mixed"
/dev_stage="mixed"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT7T3-Pac (Pharmacia) with a modified
polylinker; Site_1: EcoR I; Site_2: Not I; tissues:
Cholonic mucosa with Crohns disease, Cervix, Cervical
ulcerative colitis, Fetal thymus, Cervix, Cervical
adenosquamous carcinoma, Ligament cells, Prostate
carcinoma, Bladder carcinoma, Brain oligodendroga;
NCI_CGAP_Sub9 is a substracted cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT7T3-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is

located between the Not I site and the (dT)18 tail. The
sequence tags for this library are CGTC, AACG, GGGCC,
GGAAG, TAGC, TAAGC, ATGC, AGACA, ATCAC. For additional
information, contact: Bento Soares, bento-soares@uiowa.edu
TAG_LIB=UI-H-C00
TAG_TISSUE=Bladder Carcinoma
TAG_SEQ=AGACA"

BASE COUNT 85 a 155 c 145 g 113 t 1 others
ORIGIN

Alignment Scores:
Pred. No.: 3.18e-30 Length: 499
Score: 305.00 Matches: 60
Percent Similarity: 96.77% Conservative: 0
Best Local Similarity: 96.77% Mismatches: 2
Query Match: 82.88% Indels: 0
DB: 14 Gaps: 0

US-09-993-234-6_COPY_339_409 (1-71) x BQ027499 (1-499)

OY 10 LysGluPheValArgThrLeuGlyLeuArgGluAlaGluIleGluAlaValGlu 29
|||||
DB 499 AAGAGTTCGTGCGCAGCGCTGGGGCTGGCGGAGCAGAGATCGAAACCCGTGAGGTGAG 440
OY 30 IleGlyArgPheArgAspGlnGlnIleTyrGluMetLeuLysArgTrpArgGlnGlnPro 49
|||||
DB 439 ATCGNCCGCTTCCGAGACCAGCAGATGCTCAAGCGCTGGCGCAGCAGCAGCCC 380
OY 50 AlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMetGlyLeuAspGlyCysValGlu 69
|||||
DB 379 GCGGGCTCGAGCGCGTTACGGCGCCCTGGAGCGCATGGGGCTGGACGGCTCGTGGA 320

OY 70 AspLeu 71
|||||
DB 319 GACTTG 314

RESULT 15
AW964958 507 bp mRNA linear EST 01-JUN-2000
LOCUS AW964958/c
DEFINITION EST376926 MAGE resequences, MAGH Homo sapiens cDNA, mRNA sequence.
ACCESSION AW964958
VERSION AW964958.1 GI:8154689
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 507)
AUTHORS Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C., Holt
,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
Quackenbush,J.
TITLE Assessment of gene expression patterns in a model of colon tumor
metastasis using a 19,200 element cDNA microarray
JOURNAL Unpublished (2000)
COMMENT Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: john@tigr.org
Plate: 207
Seq primer: Forward.

FEATURES

source

Location/Qualifiers
1..507
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="MAGE resequences, MAGH"
/note="Vector: pBluescriptKm"
BASE COUNT 85 a 155 c 156 g 111 t
ORIGIN

Alignment Scores: 4.4e-30 Length: 507
Pred. No.:

Score: 304.00
Percent Similarity: 94.03%
Best Local Similarity: 89.55%
Query Match: 82.61%
DB: 10
Matches: 60
Conservative: 3
Mismatch: 4
Indels: 0
Gaps: 0

US-09-993-234-6_COPY_339_409 (1-71) x AW964958 (1-507)

QY 5 ProAlaArgTrpLysGluPheValArgThrLeuGlyLeuArgGluAlaGluIleGlu 24
DB 505 CCAGCCCGCGGATGAAGAAGTTCGTGCGCACGCTGGGCTCGCGAGCAAGATCAAA 446
QY 25 AlavaGluValGluIleGlyArgPheArgAspGlnGlnTyrGluMetLeuLysArgTrp 44
DB 445 CCCGTGAAGGTGAAGATCGGCCGCTCCCGAGACCAAGTACGAGATGCTCAAGCGCTG 386
QY 45 ArgGlnGlnGlnProAlaGlyLeuGlyAlaValTyrAlaAlaLeuGluArgMetGlyLeu 64
DB 385 CGCCAGCAGCAGCCCGCGGCTCGAGCCGTTTACGCGCCCTGAGCGCATGGGGCTG 326
QY 65 AspGlyCysValGluAspLeu 71
DB 325 GACGGCTGCGTGAAGACTTG 305

Search completed: April 6, 2003, 23:25:32
Job time : 447.113 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: Apr11 6, 2003, 13:30:03 ; Search time 2014 Seconds

(without alignments)
8019.889 Million cell updates/sec

Title: US-09-993-234-9_COPY_146_700

Perfect score: 555

Sequence: 1 CTGGGGGGCCCCGGCCACAGG.....GGCAGATGTTCTGGGTCCAG 555

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: gb_da:*
- 2: gb_htg:*
- 3: gb_in:*
- 4: gb_om:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_sts:*
- 12: gb_sy:*
- 13: gb_un:*
- 14: gb_vl:*
- 15: em_ba:*
- 16: em_fun:*
- 17: em_hum:*
- 18: em_in:*
- 19: em_mu:*
- 20: em_om:*
- 21: em_or:*
- 22: em_ov:*
- 23: em_pat:*
- 24: em_ph:*
- 25: em_pl:*
- 26: em_ro:*
- 27: em_sts:*
- 28: em_un:*
- 29: em_vl:*
- 30: em_htg_hum:*
- 31: em_htg_inv:*
- 32: em_htg_other:*
- 33: em_htg_mus:*
- 34: em_htg_pln:*
- 35: em_htg_rod:*
- 36: em_htg_mam:*
- 37: em_htg_vrt:*
- 38: em_sy:*
- 39: em_htgo_hum:*
- 40: em_htgo_mus:*
- 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	555	100.0	1254	6 ARI19657	ARI19657 Sequence
2	555	100.0	1254	9 HSU72763	U72763 Human death
3	555	100.0	1254	9 HSU78029	U78029 Human apopto
4	555	100.0	1254	9 HSU94501	U94501 Human lymph
5	555	100.0	1257	9 HSU94502	U94502 Human lymph
6	555	100.0	1634	9 HSU74611	U74611 Human Apo-3
7	555	100.0	1662	6 AX055442	AX055442 Sequence
8	555	100.0	1662	6 AX201344	AX201344 Sequence
9	555	100.0	1783	6 ARI19656	ARI19656 Sequence
10	553.4	99.7	1528	9 HSU83597	U83597 Human death
11	553.4	99.7	1557	9 HSU75380	U75380 Human apopt
12	541	97.5	1143	9 HSU94510	U94510 Human lymph
13	541	97.5	1355	9 HSU94503	U94503 Human lymph
14	541	97.5	1743	6 AX331947	AX331947 Sequence
15	541	97.5	1743	9 HSWSL1	Y09392 H.sapiens m
16	531	95.7	1250	6 AX150176	AX150176 Sequence
17	512.2	92.3	1669	9 AF026070	AF026070 Homo sapi
18	511	92.1	1763	9 AF026071	AF026071 Homo sapi
19	488	87.9	1087	9 HSU94505	U94505 Human lymph
20	486.4	87.6	808	9 HSU75381	U75381 Human apopt
21	486.4	87.6	809	9 HSU94512	U94512 Human lymph
22	486.4	87.6	816	6 AX335086	AX335086 Sequence
23	486.4	87.6	816	9 HSU83598	U83598 Human death
24	485	87.4	1198	9 HSU94504	U94504 Human lymph
25	322	58.0	651	9 HSU83599	U83599 Human alter
26	319	57.5	1119	9 HSU94509	U94509 Human lymph
27	252	45.4	952	9 HSU94506	U94506 Human lymph
28	242.6	43.7	1665	10 AF329969	AF329969 Mus muscu
29	206	37.1	1619	10 BC017526	BC017526 Mus muscu
30	171.2	30.8	838	9 HSU94507	U94507 Human lymph
31	171	30.8	4811	9 AB051851	AB051851 Homo sapi
32	171	30.8	4825	9 AB051850	AB051850 Homo sapi
33	171	30.8	53982	9 AL158217	AL158217 Human DNA
34	134.8	24.3	665	9 HSU83600	U83600 Human death
35	103	18.6	705	9 HSU94508	U94508 Human lymph
36	95.4	17.2	196368	2 AL772240	AL772240 Mus muscu
37	90.8	16.4	97483	2 AC118359	AC118359 Rattus no
38	85.4	15.4	281	9 HSU94511	U94511 Human lymph
39	57.4	10.3	1581	9 AK094463	AK094463 Homo sapi
40	51.6	9.3	125020	9 AF429315	AF429315 Homo sapi
41	50.2	9.0	667	9 HSA329641	AF429315 Homo sapi
42	50.2	8.0	125020	9 AF429315	AF429315 Homo sapi
43	44.4	7.6	2440	4 BTU90937	U90937 Bos taurus
44	42.2	7.0	280473	2 AC068823	AC068823 Homo sapi
45	39	7.0	280473	2 AC068823	AC068823 Homo sapi

ALIGNMENTS

RESULT 1	ARI19657	ARI19657	1254 bp	DNA	linear	PAT 16-MAY-2001
LOCUS	ARI19657	Sequence 3 from patent US 6153402.				
DEFINITION	ARI19657					
ACCESSION	ARI19657					
VERSION	ARI19657.1	GI:14102356				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 1254)					
AUTHORS	Yu,G.-L., Ni,J., Gentz,R.L. and Dillon,P.J.					
TITLE	Death domain containing receptors					
JOURNAL	Patent: US 6153402-A 3 28-NOV-2000;					
FEATURES	Location/Qualifiers					

source	1. .1254	/organism="unknown"
BASE COUNT	201 a	420 c 407 g 226 t
ORIGIN		

Query Match	100.0%;	Score 555;	DB 6;	Length 1254;
Best Local Similarity	100.0%;	Pred. No. 9.6e-133;		
Matches 555; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	CTGGGGGGCCCCCGAGGGCGGGCACTGTAGCCCCAGGTGTACTGTGCCGGTGACTTC	60
Db	58	CTGGGGGGCCCCCGAGGGCGGGCACTGTAGCCCCAGGTGTACTGTGCCGGTGACTTC	117
QY	61	CACAAGAAATTTGGTCTGTTTGTGTGCAGAGGCTGCCAGCGGGGCACACTACCTGAAGCC	120
Db	118	CACAAGAAATTTGGTCTGTTTGTGTGCAGAGGCTGCCAGCGGGGCACACTACCTGAAGCC	177
QY	121	CCTTGCACGAGCCCTGCGGCACTCCACCTGCGTTGTGTGTCCCAAGACACCTTCTTG	180
Db	178	CCTTGCACGAGCCCTGCGGCACTCCACCTGCGTTGTGTGTCCCAAGACACCTTCTTG	237
QY	181	GCCCTGGGAGAACCCACCATTAATTTCTGAATGTGCCCGCTGCCAGGCCCTGTATGAGCAGGCC	240
Db	238	GCCCTGGGAGAACCCACCATTAATTTCTGAATGTGCCCGCTGCCAGGCCCTGTATGAGCAGGCC	297
QY	241	TCCCAGTGGCGCTGGAGAACTGTTTACAGAGTGGCCGACACCCGCTGTGGCTGTAAGCCA	300
Db	298	TCCCAGTGGCGCTGGAGAACTGTTTACAGAGTGGCCGACACCCGCTGTGGCTGTAAGCCA	357
QY	301	GGCTGGTTTGTGGAGTGCACAGGTACGCCAATGTGTACAGAGTTCACCCCTTACTGCCAA	360
Db	358	GGCTGGTTTGTGGAGTGCACAGGTACGCCAATGTGTACAGAGTTCACCCCTTACTGCCAA	417
QY	361	CCATGCTAGACTGCGGGGCCCTGCACCGCCACACACAGCGCTACTCTGTTCGCCGAGAGAT	420
Db	418	CCATGCTAGACTGCGGGGCCCTGCACCGCCACACACAGCGCTACTCTGTTCGCCGAGAGAT	477
QY	421	ACTGACTGTGGGACCTGCTGCTTGCTTCTATGAAATGGCGATGGCTGCTGTCTCTGC	480
Db	478	ACTGACTGTGGGACCTGCTGCTTGCTTCTATGAAATGGCGATGGCTGCTGTCTCTGC	537
QY	481	CCCAAGAGCACCCTGGGGAGCTGTCCAGAGCGCTGTGCCCTGTCTGTGGCTGGAGGCAG	540
Db	538	CCCAAGAGCACCCTGGGGAGCTGTCCAGAGCGCTGTGCCCTGTCTGTGGCTGGAGGCAG	597
QY	541	ATGTTCCTGGGTCAG	555
Db	598	ATGTTCCTGGGTCAG	612

RESULT	2
LOCUS	HSU72763
DEFINITION	Human death receptor 3 (DR3) mRNA, complete cds.
ACCESSION	H08927
VERSION	U72763.1 GI:1669511
KEYWORDS	.
SOURCE	Homo sapiens. Homo sapiens
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1 (bases 1 to 1254) Chinnaiyan,A.M., O'Rourke,K., Yu,G.-L., Lyons,R.H., Garg,M., Duan,D.R., Xing,L., Gentz,R., Ni,J. and Dixit,V.M. Signal transduction by DR3, a death domain-containing receptor related to TNFR-1 and CD95 <i>Science</i> 274 (5289), 990-992 (1996)
TITLE	JOURNAL MEDLINE PUBMED 97081063 8875942
AUTHORS	Duan,R., Xing,L., Gentz,R., Ni,J. and Dixit,V.M. Direct Submission

JOURNAL Submitted (29-SEP-1996) Pathology, University of Michigan Medical School, 1301 Catherine St., Box 0602, Ann Arbor, MI 48109, USA

FEATURES Location/Qualifiers

source 1. .1254

gene	locus_tag	locus_tag
gene	1. .1254	/gene="DR3"
CDS	1. .1254	

```

/codon_start=1
/product="death receptor 3"
/protein_id="AAC50819.1"
/db_xref="GI:1669512"
/translation="MEQRRPGCAVAANAALLVLLGARAQGGTRSPRCDCAGDFHKKIG
LECCRCGPAGHYLKAPCTEPCGNSTCLVCPDTEFLAWENHHNSECARCOACDEOASQW
ALENCSAVADTRCGCKPGWFVEQVQSQCVSPPYQCPCLDCGALHRTTRLCSRRDT
DCGTCLEPGFEYEHGDGCVSCTSLGSCBERCAAVCGWRQMFVQVLLAGLVYPLLGA
TLITYYRHCWPHKPLVTADAEAGMALPTPSPATHLSPLDSAHTLAPDSEKICTVQL
VGNSTWTPGYPETQELACPQVWTSMWDLPSRALGPAAPTLSPESPAGSPAMLQPGPO
LYDVMDAVPARRMKEFVRTIGLREALEIAEVEIGRFRDQQYEMLKRWKQOQPAGLGA
VYAALERMGLDGCVEDLRSRLQRP"

```

Query Match	100.0%;	Score 555;	DB 9;	Length 1254;
Best Local Similarity	100.0%;	Pred. NO. 9.6e-133;		
Matches 555; Conservative	0;	Mismatches	0;	Gaps 0;

QY	1	CTGGGGGGCCCCGGCCAGAGGGGGGCGACCTGTAAGCCAGGTGTGACTGTGCGCGGTGACTTC	60
Db	58	CTGGGGGGCCCCGGCCAGAGGGGGGCGACCTGTAAGCCAGGTGTGACTGTGCGCGGTGACTTC	117
QY	61	CACAAGAAGATGCTCTGTTTTGTTGACAGAGGCTGCCACAGCGGGGCGACTACCTGAAGCC	120
Db	118	CACAAGAAGATGCTCTGTTTTGTTGACAGAGGCTGCCACAGCGGGGCGACTACCTGAAGCC	177
QY	121	CCTTGACGAGAGCCCTGCGGCACTCCACCTGCCCTTGTGTGTCCCAAGACACACTTCTTG	180
Db	178	CCTTGACGAGAGCCCTGCGGCACTCCACCTGCCCTTGTGTGTCCCAAGACACACTTCTTG	237
QY	181	GCCTGGAGAACCAACCATATTTCTGAATGTGCCCGCTGCCAGGCGTGTATGACAGGCC	240
Db	238	GCCTGGAGAACCAACCATATTTCTGAATGTGCCCGCTGCCAGGCGTGTATGACAGGCC	297
QY	241	TCCCAGGTGCGCGCTGGAGAACTGTTACAGCAGTGGCCGACACACCCGCTGTGGCTGAAGCCA	300
Db	298	TCCCAGGTGCGCGCTGGAGAACTGTTACAGCAGTGGCCGACACACCCGCTGTGGCTGAAGCCA	357
QY	301	GGCTGTTTTGTGGAGTGGCCAGGTACAGCCAAATGTGTCAGCAGTTCACCCCTTCTACTGCCAA	360
Db	358	GGCTGTTTTGTGGAGTGGCCAGGTACAGCCAAATGTGTCAGCAGTTCACCCCTTCTACTGCCAA	417
QY	361	CCATGCTAGACTGCGGGGGCCCTGCACCCGACACACCGGCTACTCTGTGCCGACAGAGAT	420
Db	418	CCATGCTAGACTGCGGGGGCCCTGCACCCGACACACCGGCTACTCTGTGCCGACAGAGAT	477
QY	421	ACTGACTGTGGGACCTGCGCTGCGCTTATGAACATGGCGATGGCTGCGTGTCTTC	480
Db	478	ACTGACTGTGGGACCTGCGCTGCGCTTATGAACATGGCGATGGCTGCGTGTCTTC	537
QY	481	CCCACGAGCACCCCTGGGAGCTGTCCAAGCGCTGTGCCGCTGTGTGGCTGAGGCGAG	540
Db	538	CCCACGAGCACCCCTGGGAGCTGTCCAAGCGCTGTGCCGCTGTGTGGCTGAGGCGAG	597
QY	541	ATGTTCTGGGCTCCAG	555
Db	598	ATGTTCTGGGCTCCAG	612

RESULT 3	
HSU78029	
LOCUS	
HSU78029	
1254 bp	
mRNA	
linear	
PRI 15-JAN-1997	

DEFINITION Human apoptosis inducing receptor AIR mRNA, complete cds.
ACCESSION U78029
VERSION U78029.1 GI:1778763
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 1254)
Degli-Esposti,M.A., Din,W.S., Cosman,D., Smith,C.A. and
Goodwin,R.G.
TITLE AIR, A Novel Member of the TNF Receptor Family, Is a Strong Inducer
of Apoptosis
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1254)
AUTHORS Degli-Esposti,M.A. and Goodwin,R.G.
TITLE Direct Submission
JOURNAL Submitted (12-NOV-1996) Biochemistry, Immunex Corporation, 51
University St., Seattle, WA 98101, USA
FEATURES
source
1..1254
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/map="1pter"
/cell_type="peripheral blood T-cells"
1..1254
/codon_start=1
/product="apoptosis inducing receptor AIR"
/protein_id="AAB40918.1"
/db_xref="GI:1778764"
/translation="MEQRPFGCAVAALLLVLGARAQGGTRSPRCDCAGDFHKKIG
LFCRCGPAGHYLKAPCTEPGNSCLVCPQDTFLAMENHNHNSCARQACDEQASQV
ALENCASAVADTRCGCKPGWFEQVSCVSSSPFYCQPCLDGALHRTLLCSRRDT
DCGTCCLPGFYEHDGCVSPTSTIGSCPERCAAVCGWRQMFVQVLLAGLVPLLLGA
TLTTYRHGWPBKPLVTADAGMEALTPPATHLSPDLSAHTLLAPPDSEKICTVOL
VGNSTPGYPETQDALCPQVTWSMDQLPSRALGPAAPTLSPSPAGSPAMMLQPGPO
LYDVMADVAPARWKEFVRTLGLREAIEIENAVEIGRFRDQYEMLKRWROQOPAGLGA
VYALERMGLDGCVEDLRSRLQRG"

BASE COUNT 201 a 420 c 407 g 226 t
ORIGIN

Query Match 100.0%; Score 555; DB 9; Length 1254;
Best Local Similarity 100.0%; Pred. No. 9.6e-133;
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTGGGGGGCCCCAGGGCCGACCTGCTAGCCCCAGGTGTGACTGTGCGGTGACTTC 60
|||||
Db 58 CTGGGGGGCCCCAGGGCCGACCTGCTAGCCCCAGGTGTGACTGTGCGGTGACTTC 117
OY 61 CACAAGAAGATTGCTGTGTTTGTGACAGAGGCTGCCAGCGGGGCACTACCTGAAGGCC 120
|||||
Db 118 CACAAGAAGATTGCTGTGTTTGTGACAGAGGCTGCCAGCGGGGCACTACCTGAAGGCC 177
OY 121 CCTTGACAGGAGCCCTGGGGCACTCCACCTGCTGTGTGTCGCCAAGACACCTTCTG 180
|||||
Db 178 CCTTGACAGGAGCCCTGGGGCACTCCACCTGCTGTGTGTCGCCAAGACACCTTCTG 237
OY 181 GCCTGGGAGAACCACTAATTTCTGAATGTGCCCGCTGCCAGGCGCTGTGATGAGCAGGCC 240
|||||
Db 238 GCCTGGGAGAACCACTAATTTCTGAATGTGCCCGCTGCCAGGCGCTGTGATGAGCAGGCC 297
OY 241 TCCCAGGTGGCGCTGGAGAACTGTTACAGAGTGGCGGACACCCGCTGTGGCTGTAAAGCA 300
|||||
Db 298 TCCCAGGTGGCGCTGGAGAACTGTTACAGAGTGGCGGACACCCGCTGTGGCTGTAAAGCA 357
OY 301 GGCTGTTTGTGAGTGCAGGTGACCAATGTGTGACAGAGTTACCCCTTCTACTGCCAA 360
|||||
Db 358 GGCTGTTTGTGAGTGCAGGTGACCAATGTGTGACAGAGTTACCCCTTCTACTGCCAA 417
OY 361 CCATGCCTAGACTGGGGCCCTGCACCGCCACACAGCGGCTACTCTGTTCGGCAGAGAT 420
|||||
Db 418 CCATGCCTAGACTGGGGCCCTGCACCGCCACACAGCGGCTACTCTGTTCGGCAGAGAT 477

OY 421 ACTGACTGTGGGACCTGCGCTGCGCTTCTATGAACATGGCGATGGCTGCTGCTGC 480
|||||
Db 478 ACTGACTGTGGGACCTGCGCTGCGCTTCTATGAACATGGCGATGGCTGCTGCTGC 537
OY 481 CCCACGAGCACCCCTGGGAGCTGTCCAGAGCGGCTGTGCCGCTGTCTGTGGCTGAGAGCAG 540
|||||
Db 538 CCCACGAGCACCCCTGGGAGCTGTCCAGAGCGGCTGTGCCGCTGTCTGTGGCTGAGAGCAG 597
OY 541 ATGTTCTGGGCTCCAG 555
|||||
Db 598 ATGTTCTGGGCTCCAG 612

RESULT 4
LOCUS HSU94501
DEFINITION Human lymphocyte associated receptor of death 1a mRNA, complete
cds.
ACCESSION U94501
VERSION U94501.1 GI:2071948
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 1254)
Screation,G.R., Xu,X.N., Olsen,A.L., Cowper,A.E., Tan,R.,
McMichael,A.J. and Bell,J.I.
TITLE LARD: a new lymphoid-specific death domain containing receptor
regulated by alternative pre-mRNA splicing
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)
MEDLINE 9114039
PUBMED 9114039
REFERENCE 2 (bases 1 to 1254)
AUTHORS Screation,G.R.
TITLE Direct Submission
JOURNAL Submitted (19-MAR-1997) Molecular Immunology Group, Institute of
Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3
9DU, UK
FEATURES
source
Location/Qualifiers
1..1254
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Hela"
/cell_type="lymphocyte"
1..1254
/function="mediates apoptosis"
/note="LARD-1a; membrane protein; similar to Fas and
TNF-R1; contains a death domain"
/codon_start=1
/product="lymphocyte associated receptor of death 1a"
/protein_id="AAC51306.1"
/db_xref="GI:2071949"
/translation="MEQRPFGCAVAALLLVLGARAQGGTRSPRCDCAGDFHKKIG
LFCRCGPAGHYLKAPCTEPGNSCLVCPQDTFLAMENHNHNSCARQACDEQASQV
ALENCASAVADTRCGCKPGWFEQVSCVSSSPFYCQPCLDGALHRTLLCSRRDT
DCGTCCLPGFYEHDGCVSPTSTIGSCPERCAAVCGWRQMFVQVLLAGLVPLLLGA
TLTTYRHGWPBKPLVTADAGMEALTPPATHLSPDLSAHTLLAPPDSEKICTVOL
VGNSTPGYPETQDALCPQVTWSMDQLPSRALGPAAPTLSPSPAGSPAMMLQPGPO
LYDVMADVAPARWKEFVRTLGLREAIEIENAVEIGRFRDQYEMLKRWROQOPAGLGA
VYALERMGLDGCVEDLRSRLQRG"

BASE COUNT 201 a 420 c 407 g 226 t
ORIGIN

Query Match 100.0%; Score 555; DB 9; Length 1254;
Best Local Similarity 100.0%; Pred. No. 9.6e-133;
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTGGGGGGCCCCAGGGCCGACCTGCTAGCCCCAGGTGTGACTGTGCGGTGACTTC 60
|||||
Db 58 CTGGGGGGCCCCAGGGCCGACCTGCTAGCCCCAGGTGTGACTGTGCGGTGACTTC 117

QY 61 CACAAGAGATTGCTGTTTGTGTCAGAGGCTGCCAGCGGGGACACTACCTGAAGGCC 120
|||||
Db 118 CACAAGAGATTGCTGTTTGTGTCAGAGGCTGCCAGCGGGGACACTACCTGAAGGCC 177
QY 121 CCTGCACGAGCCCTGCGGCACTCCACCCTGCTGTGTGTCTCCCAAGACACTTCTTG 180
|||||
Db 178 CCTGCACGAGCCCTGCGGCACTCCACCCTGCTGTGTGTCTCCCAAGACACTTCTTG 237
QY 181 GCCTGGAGAACCACTAATTTCTGAATGTGCCCCCTGCCAGGCTGTGATGAGCAGGCC 240
|||||
Db 238 GCCTGGAGAACCACTAATTTCTGAATGTGCCCCCTGCCAGGCTGTGATGAGCAGGCC 297
QY 241 TCCAGAGTGGCGTGGAGAACTGTTTCAGCAGTGGCCGACACCCGCTGTGCTGTAAGCCA 300
|||||
Db 298 TCCAGAGTGGCGTGGAGAACTGTTTCAGCAGTGGCCGACACCCGCTGTGCTGTAAGCCA 357
QY 301 GGCTGTTTGTGAGTGCCAGGTCCAGCAATGTGTGACAGTTTCACTTCTACTGCCAA 360
|||||
Db 358 GGCTGTTTGTGAGTGCCAGGTCCAGCAATGTGTGACAGTTTCACTTCTACTGCCAA 417
QY 361 CCATGCTAGACTGCGGGCCCTGCACCGCCACACAGCGCTACTCTGTTCCCGCAGAGAT 420
|||||
Db 418 CCATGCTAGACTGCGGGCCCTGCACCGCCACACAGCGCTACTCTGTTCCCGCAGAGAT 477
QY 421 ACTGACTGTGGACCTGCTGCTGCTGCTATGAACATGCGCATGCGCTGCTGCTGC 480
|||||
Db 478 ACTGACTGTGGACCTGCTGCTGCTGCTATGAACATGCGCATGCGCTGCTGCTGC 537
QY 481 CCCACGAGACCCCTGGGGAGCTGTCCAGAGCGCTGTGCCGTGTGTGCGCTGGAGGCG 540
|||||
Db 538 CCCACGAGACCCCTGGGGAGCTGTCCAGAGCGCTGTGCCGTGTGTGCGCTGGAGGCG 597
QY 541 ATGTTCTGGGTCCAG 555
|||||
Db 598 ATGTTCTGGGTCCAG 612

RESULT 5
HSU94502
LOCUS 1257 bp mRNA linear PRI 15-MAY-1997
DEFINITION Human lymphocyte associated receptor of death 1b mRNA,
alternatively spliced, complete cds.
ACCESSION U94502.1 GI:2071950
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens.
Homo sapiens.
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 1257)
Screation,G.R., Xu,X.N., Olsen,A.L., Cowper,A.E., Tan,R.,
McMichael,A.J. and Bell,J.I.
LARD: a new lymphoid-specific death domain containing receptor
regulated by alternative pre-mRNA splicing
Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)
JOURNAL
MEDLINE 97272273
PUBMED 9114039
REFERENCE 2 (bases 1 to 1257)
AUTHORS Screation,G.R.
TITLE Direct Submission
JOURNAL Submitted (19-MAR-1997) Molecular Immunology Group, Institute of
Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3
9DU, UK

FEATURES
source
1. .1257
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Hela"
/cell_type="lymphocyte"
1. .1257
/function="mediates apoptosis"
/note="LARD-1b; membrane protein; similar to Fas and
TNF-R1; contains a death domain"

/codon_start=1
/product="lymphocyte associated receptor of death 1b"
/protein_id="AAC51307.1"
/db_xref="GI:2071951"
/translation="MEORPRGCAVAALLLVLGARAQGTGTRSPRCDAGDFHKKIG
LFCRRGCPAGHYLKAPECIEGNSSTLCVPODFTLAWENHNHNSCARCQACDEASQY
ALENCSAVADTRCGCKPGWFEQVSOVSSSPFYCOPLDCGALHRTLRSLCSRD
DCGTCCLPGFYEHDGCVSCPSTLGSCEPERCAAVCGNRQFWVQVLLAGLVPLLGA
TLTYTYRHQWPHKPLVRADEAGMEALTPPATHTLSPLDSAHLLAPDSSEKICTYO
LVGNSWTPGYPETQELCPQVTSWDQLPSRALPAAPTLSPESPAGSPAMLOQGP
OLYDMDAVPARRWKEFYRTGLREAIEAVEVEIGFRDQYEMLRWRQDQPAIGL
AVYALERMGLDGVEDLRSRLQRP"
misc_feature
708..711
/note="insertion compared to LARD-1a, deposited in GenBank
Accession Number U94501, probably represents alternative
3' splice site"
BASE COUNT 202 a 421 c 408 g 226 t
ORIGIN

Query Match 100.0%; Score 555; DB 9; Length 1257;
Best Local Similarity 100.0%; Pred. No. 9.6e-133;
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGGGCCCCCGCCAGGGCGGCACTGTAACCCAGGTGTGACTGTGCCGGTACTTC 60
|||||
Db 58 CTGGGGCCCCCGCCAGGGCGGCACTGTAACCCAGGTGTGACTGTGCCGGTACTTC 117
QY 61 CACAAGAGATTGCTGTTTGTGTCAGAGGCTGCCAGCGGGGCACTAAGAGGCC 120
|||||
Db 118 CACAAGAGATTGCTGTTTGTGTCAGAGGCTGCCAGCGGGGCACTAAGAGGCC 177
QY 121 CCTGCACGAGACCCCTGCGGCACTGCACTGCTGTGTGTGCCAAGACACCTTCTTG 180
|||||
Db 178 CCTGCACGAGACCCCTGCGGCACTGCACTGCTGTGTGTGCCAAGACACCTTCTTG 237
QY 181 GCCTGGAGAACCACTAATTTCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCC 240
|||||
Db 238 GCCTGGAGAACCACTAATTTCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCC 297
QY 241 TCCAGAGTGGCGCTGGAGAACTGTTTCAGCAGTGGCCGACACCGGCTGTGCTGAAGCCA 300
|||||
Db 298 TCCAGAGTGGCGCTGGAGAACTGTTTCAGCAGTGGCCGACACCGGCTGTGCTGAAGCCA 357
QY 301 GGCTGTTTGTGAGTGCACAGTCAACCAATGTGTACAGATTCACCTTCTACTGCCAA 360
|||||
Db 358 GGCTGTTTGTGAGTGCACAGTCAACCAATGTGTACAGATTCACCTTCTACTGCCAA 417
QY 361 CCATGCTAGACTGCGGGCCCTGCACCGCCACACAGCGCTACTCTGTCCGACAGAGAT 420
|||||
Db 418 CCATGCTAGACTGCGGGCCCTGCACCGCCACACAGCGCTACTCTGTGTCCGACAGAGAT 477
QY 421 ACTGACTGTGGAGACCTGCTGCTGCTTCTATGAACATGGCGATGGCTGCTGCTGC 480
|||||
Db 478 ACTGACTGTGGAGACCTGCTGCTGCTTCTATGAACATGGCGATGGCTGCTGCTGC 537
QY 481 CCCACGAGACCCCTGGGGAGCTGTCCAGAGCGCTGTGCCGTGTGTGCTGGAGGCG 540
|||||
Db 538 CCCACGAGACCCCTGGGGAGCTGTCCAGAGCGCTGTGCCGTGTGTGCTGGAGGCG 597
QY 541 ATGTTCTGGGTCCAG 555
|||||
Db 598 ATGTTCTGGGTCCAG 612

RESULT 6
HSU74611
LOCUS HSU74611 1634 bp mRNA linear PRI 02-JAN-1997
DEFINITION Human Apo-3 mRNA, complete cds.
ACCESSION U74611
VERSION U74611.1 GI:1763292
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1634)
AUTHORS Marsters,S.A., Sheridan,J.P., Donahue,C.J., Pittl,R.M., Gray,C.L.,
Goddard,A.D., Bauer,K.D. and Ashkenazi,A.
TITLE Apo-3, a new member of the tumor necrosis factor receptor family,
contains a death domain and activates apoptosis and NF-kB
JOURNAL Curr. Biol. (1996) In press
REFERENCE 2 (bases 1 to 1634)
AUTHORS Marsters,S.A., Sheridan,J.P., Donahue,C.J., Pittl,R.M., Gray,C.L.,
Goddard,A.D., Bauer,K.D. and Ashkenazi,A.
TITLE Direct Submission
JOURNAL Submitted (15-OCT-1996) Molecular Oncology, Genentech, 460 Pt. San
Bruno Blvd., South San Francisco, CA 94080, USA
FEATURES
source
Location/Qualifiers
1. 1634
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/map="1p36.3"
/tissue_type="heart"
/dev_stage="fetal"
89. 1342
/note="contains death domain, activates apoptosis and
NF-kB; TNF receptor family member"
/codon_start=1
/product="Apo-3"
/protein_id="AAB39714.1"
/db_xref="GI:1763293"
/translation="MEQRPKCAVAALLLVLGARAQGTSPKDCADGFHKKIG
LFCRGGCPAGHYLKAPCTEPCNSICLVCPDPTFLAMENHNHNSCARCQACDEQASOV
ALENCSAVADTRCGCKPGWFEVCOVSCVSSPEYCOPLDCGALHRTLLCSRDY
DCGTCLPGEYEHGDGCVSPTSLGSCPERCAVCGWROMENYQVLLAGLVPLLGA
TLTYTRHCWPHKPLVTADAGMALTPPATHLSPDLSAHTLAPDSSEKICTVOL
VGNWTPGYPETQALCPQVYMSNDQLPSRALPAAPTLSPSPAGSPAMLOPQPO
LYVMDAVPARRWKEFVRTLGLREAEIEAVEIGRFRDQYEMLKRWKQQQPAIGLA
VVALERMGLDGCVEDLRSLQRP"
BASE COUNT 300 a 528 c 519 g 287 t
ORIGIN
Query Match 100.0%; Score 555; DB 9; Length 1634;
Best Local Similarity 100.0%; Pred. No. 9.4e-133;
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 566 ACTGACTGTGGAGACCTGCTCCCTGGCTTCTATGAACATGCGCATGGCTGCTGCTGC 625
QY 481 CCCACGAGCACCCCTGGGAGCTGTCCAGAGCGCTGTGCCGTGTCTGTGGCTGAGGCGAG 540
Db 626 CCCACGAGCACCCCTGGGAGCTGTCCAGAGCGCTGTGCCGTGTCTGTGGCTGAGGCGAG 685
QY 541 ATGTTCTGGGTCCAG 555
Db 686 ATGTTCTGGGTCCAG 700
RESULT 7
AX055442
LOCUS AX055442 1662 bp DNA linear PAT 13-JAN-2001
DEFINITION Sequence 72 from Patent WO0073452.
ACCESSION AX055442
VERSION AX055442.1 GI:12228713
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1662)
AUTHORS Ashkenazi,A.J., Baker,K.P., Chan,B., Goddard,A., Godowski,P.J.,
Gurney,A.L., Hebert,C., Henzel,W., Kabakoff,R.C., Shelton,D.L.,
Tumas,D., Watanabe,C.K. and Wood,W.I.
TITLE Compositions and methods for the treatment of immune related
diseases
JOURNAL Patent: WO 0073452-A 72 07-DEC-2000;
Genentech, Inc. (US)
FEATURES
source
1. 1662
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 302 a 540 c 531 g 289 t
ORIGIN
Query Match 100.0%; Score 555; DB 6; Length 1662;
Best Local Similarity 100.0%; Pred. No. 9.4e-133;
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 481 CCCACGAGCACCCTGGGAGCTGTCCAGAGCGCTGTGCTGTGCTGTGAGGCGAG 540
|||||
Db 640 CCCACGAGCACCCTGGGAGCTGTCCAGAGCGCTGTGCTGTGCTGTGAGGCGAG 699
QY 541 ATGTTCTGGGTCCAG 555
|||||
Db 700 ATGTTCTGGGTCCAG 714

RESULT 8
AX201344
LOCUS AX201344 1662 bp DNA linear PAT 30-AUG-2001
DEFINITION Sequence 23 from Patent WO0153486.
ACCESSION AX201344
VERSION AX201344.1 GI:15391165
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1662)
AUTHORS Ashkenazi,A.J., Goddard,A., Godowski,P.J., Gurney,A.L.,
Hillan,K.J., Marsters,S.A., Pan,J., Pilti,R.M., Roy,M.A., Smith,V.,
Stone,D.M., Watanabe,C.K. and Wood,W.I.
TITLES Positions and methods for the treatment of tumour
JOURNAL Patent: WO 0153486-A 23 26-JUL-2001;
Genentech, Inc. (US)
FEATURES
source location/Qualifiers
1..1662
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 302 a 540 c 531 g 289 t
ORIGIN

Query Match 100.0%; Score 555; DB 6; Length 1662;
Best Local Similarity 100.0%; Pred. No. 9.4e-133;
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGGGCCCCGGCCAGGGGGGCGACTGTAGCCCCAGGTGTGACTGTCCGGTACTTC 60
|||||
Db 160 CTGGGGCCCCGGCCAGGGGGGCGACTGTAGCCCCAGGTGTGACTGTCCGGTACTTC 219
QY 61 CACAAGAGATTGCTGTTTGTGTCAGAGGCTGCCAGCGGGGCACTACCTGAAGGCC 120
|||||
Db 220 CACAAGAGATTGCTGTTTGTGTCAGAGGCTGCCAGCGGGGCACTACCTGAAGGCC 279
QY 121 CCTTGACGAGAGCCCTGCGCAACTCCACTGCTGTGTGTCCCAAGACACTTCTTG 180
|||||
Db 280 CCTTGACGAGAGCCCTGCGCAACTCCACTGCTGTGTGTCCCAAGACACTTCTTG 339
QY 181 GCCTGGGAGAACCAACCATATTCGATGTGCCCCGCTGCCAGGCTGTGATGAGCAGGCC 240
|||||
Db 340 GCCTGGGAGAACCAACCATATTCGATGTGCCCCGCTGCCAGGCTGTGATGAGCAGGCC 399
QY 241 TCCCAAGTGGCGCTGGAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGGTGAAGCCA 300
|||||
Db 400 TCCCAAGTGGCGCTGGAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGGTGAAGCCA 459
QY 301 GGCTGGTTTGTGAGTGCAGGTGACCAATGTGTACAGCACTACCTTCTACTGCCAA 360
|||||
Db 460 GGCTGGTTTGTGAGTGCAGGTGACCAATGTGTACAGCACTACCTTCTACTGCCAA 519
QY 361 CCATGCTTAGACTGCGGGGCTGCACCGCCACACAGCGCTACTCTGTCCCGCAGAGAT 420
|||||
Db 520 CCATGCTTAGACTGCGGGGCTGCACCGCCACACAGCGCTACTCTGTCCCGCAGAGAT 579
QY 421 ACTGACTGTGGAGCTGCGCTGCTCTATGACATGCGGATGGCTGCTGCTGC 480
|||||
Db 580 ACTGACTGTGGAGCTGCGCTGCTCTATGACATGCGGATGGCTGCTGCTGC 639
QY 481 CCCACGAGCACCCTGGGAGCTGTCCAGAGCGCTGTGCTGTGCTGTGAGGCGAG 540
|||||

Db 640 CCCACGAGCACCCTGGGAGCTGTCCAGAGCGCTGTGCTGTGCTGTGAGGCGAG 699
QY 541 ATGTTCTGGGTCCAG 555
|||||
Db 700 ATGTTCTGGGTCCAG 714

RESULT 9
AR119656
LOCUS AR119656 1783 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 1 from patent US 6153402.
ACCESSION AR119656
VERSION AR119656.1 GI:14102355
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1783)
AUTHORS Yu,G.-L., Ni,J., Gentz,R.L. and Dillon,P.J.
TITLES Death domain containing receptors
JOURNAL Patent: US 6153402-A 1 28-NOV-2000;
FEATURES
source location/Qualifiers
1..1783
/organism="unknown"

BASE COUNT 330 a 562 c 564 g 327 t
ORIGIN

Query Match 100.0%; Score 555; DB 6; Length 1783;
Best Local Similarity 100.0%; Pred. No. 9.3e-133;
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGGGCCCCGGCCAGGGGGGCGACTGTAGCCCCAGGTGTGACTGTCCGGTACTTC 60
|||||
Db 288 CTGGGGCCCCGGCCAGGGGGGCGACTGTAGCCCCAGGTGTGACTGTCCGGTACTTC 347
QY 61 CACAAGAGATTGCTGTTTGTGTCAGAGGCTGCCAGCGGGGCACTACCTGAAGGCC 120
|||||
Db 348 CACAAGAGATTGCTGTTTGTGTCAGAGGCTGCCAGCGGGGCACTACCTGAAGGCC 407
QY 121 CCTTGACGAGAGCCCTGCGCAACTCCACTGCTGTGTGTCCCAAGACACTTCTTG 180
|||||
Db 408 CCTTGACGAGAGCCCTGCGCAACTCCACTGCTGTGTGTCCCAAGACACTTCTTG 467
QY 181 GCCTGGGAGAACCAACCATATTCGATGTGCCCCGCTGCCAGGCTGTGATGAGCAGGCC 240
|||||
Db 468 GCCTGGGAGAACCAACCATATTCGATGTGCCCCGCTGCCAGGCTGTGATGAGCAGGCC 527
QY 241 TCCCAAGTGGCGCTGGAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGGTGAAGCCA 300
|||||
Db 528 TCCCAAGTGGCGCTGGAGAACTGTTCAGCAGTGGCCGACACCCGCTGTGGTGAAGCCA 587
QY 301 GGCTGGTTTGTGAGTGCAGGTGACCAATGTGTACAGCACTACCTTCTACTGCCAA 360
|||||
Db 588 GGCTGGTTTGTGAGTGCAGGTGACCAATGTGTACAGCACTACCTTCTACTGCCAA 647
QY 361 CCATGCTTAGACTGCGGGGCTGCACCGCCACACAGCGCTACTCTGTTCGCCAGAGAT 420
|||||
Db 648 CCATGCTTAGACTGCGGGGCTGCACCGCCACACAGCGCTACTCTGTTCGCCAGAGAT 707
QY 421 ACTGACTGTGGAGCTGCGCTGCTCTATGACATGCGGATGGCTGCTGCTGC 480
|||||
Db 708 ACTGACTGTGGAGCTGCGCTGCTCTATGACATGCGGATGGCTGCTGCTGC 767
QY 481 CCCACGAGCACCCTGGGAGCTGTCCAGAGCGCTGTGCTGTGCTGTGAGGCGAG 540
|||||
Db 768 CCCACGAGCACCCTGGGAGCTGTCCAGAGCGCTGTGCTGTGCTGTGAGGCGAG 827
QY 541 ATGTTCTGGGTCCAG 555
|||||
Db 828 ATGTTCTGGGTCCAG 842
RESULT 10

HSU83597	1528 bp	mRNA	linear	PRI 27-JAN-1997
LOCUS				
DEFINITION	Human death domain receptor 3 (DDR3)	mRNA,	partial	cds.
ACCESSION	U83597			
VERSION	U83597.1	GI:1800292		
KEYWORDS				
SOURCE	Homo sapiens.			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE	1 (bases 1 to 1528)			
AUTHORS	Chaudhary, P.M. and Hood, L.E.			
TITLE	Direct Submission			
JOURNAL	Submitted (03-JAN-1997) Molecular Biotechnology, University of			
	Washington, 1705 NE Pacific Street, HSB-K360, Seattle, WA 98195,			
	USA			

FEATURES	Location/Qualifiers
source	1. .1528

gene
CDS

```

/function="mediates apoptosis when cross-linked"
/note="A TNFR1-related death-domain containing receptor;
DR3, WSL-LR, Apo-3, TRAMP; transmembrane form; similar to
human EST clone 298913, GenBank Accession Number N71143"
/codon_start=3
/product="death domain receptor 3"
/protein_id="AAB41432.1"

```

```

/translation="GCAAVAAALLLVLLGARAÖGGTRSPRCDCAGDFHKKIGLFCRG
CPAGHTLAKPCTEPCNGSTGLVCPODFELAMENHNHNSCARCOACBOASQVLALES
AVADTRCGCKPWFVEVCQVSCVSSSPFYCQPCLDGALHRTLRLLCSRDYDGCGL
LGFVEHSDGCVSCPTSTIGSCPERCAYCGWRMFVQVLLAGLVPLLDGATLTYTY
RHCPHNPRLVLTADAGMEALTPPPATHSLPDSANTLLAPPDSEKICTVQLVGNSWT
PGYPEIQEOLACPOVWTSMQDLPSRALGPAAPTLSPSPAGSPAMMIOGPOLYDVMD
AVPARRKEFVTRTGLRLEAEI EAVEVEIGRFRDQYEMLKRWKQQCPAGLGAVYAALE
RMGDCGCEVDLRSLRQGP"

```

BASE COUNT	280 a	496 c	470 g	282 t
ORIGIN				

Query Match	99.7%;	Score 553.4;	DB 9;	length 1528;
Best Local Similarity	99.8%;	Pred. No. 2.4e-132;		
Matches 554; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

Qy 1 CTGGGGCCCCGGGCCAGGGCGGCACTGTAGCCCCAGGTGTGACTGTGCCGCTGACTTC 60
|||||
42 CTGGGGCCCCGGGCCAGGGCGGCACTGTAGCCCCAGGTGTGACTGTGCCGCTGACTTC 101

QY 61 CACAGAGAATTGCTCTGTTTGTTCAGAGGCTGCCAGCGGGCAGTACCTGAAGGCC 120
|||||
102 CACAGAGAATTGCTCTGTTTGTTCAGAGGCTGCCAGCGGGGCACTAAGGCC 161

QY	121	CCCTGCACGGAGCCCTGCGGCACTCCACCTGCCTGTGTGTCCCAAGACACCTTCTTG	180
Db	162	CCCTGCACGGAGCCCTGCGGCACTCCACCTGCCTGTGTGTCCCAAGACACCTTCTTG	221

[illegible]

QY 241 TCCAGCTGGCGCTGAGAACTGTTACAGAGTGCCGACACCCGCTGTGGCTGTAAGCCA 300
|||||
Db 282 TCCAGGTGGCGCTGGAGAACTGTTACAGAGTGCCGACACCCGCTGTGGCTGTAAGCCA 341

QY 301 GCGTCGTTTGTGAGTGCAGGTCAGCCAATGTGTACAGAGTTCACCCCTTCTACTGCCAA 360
|||||
Db 342 GCGTCGTTTGTGAGTGCAGGTCAGCCAATGTGTACAGAGTTCACCCCTTCTACTGCCAA 401

QY 361 CCATGCTAGACTGCGGGGCCCTGCACCGCCACACACGGCTACTGTGTCCCGCAGAGAT 420
|||||
Db 402 CCATGCTTAGACTGCGGGGCCCTGCACCGCCACACACGGCTACTGTGTCCCGCAGAGAT 461

QY 421 ACTGACTGTGGGACCTGCCTGCCTGGCTTCTATGAACATGGCGATGGCTGCCTGTCTCTGC 480
|||||
Db 462 ACTGACTGTGGGACCTGCCTGCCTGGCTTCTATGAACATGGCGATGGCTGCCTGTCTCTGC 521

QY 481 CCCACGACCAACCCTGGGGAGCTGTCCAGACCGCTGTGCCGCTGTCTGTGGCTGGAGGCAG 540
|||||
Db 522 CCCACGACCAACCCTGGGGAGCTGTCCAGACCGCTGTGCCGCTGTCTGTGGCTGGAGGCAG 581

QY 541 ATGTTCTGGGTCCAG 555
|||||
Db 582 ATGTTCTGGGTCCAG 596

RESULT	11
HSU75380	
LOCUS	HSU75380
DEFINITION	Human apoptosis-mediating receptor TRAMP mRNA, partial cds.
ACCESSION	U75380
VERSION	U75380.1 GI:1695924
	1557 bp
	mRNA linear PRI 05-APR-1997

SOURCE ORGANISM	Homo sapiens . Homo sapiens
-----------------	--------------------------------

REFERENCE
Bodmer, J.L., Burns, K., Schneider, P., Hofmann, K., Steiner, V.
AUTHORS

JOURNAL	TITLE
Immunitivity 6 (1): 79-88 (1997)	French, L.E., Browning, J.L., MacDonald, R. and Tschopp, J. TRAMP, a novel apoptosis-mediating receptor with sequence homology to tumor necrosis factor receptor 1 and Fas(Apo-1/CD95)

COGNATE	97205335	9052839
MEDLINE	97205335	9052839
PUBMED	97205335	9052839

REFERENCE	AUTHORS
2 (bases 1 to 1557)	Bodmer, J.L., Burns, K., Schneider, P., Hofmann, K., Steiner, V., Thome, M., Bornaand, T., Hahne, M., Schroter, M., Wilson, A., French, L.E., Browning, J.L., Macdonald, R. and Tschopp, J.

JOURNAL
 Submitted (18-OCT-1996) Institute of Biochemistry, University of
 Lausanne, 155 Chemin des Boveresses, Epalinges, CH 1066,
 Switzerland

FEATURES	Location/Qualifiers
source	1. .1557

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/map="1p36.2"
/tissue-type="fetal lung"
<1.1245
CDS

```

```

/function="activates NF- $\kappa$ B"
/function="mediates apoptosis"
/note="contains a death domain; similar to TNF receptor"
/codon_start=1
/product="apoptosis-mediating receptor TRAMP"
/protein_id="AAC51192.1"
/db_xref="GI:1695925"
/translation="AAAGCAVAMALLLVLGARAQGGRSPRCDCAGDFHKKIGLFC
CRGCPAGHYLKAPCTEPFCGNSTCLVCPDPTFLAMENHHNSECARCDDEASOVALE
NCSAVADTRCGCKPGMFEVCQVSQCVSSFFPYCQPLDCGALHRRHTRLLCSRDDTDCG
TCLIGFYEHGDCVSCPTSTGLSCPERCAVCGRMFVWQVLLAGLVPLLGATLT
YTYRHCMPHKPLVLTADAGMEALTPPATHTSLPDSAHNTLLAPPDSSERICTVQLVGN
SWTPGYPETQEALECPQVLTWSMDQLPSRALGPAAPTLSPESPAGSPAMMLQPGPOLYD
VMDVAPARRMKEFVRTGLRREAIEAVEVEIGRFRDQYEMLKRMWQQPAGLGAVYA
ALERMGLDGCVEDLRSRLQGRP"

```

BASE COUNT	286 a	508 c	477 g	286 t
ORIGIN				
Query Match		99.7%;	Score 553.4;	DB 9;
Best Local Similarity		99.8%;	Pred. No. 2.4e-132;	Length 1557;

Matches 554; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGGGGCCCCCAGGGGGGCGACCTCGTAGCCCCCAGGTGTGACTGTGCGGCTGACTTC 60
Db 49 CTGGGGCCCCCAGGGGGGCGACCTCGTAGCCCCCAGGTGTGACTGTGCGGCTGACTTC 108
QY 61 CACAAGAGATTGGTCTGTTTGTTCAGAGGCTGCCAGCGGGGCACTACTGAAGGCC 120
Db 109 CACAAGAGATTGGTCTGTTTGTTCAGAGGCTGCCAGCGGGGCACTACTGAAGGCC 168
QY 121 CCTTGCACGGAGCCCTGCGGCACTCCACTGCTGTGTGTCCCAAGACACCTTCTTG 180
Db 169 CCTTGCACGGAGCCCTGCGGCACTCCACTGCTGTGTGTCCCAAGACACCTTCTTG 228
QY 181 GCGTGGAGAACCAACCATATTTCTGAATGTGCCCCGCTGCCAGGCGCTGTATGAGAGGCC 240
Db 229 GCGTGGAGAACCAACCATATTTCTGAATGTGCCCCGCTGCCAGGCGCTGTATGAGAGGCC 288
QY 241 TCCAGGTGGCGCTGGAGAACTGTTCAAGAGTGGCCGACACCCGCTGTGGCTGAAGCCA 300
Db 289 TCCAGGTGGCGCTGGAGAACTGTTCAAGAGTGGCCGACACCCGCTGTGGCTGAAGCCA 348
QY 301 GCGTGGTGTGTGAGTGCAGGTCCAGGCAATGTGTACAGAGTTACCCCTTCTACTGCCAA 360
Db 349 GCGTGGTGTGTGAGTGCAGGTCAGGCAATGTGTACAGAGTTACCCCTTCTACTGCCAA 408
QY 361 CCATGCTTAGACTGCGGGGCGCTGCACCGCCACACACGGCTACTGTGTCCCGAGAGAT 420
Db 409 CCATGCTTAGACTGCGGGGCGCTGCACCGCCACACACGGCTACTGTGTCCCGAGAGAT 468
QY 421 ACTGACTGTGGAGACCTGCGCTGCTCTATGAACATGGCGATGGCTGCTCCTGC 480
Db 469 ACTGACTGTGGAGACCTGCGCTGCTCTATGAACATGGCGATGGCTGCTCCTGC 528
QY 481 CCCACGAGCAACCTGGGAGCTGTCCAGAGCGCTGTGCCGTGTGTGGCTGAGAGCAG 540
Db 529 CCCACGAGCAACCTGGGAGCTGTCCAGAGCGCTGTGCCGTGTGTGGCTGAGAGCAG 588
QY 541 ATGTTCTGGGTCCAG 555
Db 589 ATGTTCTGGGTCCAG 603

RESULT 12
HSU94510

LOCUS 1143 bp mRNA linear PRI 15-MAY-1997
DEFINITION Human lymphocyte associated receptor of death 9 mRNA, alternatively
spliced, complete cds.

ACCESSION U94510
VERSION U94510.1 GI:2071966
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens.

REFERENCE 1 (bases 1 to 1143)
AUTHORS McMichael,A.J. and Bell,J.I.
TITLE LARD: a new lymphoid-specific death domain containing receptor
regulated by alternative pre-mRNA splicing
Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)

JOURNAL MEDLINE 97272273
PUBMED 9114039
REFERENCE 2 (bases 1 to 1143)
AUTHORS Sreaton,G.R.
TITLE Direct Submission
JOURNAL Submitted (19-MAR-1997) Molecular Immunology Group, Institute of
Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3
9DU, UK

FEATURES
source location/Qualifiers
1..1143
/organism="Homo sapiens"
/db_xref="taxon:9606"

CDS
/cell_line="Hela"
/cell_type="lymphocyte"
1..1143
/function="mediates apoptosis"
/note="LARD-9; NGFR family member; similar to Fas and
TNF-R1"
/codon_start=1
/product="lymphocyte associated receptor of death 9"
/protein_id="A051315.1"
/db_xref="GI:2071967"

misc_feature
598..599
/note="deletion compared to LARD 1a, deposited in GenBank
Accession Number U94501, probable skipping of putative
exon 7 encoding the transmembrane domain"

BASE COUNT 188 a 378 c 378 g 199 t
ORIGIN

Query Match 97.5%; Score 541; DB 9; Length 1143;
Best Local Similarity 100.0%; Pred. No. 4e-129;
Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGGGCCCCCAGGGGGGCGACCTCGTAGCCCCCAGGTGTGACTGTGCGGCTGACTTC 60
Db 58 CTGGGGCCCCCAGGGGGGCGACCTCGTAGCCCCCAGGTGTGACTGTGCGGCTGACTTC 117
QY 61 CACAAGAGATTGGTCTGTTTGTTCAGAGAGGCTGCCAGCGGGCACTACTGAAGGCC 120
Db 118 CACAAGAGATTGGTCTGTTTGTTCAGAGAGGCTGCCAGCGGGCACTACTGAAGGCC 177
QY 121 CCTTGCACGGAGCCCTGCGGCACTCCACTGCTGTGTGTCCCAAGACACCTTCTTG 180
Db 178 CCTTGCACGGAGCCCTGCGGCACTCCACTGCTGTGTGTCCCAAGACACCTTCTTG 237
QY 181 GCGTGGAGAACCAACCATATTTCTGAATGTGCCCCGCTGCCAGCGCTGTATGAGAGGCC 240
Db 238 GCGTGGAGAACCAACCATATTTCTGAATGTGCCCCGCTGCCAGCGCTGTATGAGAGGCC 297
QY 241 TCCAGGTGGCGCTGGAGAACTGTTCAAGAGTGGCCGACACCCGCTGTGGCTGAAGCCA 300
Db 298 TCCAGGTGGCGCTGGAGAACTGTTCAAGAGTGGCCGACACCCGCTGTGGCTGAAGCCA 357
QY 301 GCGTGGTGTGTGAGTGCAGGTCCAGGCAATGTGTACAGAGTTACCCCTTCTACTGCCAA 360
Db 358 GCGTGGTGTGTGAGTGCAGGTCAGGCAATGTGTACAGAGTTACCCCTTCTACTGCCAA 417
QY 361 CCATGCTTAGACTGCGGGGCGCTGCACCGCCACACACGGCTACTCTGTCCCGAGAGAT 420
Db 418 CCATGCTTAGACTGCGGGGCGCTGCACCGCCACACACGGCTACTCTGTCCCGAGAGAT 477
QY 421 ACTGACTGTGGAGACCTGCGCTGCTCTATGAACATGGCGATGGCTGCGTGTCTGC 480
Db 478 ACTGACTGTGGAGACCTGCGCTGCTCTATGAACATGGCGATGGCTGCGTGTCTGC 537
QY 481 CCCACGAGCAACCTGGGAGCTGTCCAGAGCGCTGTGCCGTGTGTGGCTGAGAGCAG 540
Db 538 CCCACGAGCAACCTGGGAGCTGTCCAGAGCGCTGTGCCGTGTGTGGCTGAGAGCAG 597
QY 541 A 541
Db 598 A 598

RESULT 13
HSU94503

LOCUS 1355 bp mRNA linear PRI 15-MAY-1997
DEFINITION Human lymphocyte associated receptor of death 2 mRNA, alternatively

spliced, complete cds.
ACCESSION U94503
VERSION U94503.1 GI:2071952
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
REFERENCE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS 1 (bases 1 to 1355)
Screation,G.R., Xu,X.N., Olsen,A.L., Cowper,A.E., Tan,R.,
McMichael,A.J. and Bell,J.I.
TITLE LARD: a new lymphoid-specific death domain containing receptor
JOURNAL regulated by alternative pre-mRNA splicing
MEDLINE Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)
PUBMED 97272273
REFERENCE 9114039
AUTHORS 2 (bases 1 to 1355)
Screation,G.R.
TITLE Direct Submission
JOURNAL Submitted (19-MAR-1997) Molecular Immunology Group, Institute of
Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3
9DU, UK
FEATURES
source Location/Qualifiers
1..1355
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Hela"
/cell_type="lymphocyte"
1..762
/function="mediates apoptosis"
/note="LARD-2; similar to Fas and TNF-R1; possibly
soluble; truncated before the transmembrane domain"
/codon_start=1
/product="lymphocyte associated receptor of death 2"
/protein_id="AAC51308.1"
/db_xref="GI:2071953"
/translation="MEQRPRGCAVAALLLVLGARAQGRSPRCDCAGDFHKIG
LFCRCGPAGHYLKAPCTEPCNSTCLVCPQDTFLAWENHNHSECARCOACDEQASQV
ALENCASAVADTRCGCKPGWFEQVSOQVSSSPFYCQPCLDGALHRTLRLLCSRRDT
DCGTCLPGFEYHGDGCVSCPSTLGSCEPERCAVCGWROSRWCAGNASGRTGMDRGEA
GEEGNNHPTPTSCFQCSGSRCSWLALWSPSCLGPP"
misc_feature
599..700
/note="insertion compared to LARD 1a, deposited in GenBank
Accession Number U94501, probable retained intron leading
to premature transcriptional termination"
BASE COUNT 223 a 441 c 451 g 240 t
ORIGIN
Query Match 97.5%; Score 541; DB 9; Length 1355;
Best Local Similarity 99.1%; Pred. No. 3.9e-129;
Matches 544; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 CTGGGGCCCCGGCCAGGGCGCACTCGTACGCCAGGTGTGACTGTGCCGTGACTTC 60
DB 58 CTGGGGCCCCGGCCAGGGCGCACTCGTACGCCAGGTGTGACTGTGCCGTGACTTC 117
QY 61 CACAAGAAGATGTGCTGTTTGTGTCAGAGGCTGCCAGCGGGGCACTACTGAAGGCC 120
DB 118 CACAAGAAGATGTGCTGTTTGTGTCAGAGGCTGCCAGCGGGGCACTACTGAAGGCC 177
QY 121 CCTTGCACGGAGCCCTGCGGCACTCCACCTGCTGTGTGTCCCAAGACACTTCTTG 180
DB 178 CCTTGCACGGAGCCCTGCGGCACTCCACCTGCTGTGTGTCCCAAGACACTTCTTG 237
QY 181 GCCTGGAGAACCATTAATTCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCC 240
DB 238 GCCTGGAGAACCATTAATTCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCC 297
QY 241 TCCCAGGTGGCGCTGGAGAAGTGTTCAGCAGTGGCCGACACCCGCTGTGGCTGAAGCCA 300
DB 298 TCCCAGGTGGCGCTGGAGAAGTGTTCAGCAGTGGCCGACACCCGCTGTGGCTGAAGCCA 357
QY 301 GGCTGTTTGTGAGTGCACAGTCAAGCCAAATGTGTACGAGTTACCCCTTCTACTGCCAA 360

|||||
DB 358 GGCTGTTTGTGAGTGCACAGTCAAGCCAAATGTGTACAGTTCACCCCTTCTACTGCCAA 417
QY 361 CCATGCCCTAGACTGCGGGCCCTGACACCGCCACACACAGGCTACTCTGTCCCGCAGAGAT 420
DB 418 CCATGCCCTAGACTGCGGGCCCTGACACCGCCACACACAGGCTACTCTGTCCCGCAGAGAT 477
QY 421 ACTGACTGTGGAGCTGCTGCTGCTGCTTCTATGAACATGGCGATGGCTGCGTGTCTGC 480
DB 478 ACTGACTGTGGAGCTGCTGCTGCTGCTTCTATGAACATGGCGATGGCTGCGTGTCTGC 537
QY 481 CCCACGAGCACCCCTGGGGAGCTGTCCAGAGCGGCTGTGCCGCTGTCTGTGGCTGAGGAG 540
DB 538 CCCACGAGCACCCCTGGGGAGCTGTCCAGAGCGGCTGTGCCGCTGTCTGTGGCTGAGGAG 597
QY 541 ATGTTCTGG 549
DB 598 AGTAGGTGG 606
RESULT 14
AX331947 1743 bp DNA linear PAT 09-JAN-2002
LOCUS AX331947
DEFINITION Sequence 2456 from Patent WO0194629.
ACCESSION AX331947
VERSION AX331947.1 GI:18122581
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1
TITLE Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
Horriqan,S., Soppet,D.R. and Weaver,Z.
Cancer gene determination and therapeutic screening using signature
gene sets
JOURNAL Patent: WO 0194629-A 2456 13-DEC-2001;
FEATURES Avalon Pharmaceuticals (US)
source Location/Qualifiers
1..1743
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 347 a 543 c 549 g 304 t
ORIGIN
Query Match 97.5%; Score 541; DB 6; Length 1743;
Best Local Similarity 99.1%; Pred. No. 3.8e-129;
Matches 544; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 CTGGGGCCCCGGCCAGGGCGCACTCGTAGCCCAAGTGTGACTGTGCCGTGACTTC 60
DB 126 CTGGGGCCCCGGCCAGGGCGCACTCGTAGCCCAAGTGTGACTGTGCCGTGACTTC 185
QY 61 CACAAGAAGATGTGCTGTTTGTGTCAGAGGCTGCCAGCGGGGCACTACTGAAGGCC 120
DB 186 CACAAGAAGATGTGCTGTTTGTGTCAGAGGCTGCCAGCGGGGCACTACTGAAGGCC 245
QY 121 CCTTGCACGGAGCCCTGCGGCAACTCCACCTGCTGTGTGTCCCAAGACACTTCTTG 180
DB 246 CCTTGCACGGAGCCCTGCGGCAACTCCACCTGCTGTGTGTCCCAAGACACTTCTTG 305
QY 181 GCCTGGAGAACCATTAATTCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCC 240
DB 306 GCCTGGAGAACCATTAATTCTGAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCC 365
QY 241 TCCCAGGTGGCGCTGGAGAAGTGTTCAGCAGTGGCCGACACCCGCTGTGGCTGAAGCCA 300
DB 366 TCCCAGGTGGCGCTGGAGAAGTGTTCAGCAGTGGCCGACACCCGCTGTGGCTGAAGCCA 425
QY 301 GGCTGTTTGTGAGTGCACAGTCAAGCCAAATGTGTACGAGTTACCCCTTCTACTGCCAA 360
DB 426 GGCTGTTTGTGAGTGCACAGTCAAGCCAAATGTGTACGAGTTACCCCTTCTACTGCCAA 485

QY 361 CCATGCTAGACTGCGGGCCCTGCACGGCCACACAGCGTACTCTGTCCCGCAGAGAT 420
|||||
Db 486 CCATGCTAGACTGCGGGCCCTGCACGGCCACACAGCGTACTCTGTCCCGCAGAGAT 545
QY 421 ACTGACTGTGGGACCTGCCCTGCGCTTCTATGAACATGGCGATGGCTGCTGCTGC 480
|||||
Db 546 ACTGACTGTGGGACCTGCCCTGCGCTTCTATGAACATGGCGATGGCTGCTGCTGC 605
QY 481 CCCACGAGCACCCTGGGGAGCTGTCCAGAGCGCTGTGCCGCTGTCTGTGGCTGAGGCAG 540
|||||
Db 606 CCCACGAGCACCCTGGGGAGCTGTCCAGAGCGCTGTGCCGCTGTCTGTGGCTGAGGCAG 665
QY 541 ATGTTCTGG 549
| |||
Db 666 AGTAGGTGG 674
RESULT 15
HSMWL1 1743 bp mRNA linear PRI 16-DEC-1996
LOCUS H.sapiens mRNA for WSL-LR, WSL-S1 and WSL-S2 proteins.
DEFINITION Y09392
ACCESSION Y09392
VERSION Y09392.1 GI:1669690
KEYWORDS wsl-1 gene; WSL-1R protein; WSL-S1 protein; WSL-S2 protein.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1743)
AUTHORS Kitson,J., Raven,T., Jiang,Y.P., Goeddel,D.V., Gilles,K.M.,
Pun,K.T., Grinham,C.J., Brown,R. and Farrow,S.N.
TITLE A death-domain-containing receptor that mediates apoptosis
JOURNAL Nature 384 (6607), 372-375 (1996)
MEDLINE 97088617
PUBMED 8934525
REFERENCE 2 (bases 1 to 1743)
AUTHORS Kitson,J.
TITLE Direct Submission
JOURNAL Submitted (12-NOV-1996) J. Kitson, GLAXO-Wellcome, Medicines
Research Centre, Gunneis Wood Road, Stevenage, SG1 2NY, UK
FEATURES
source
1. .1743
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_type="T-lymphocyte"
/tissue_type="lymphoid"
1. .1742
/gene="wsl-1"
1. .610
/gene="wsl-1"
/number=1
join(69. .666,768. .1423)
/gene="wsl-1"
/codon_start=1
/product="WSL-1R protein"
/protein_id="CAA70561.1"
/db_xref="GI:1669693"
/db_xref="SWISS-PROT:Q93038"
/translation="MEQRPBGCAVAALLLVLLGARAQGGTRSPRCDGADDFHKKIG
LFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDFTFLAMENHNHNSCARCQACDEQASQY
ALENCASAVADTRCGCKPGWFEVCQVSQCVSSSPFYCQPCLDGALHHRTRLCSRRDT
DCGTCCLPGFYEHEGDCVSCPTSLGSCPERCAAVCGWRQSRWCAGNARGRTGMDRGEA
GEEGHNPTPTSCFQCSGSRCSWLALMSPSCLGPP"
LYDVMADAVPARRWKEFVRTLGLREAEIENAVEVEIGLFRDQYEMLKHWROQQPAGLGA
VYAALERMGLDGCVEDLRSRLQRP"
join(69. .610,768. .882)
/gene="wsl-1"
/codon_start=1
/product="WSL-S1 protein"
/protein_id="CAA70560.1"
/db_xref="GI:1669692"
/db_xref="SWISS-PROT:Q93038"

/translation="MEQRPBGCAVAALLLVLLGARAQGGTRSPRCDGADDFHKKIG
LFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDFTFLAMENHNHNSCARCQACDEQASQY
ALENCASAVADTRCGCKPGWFEVCQVSQCVSSSPFYCQPCLDGALHHRTRLCSRRDT
DCGTCCLPGFYEHEGDCVSCPTSLGSCPERCAAVCGWRQSRWCAGNARGRTGMDRGEA
GEEGHNPTPTSCFQCSGSRCSWLALMSPSCLGPP"
LYDVMADAVPARRWKEFVRTLGLREAEIENAVEVEIGLFRDQYEMLKHWROQQPAGLGA
VYAALERMGLDGCVEDLRSRLQRP"
join(69. .830
/gene="wsl-1"
/codon_start=1
/product="WSL-S2 protein"
/protein_id="CAA70559.1"
/db_xref="GI:1669691"
/db_xref="SWISS-PROT:Q93038"
/translation="MEQRPBGCAVAALLLVLLGARAQGGTRSPRCDGADDFHKKIG
LFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDFTFLAMENHNHNSCARCQACDEQASQY
ALENCASAVADTRCGCKPGWFEVCQVSQCVSSSPFYCQPCLDGALHHRTRLCSRRDT
DCGTCCLPGFYEHEGDCVSCPTSLGSCPERCAAVCGWRQSRWCAGNARGRTGMDRGEA
GEEGHNPTPTSCFQCSGSRCSWLALMSPSCLGPP"
LYDVMADAVPARRWKEFVRTLGLREAEIENAVEVEIGLFRDQYEMLKHWROQQPAGLGA
VYAALERMGLDGCVEDLRSRLQRP"
join(69. .610,768. .882)
/gene="wsl-1"
/codon_start=1
/product="WSL-S1 protein"
/protein_id="CAA70560.1"
/db_xref="GI:1669692"
/db_xref="SWISS-PROT:Q93038"

BASE COUNT 347 a 543 c 549 g 304 t
ORIGIN
Query Match 97.5%; Score 541; DB 9; Length 1743;
Best Local Similarity 99.1%; Pred. No. 3,8e-129;
Matches 544; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 CTGGGGGCCCCGGGCCAGGGGCGGCACTCGTAGCCCCAGGCTGTGACTGTGCCGGTACTTC 60
Db 126 CTGGGGGCCCCGGGCCAGGGGCGGCACTCGTAGCCCCAGGCTGTGACTGTGCCGGTACTTC 185
QY 61 CACAAGAGATTGGTCTGTTTGTGTCAGAGGCTGCCAGCGGGCACTACCTGAAGGCC 120
Db 186 CACAAGAGATTGGTCTGTTTGTGTCAGAGGCTGCCAGCGGGCACTACCTGAAGGCC 245
QY 121 CCTTGCAAGGAGCCCTGCGGCACTCCACCTGCTGTGTGTGCCAAGACACCTTCTTG 180
Db 246 CCTTGCAAGGAGCCCTGCGGCACTCCACCTGCTGTGTGTGCCAAGACACCTTCTTG 305
QY 181 GCCTGGAGAGAACCAACCATATTTGTAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCC 240
Db 306 GCCTGGAGAGAACCAACCATATTTGTAATGTGCCCGCTGCCAGGCTGTGATGAGCAGGCC 365
QY 241 TCCAGAGTGGCGCTGGAGACTGTTCAGCAGTGGCCGACACCGCTGTGGCTGTAAGCA 300
Db 366 TCCAGAGTGGCGCTGGAGACTGTTCAGCAGTGGCCGACACCGCTGTGGCTGTAAGCA 425
QY 301 GGCTGTTTGTGAGTGCAGGTCAGCCAAATGTGTCAAGCAGTTCACCTTACTGCCAA 360
Db 426 GGCTGTTTGTGAGTGCAGGTCAGCCAAATGTGTCAAGCAGTTCACCTTACTGCCAA 485
QY 361 CCATGCTAGACTGCGGGCCCTGCACCGCCACACAGCGGCTACTCTGTCCCGCAGAGAT 420
Db 486 CCATGCTAGACTGCGGGCCCTGCACCGCCACACAGCGGCTACTCTGTCCCGCAGAGAT 545
QY 421 ACTGACTGTGGGACCTGCCCTGCGCTTCTATGAACATGGCGATGGCTGCTGCTGC 480
Db 546 ACTGACTGTGGGACCTGCCCTGCGCTTCTATGAACATGGCGATGGCTGCTGCTGC 605
QY 481 CCCACGAGCACCCTGGGGAGCTGTCCAGAGCGCTGTGCCGCTGTGTGGCTGAGGCAG 540
Db 606 CCCACGAGCACCCTGGGGAGCTGTCCAGAGCGCTGTGCCGCTGTGTGGCTGAGGCAG 665
QY 541 ATGTTCTGG 549
| |||
Db 666 AGTAGGTGG 674

Search completed: April 6, 2003, 15:03:52
Job time : 2023 secs



THIS PAGE BLANK (USPTO)